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Composition of protein complexes of the app-processing pathway

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1: FIELD OF THE INVENTION

The present invention relates to protein complexes of the beta-amyloid precursor protein (APP) processing pathway, component proteins of the said complexes, fragments and derivatives of the component proteins, and antibodies specific to the complexes. The present invention also relates to methods for use of the complexes of the APP processing pathway and their interacting proteins in, inter alia, screening, diagnosis, and therapy, as well as to methods of preparing the complexes.

2. BACKGROUND OF THE INVENTION (cited references are listed in supra)

Alzheimer's disease is a chronic condition that affects millions of individuals worldwide. After onset of the disease sufferers require a high degree of supervision and care. As the proportion of aged individuals in the population increases, the number of sufferers of Alzheimer's disease is expected to expand dramatically. Current top drugs (e.g. Aricept®/donepezil) attempt to achieve a temporary improvement of cognitive functions by inhibiting acetylcholinesterase, which results in increased levels of the neurotransmitter acetylcholine in the brain. These therapies are not suitable for later stages of the disease, they do not treat the underlying disease pathology, and they do not halt disease progression. The growing need for an effective therapy, coupled with the absence of effective treatments, presents a significant opportunity for drug target development and drug discovery.

The brains of sufferers of Alzheimer's disease show a characteristic pathology of prominent neuropathologic lesions, such as the initially intracellular neurofibrillary tangles (NFTs), and the extracellular amyloid-rich senile plaques. These lesions are associated with massive loss of populations of CNS neurons and their progression accompanies the clinical dementia associated with AD. The major component of amyloid plaques is the amyloid beta peptide. Amyloid beta is the proteolytic product of a precursor protein, beta amyloid precursor protein (beta-APP or APP). APP is a type-I trans-membrane protein which is cleaved by several different membrane-associated proteases. The first cleavage of APP occurs extracellularly by one of two proteases, alpha-secretase or beta-secretase. Beta-secretase or BACE1 (beta-site APP-cleaving enzyme) is a type-I transmembrane protein containing an aspartyl protease activity (described in detail below). Alpha secretase is a metalloprotease whose activity is most likely to be provided

by one or a combination of the proteins ADAM10 and ADAM17. Following either the beta or alpha cleavage of APP, the final cleavage event occurs within the membrane and is carried out by a protein complex called gamma secretase. It is the combination of the beta and gamma secretase activities that results in the liberation of the Abeta peptides of 40 and 42 residues (there are also lower levels of other forms) from the APP and ultimately the formation of the amyloid plaques responsible for the pathology of Alzheimer's disease. It is believed that the Abeta-42 peptide is the most critical Abeta species, because it shows the most pronounced neurotoxicity, and can aggregate easily, thus forming a nucleus for the aggregation of other Abeta peptides, such as the Abeta-40 which is typically produced at higher levels than the other species.

The applicant's proprietary proteomics technology (TAP/LC-MS/MS) is particularly successful in the elucidation of membrane protein complexes. These multiprotein complexes form the core of the APP processing pathway and are not amenable to other techniques. Known proteins with an important functional role in APP processing were analysed with The applicant's technology to comprehensively chart the dynamic protein interactions that contribute to Abeta production. Selected novel targets are subsequently validated using cellular or biochemical assays. Moreover, purified multi-protein complexes (e.g. beta- or gamma-secretase) do represent defined functional molecular machines, which are used to evaluate the mechanism of known compounds and for the optimisation of leads.

Presenilins

Presenilins 1 and 2 (PS1 and PS2) are integral membrane proteins which are localised in the endoplasmic reticulum, the Golgi and also at the cell surface (1). They are predominantly found as a heterodimers of the NTF and CTF endoproteolytic fragments. The protease that cleaves presenilins (the "presenilinase") is not known, it is likely that the process is autocatalytic, also the functional significance of PS (auto)proteolysis is unclear.

Presenilins are involved in the proteolytical processing of Amyloid precursor protein (APP) (2,3) and the Notch receptor (4,5). In addition, Presenilins are associated with the cell-adhesion proteins alpha and beta-catenin, N-cadherin, and E-cadherin (6) (7) and other members of the armadillo family (8) (9) (10) (11).

APP processing by Presenilins is through their effects on gamma-secretase which cleaves APP, generating the C-terminus of the A-beta peptide. PS1 associates with the C83 and C99 processed C-terminal fragments of APP (12), Nicastrin (13) and Pen-2 (14). Aph-1 (15) (14) is required in Presenilin processing. It is not clear whether Presenilins regulate gamma-secretase activity directly or whether they are protease enzymes themselves (16). The gamma secretase activity could comprise a multimeric complex of these proteins (13) (17) but it is not known how the relationship between these proteins affects secretase activity.

Familial Alzheimer's disease (FAD) patients carry mutations in the presenilin proteins (PS1; PS2) or in APP. These mutations result in increased production of A-beta42 (18) which is the main component of cerebral plaques in FAD (19).

Understanding the composition of the gamma-secretase complex, the relationship between its component parts and its regulation are important in the design of drugs for use in Alzheimer's disease patients.

Nicastrin

Nicastrin is a type 1 trans-membrane glycoprotein with a conserved transmembrane domain and DYIGS motif (13) which is constitutively expressed in neural cell lines (20). Biochemical studies have shown that Nicastrin binds to Presenilins 1 and 2, C-terminal derivatives of APP (13), membrane-tethered forms of Notch (21) and that it is a member of the gamma-secretase complex along with PS1 and PS2 (17). Gamma secretase activity is involved in the cleavage of both Notch and APP. It has been shown that Nicastrin is required for the intra-membrane cleavage of Notch (22) and APP (23), it may also have a role in post-translational stabilisation of Presenilin (24).

Aph-1 (15) and Pen-2 (14) were cloned recently in a screen for presenilin enhancers ("pen") in *C. elegans* and shown to interact genetically with Aph-2 (Nicastrin). Defects in Aph-1 affect Notch signalling and Nicastrin localisation (15). Aph-1 and Pen-2 are required for Notch cleavage, gamma-secretase activity and the accumulation of processed Presenilins. Francis et al. (14) cloned the putative human orthologues of these genes, Aph-1a, Aph-1b and Pen-2, and recently Lee et al. (25) also cloned the human Aph-1 cDNAs.

The exact components of the gamma-secretase complex are not known but these two novel proteins could be components of or accessory factors to the complex and may interact together directly with Presenilin or with a Presenilin/Nicastrin complex. Nicastrin

is therefore a member of the active gamma-secretase complex and there is recent evidence that it is the fully glycosylated form of the protein which is important in this complex. (26-30)

Aph-1

Goutte et al. (15) cloned aph-1 from *C. elegans*. Aph-1 encodes a novel conserved membrane protein with seven hydrophobic regions which are predicted to be membrane spanning. It has a 40 amino acid hydrophilic tail. *C. elegans* aph1 mutants have a phenotype which is indicative of a defect in Notch signalling. In these mutants, Aph-2 (Nicastrin) localisation is altered from being at the cell surface to being in the cytoplasm, concentrated around the nucleus. In *C. elegans*, Aph-1 interacts genetically with Aph-2 (Nicastrin) and Sel-12 (one of the *C. elegans* Presenilin genes) (14).

There are Human, Mouse, *Drosophila* Aph-1 homologues which are potential orthologues. Recently, the human Aph-1 homologues, hAph-1a and hAph-1b have been cloned (14,25). Aph-1a, the hypothetical CGI-78 protein, and Sambiasin (European Patent Application 02014244.4 are all products of the same gene. Francis et al (14) showed that Aph-1 and Pen-2 are required for Notch cleavage, gamma-secretase activity and the accumulation of processed Presenilins in cultured *Drosophila* cells.

Lee et al. (25) cloned two splice variants of Aph-1a called Aph-1aS and Aph-1aL and Aph-1b. They have shown that mammalian Aph-1aL associates with Nicastrin and PS1 NTF/CTF heterodimers and with PS2 and Nicastrin in cultured cells and that endogenous Aph1aL associates with Nicastrin and PS1 in rat brain. Inhibition of the expression of Aph1a reduces the expression of both PS1 and PS2 but not Nicastrin and results in the accumulation of gamma-secretase substrates and the reduction of Aβ. Aph1a was also shown to be required for Notch cleavage.

Aph-1 may have a role in the maturation and trafficking of Nicastrin but it is necessary for gamma-secretase function and may be a member of the gamma-secretase complex.

Pen-2

Francis et al. (14) isolated pen-1 and pen-2 as two presenilin enhancer genes in a genetic screen in *C. elegans*. Pen-1 is identical to Aph-1 (15). Pen-2 has two transmembrane domains and is thought to be a polytopic integral membrane protein. This group cloned the human homologues of Aph-1 and Pen-2. In *C. elegans*, Aph-1 and

Pen-2 interact genetically with Aph-2 (Nicastrin) but not with each other. Hop-1 and Sel-12 are the *C.elegans* presenilin genes. Aph-2 interacts with Hop-1 whereas Aph-1 and Pen-2 interact with Sel-12 (14).

Pen-2 associates with PS1, PS2 and Nicastrin in mammalian cells and Aph-1 and Pen-2 are required for Notch cleavage, gamma-secretase activity and the accumulation of processed Presenilins in cultured *Drosophila* cells (14).

Nicastrin maturation is affected by the levels of PS1 and Pen-2. Loss of PS1 or a reduction in expression of Nicastrin reduces Pen-2 protein levels and a reduction in expression of Pen-2 decreases levels of both PS1, PS2 proteins. In addition, reducing the expression of Pen-2 by RNAi reduces the level of the PS1 complex (31). These data suggest that Pen-2 is either a component of or regulates the assembly of the PS1 complex and that the expression of these proteins is co-ordinately regulated.

BACE1 (beta-secretase)

Vassar et al. (32) cloned a transmembrane aspartic protease that had the characteristics of the postulated beta-secretase of APP. Three other groups also cloned BACE1 using different approaches. BACE1 knockout mice have a normal phenotype, suggesting that therapeutic inhibition of BACE1 for AD may be free of mechanism-based toxicity. BACE1 ^{-/-} mice who are also homozygous for an amyloid precursor protein transgene lack brain beta-amyloid and beta-secretase-cleaved APP C-terminal fragments. (33). Brain and primary cortical cultures from BACE1 knockout mice showed no detectable beta-secretase activity, and primary cortical cultures from BACE knockout mice produced much less amyloid-beta from APP. This suggests that BACE1, rather than its paralogue BACE2, is the main beta-secretase for APP.

BACE1 is a protein of 501 amino acids containing a 21-aa signal peptide followed by a proprotein domain spanning aa 22 to 45. There are alternatively spliced forms, BACE-I-457 and BACE-I-476. The luminal domain of the mature protein is followed by one predicted transmembrane domain and a short cytosolic C-terminal tail of 24 aa. BACE1 is predicted to be a type 1 transmembrane protein with the active site on the luminal side of the membrane, where beta-secretase cleaves APP and possible other yet unidentified substrates. BACE1 mRNA in rat brain is present at higher levels in neurons than in glia, supporting that neurons are the primary source of the extracellular A-beta deposited in plaques. Sequence and mass spectrometry analyses showed that asn153, asn172, asn223, and asn354 of the BACE1 ectodomain are N-glycosylation

sites. In addition, the ectodomain contains 6 cys residues that form disulfide bridges between positions 216 and 420, 278 and 443, and 330 and 380. The C-terminal domain of BACE1 contains a dileucine motif (LL499/500) that can potentially regulate its trafficking and endocytosis, and an adjacent serine, which is a casein kinase 1 phosphorylation site (S498) (34). The propeptide is predominantly cleaved from BACE1 by furin (35). In cells expressing wt or Swedish mutant APP, transient overexpression of BACE1 decreased alpha-secretase cleavage and increased beta-secretase activity at the known beta-secretase positions, asp1 and glu11. Although BACE1 is clearly a key enzyme required for the processing of APP into Ab, other potential substrates and functions of BACE1 are unknown. Also, no BACE1 interacting proteins with regulatory or modulatory functions have been described. Proteins that activate BACE1 activity would form suitable intervention points for Alzheimer's disease therapy. In addition, proteins that inhibit BACE1, like substrates or pseudosubstrates, could also provide suitable means of intervention e.g. as proteins therapeutics.

APP and the beta-CTF ("C99")

APP is the precursor of Abeta, a peptide which forms the principal component of Alzheimer disease (AD) senile plaques (3) Masters et al. purified the cerebral amyloid protein that forms the plaque core in AD and Down syndrome. Van Nostrand et al. (36) presented evidence that nexin-II, a protease inhibitor that is synthesized and secreted by extravascular cells, is identical to APP. Multhaup et al. (37) demonstrated that APP is involved in copper reduction. They postulated that copper-mediated toxicity may contribute to neurodegeneration in AD, possibly by increased production of hydroxyl radicals. Yan et al. (38) reported that the receptor for advanced glycation end products RAGE is a receptor for the a-beta peptide and that expression of this receptor increases in AD. Expression of RAGE is particularly increased in neurons close to deposits of amyloid beta peptide and to neurofibrillary tangles. Kaneko et al. (39) demonstrated that nanomolar concentrations of various synthetic beta amyloids specifically impaired mitochondrial succinate dehydrogenase, and speculated that one of the primary targets of beta amyloids is the mitochondrial electron transport chain.

Several missense mutations in the APP gene have been identified that result in early-onset AD: the Swedish APP670/671 double mutation; 3 different mutations at codon 717: the London APP717 mutation, V717I, V717F, and V717G; and the Florida APP716 mutation (Reviewed by Bertram and Tanzi (40)). Most of these AD-related

mutations involve amino acid changes near the beta- and gamma-secretase cleavage sites. Two other missense mutations in the APP gene are located within A-beta near the alpha-secretase cleavage site: the Flemish APP692 mutation, which is associated with cerebral hemorrhage due to congophilic amyloid angiopathy or with early-onset AD with onset age in the mid-forties; and the Dutch APP693 mutation. Almost all AD-linked mutations do elevate secretion of A-beta-42, however, APP693 does not. (41)

Cao and Sudhof (42) demonstrated that the cytoplasmic tail of APP forms a complex with the nuclear adaptor protein Fe65 and the histone acetyltransferase TIP60. This complex stimulates transcription via heterologous Gal4 or LexA DNA binding domains, suggesting that release of the cytoplasmic tail of APP by gamma-cleavage may function in gene expression. The complex could modify expression of genes that function in inflammation (43) or apoptosis (44).

Weggen et al. (45) reported that the nonsteroidal antiinflammatory drugs ibuprofen, indomethacin, and sulindac can decrease the levels of high amyloidogenic amyloid-beta-42 peptide produced from a variety of cultured cells by as much as 80%. This effect was not seen in all NSAIDs and seemed not to be mediated by inhibition of cyclooxygenase (Cox) activity. Weggen et al. (2001) also demonstrated that short-term administration of ibuprofen to mice that produce APP lowered their brain levels of amyloid-beta-42. In cultured cells, the decrease in amyloid-beta-42 secretion was accompanied by an increase in the amyloid-beta(1-38) isoform, indicating that NSAIDs subtly alter gamma-secretase activity without significantly perturbing other APP processing pathways or Notch cleavage.

Proteins and other factors that regulate APP processing, and especially those that influence levels of Abeta-42 versus other Abeta species, form important potential targets in AD therapy.

Calsenilin

In a yeast two-hybrid screen with the C-terminus of Presenilin 2, a neuronal EF-hand (calcium-binding) protein was identified and named "calsenilin" (46). It interacted with both Presenilin 1 and Presenilin 2 in cells and regulated the levels of a proteolytic product of Presenilin 2. Calsenilin is identical to KChIP3, a protein which was found in a yeast two-hybrid screen for proteins interacting with A-type potassium channels (Kv4.3) (47). KChIP3 increased the density of Kv4.2 currents indicating a stabilisation of the

channels at the plasma membrane; ii) shifted the current to hyperpolarized potentials; iii) slowed down the kinetics of inactivation and increased the kinetics of recovery.

Calsenilin is also identical to the transcriptional repressor DREAM which acts constitutively to suppress prodynorphin expression in spinal cord neurons (48). Knocking out DREAM results in sufficient dynorphin expression to produce a strong reduction in generalized pain behavior, highlighting the role that intracellular molecules play in modulating pain gating in the spinal cord. Hence proteins that modulate Calsenilin/DREAM activity are interesting targets in nociception.

Tau

Neurofibrillary tangles (NFT), intraneuronal tau protein deposits, are hallmarks of several neurodegenerative disorders such as Alzheimer's and Pick's disease, frontotemporal dementia, cortico-basal degeneration and progressive supranuclear palsy.

The seven tau isoforms are all products of a single gene. Alternative splicing gives rise to six mRNA species differentially expressed in the CNS, depending on stage of neuronal maturation and neuron type. Tau is found mainly in the axon whereas a related protein, MAP2, is mainly found in dendrites.

Tau and MAP2 are microtubule-associated proteins (MAPs) which coassemble with microtubules and colocalise with microtubules in cells. Tau is a nonstructured molecule with a microtubule binding site containing 3 or 4 characteristic amino acid repeat in its carboxyl-terminal half. Alonso et al. (49) noted that in the brains of AD patients the neuronal cytoskeleton is progressively disrupted and replaced by tangles of paired helical filaments (PHFs), and that PHFs are composed mainly of hyperphosphorylated forms of tau. They demonstrated that in solution normal tau associated with the hyperphosphorylated AD P-tau to form large tangles of filaments. They also demonstrated that dephosphorylation with alkaline phosphatase abolished the ability of AD P-tau to aggregate in vitro. In a form of autosomal dominant inherited dementia known as FTDP17 or Pick disease, the tau gene carries missense mutations or mutations in the 5'- splice site of exon 10, which results in increased levels of tau isoforms with 4 microtubule-binding repeats. These mutations lead to tau molecules that show reduced affinity for microtubules or are more prone to self aggregation.

Proteins and other factors that influence the affinity of tau protein for microtubules, and moreover, influence the aggregation of tau, which is probably mediated by

phosphorylation and dephosphorylation events, are important potential targets in AD therapy.

Fe65

Fe65 is a PTB domain- and WW domain-containing adaptor protein that is part of protein complexes at the plasma membrane as well as in the nucleus: It interacts with the Alzheimer's disease amyloid precursor protein (APP; (50)) and related proteins APLP1 and APLP2 (51). Binding of Fe65 to the cytoplasmic tail of APP enhances production of amyloid-forming Abeta peptides (52), but the molecular mechanism of this amyloidogenic effect of Fe65 has not been elucidated. Furthermore, Fe65 stabilizes APP intracellular domain (AICD) (APP intracellular domain (AICD)), the cytosolic product of APP cleavage by gamma-secretase, (53) and forms a nuclear protein complex with TIP60 (42). Little is known about the functional consequences of Fe65-dependent transactivation. The important role of TIP60 in interleukin-1beta- and NF-KappaB-dependent transactivation (43) suggests, however, that the Fe65 complex might function in inflammation.

Fe65 has been shown to bind to the transcription factor CP2/LSF/LBP1 (54) and the low-density lipoprotein receptor-related protein (55), but the significance of these interactions is unknown. Finally, Fe65 has been observed to block cell cycle progression by downregulating thymidylate synthase expression via an unknown mechanism (56).

Understanding the composition of the Fe65 complex, the relationship between its component parts and its regulation might therefore be important in the design of drugs for use in Alzheimer's disease patients as well as for the treatment of various inflammatory conditions and cancer.

X11beta

X11beta/Mint-2 is a neuronal adaptor protein that is believed to be involved in signal transduction processes. It is also regarded as a putative vesicular trafficking protein in the brain that can form a complex with the potential to couple synaptic vesicle exocytosis to neuronal cell adhesion (57).

X11beta interacts with the Alzheimer's disease amyloid precursor protein (APP) (50). Acting synergistically with Munc18a (58), X11beta stabilises APP and inhibits production of proteolytic APP fragments including the A beta peptide that is deposited in the brains of Alzheimer's disease patients (59).

Via a mechanism that depends on its PDZ domain (yet has otherwise not been characterized), X11beta potentially inhibits transactivation by an APP-Gal4/VP16 fusion protein (58). Besides interacting with APP, X11beta binds to the C-terminus of presenilin1, although not as strongly as does X11alpha (58). In addition, X11beta has been reported to interact with XB51 (60), but the functional significance of this interaction is unknown.

In *Drosophila*, dX11beta overexpression in eye imaginal disks causes disruption of compound eye morphology due to enhanced apoptosis of neuronal cells (61). X11beta has been shown to bind to NF-KappaB-p65 through its PDZ domain. This interaction has been implicated in NF-KappaB-dependent Abeta 1-42 production (62).

Elucidation of X11beta complex composition and regulation might therefore help develop novel ways of therapeutic intervention in Alzheimer's disease and inflammation.

3. SUMMARY OF THE INVENTION

An object of the present invention was to identify protein complexes of the beta-amyloid precursor protein (APP) processing pathway, component proteins of the said complexes, fragments and derivatives of the component proteins, and antibodies specific to the complexes. The present invention also relates to methods for use of the protein complexes of the APP processing pathway and their interacting proteins in, inter alia, screening, diagnosis, and therapy, as well as to methods of preparing the complexes.

By applying the process according to the invention said complexes were identified. The components are listed in table 1.

Said object is further achieved by the characterization of component proteins. These proteins are listed in table 2.

Thus, the invention relates to the following embodiments:

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein, which first protein is selected from the group of proteins in table 1, fourth column of a given complex, or a functionally active derivative

thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; and

(b) at least one second protein, which second protein is selected from the group of proteins in table 1, fifth column of said given complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said second protein, said variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; and a complex (II) comprising at least two of said second proteins,

wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

2. A protein complex comprising a first protein selected from the proteins listed in table 1, fourth column of a given complex or a homologue or variant thereof, or a functionally active fragment or functionally active derivative of said first protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said first protein under low stringency conditions, and at least one second protein selected from the group of proteins in table 1, fifth column of a given complex, or a variant or homologue thereof, or a functionally active fragment or a functionally active derivative of said second protein, the variant of said second protein being encoded by a nucleic acid that hybridizes to the nucleic acid of said second protein under low-stringency conditions, and wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

3. A protein complex comprising all proteins selected from the proteins in table 1, third column of a given complex or at least one protein being a homologue thereof, or a variant thereof or functionally active fragment or functionally active derivative of said protein, said variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low stringency conditions; wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
4. A protein complex that comprises all proteins as listed in table 1, third column for a given complex or at least one protein being a homologue or a variant thereof, or a functionally active fragment or a functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins under low stringency conditions, except at least one protein of the proteins listed in table 5, third column, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C, with the proviso that the complex comprises at least one protein selected from table 1, fifth column of a given complex.
5. The complex of any of No. 1 - 4 comprising at least one functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.
7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of No. 1 - 7 that is involved in at least one biochemical activity as stated in table 3.
9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps:
expressing a protein of the complex, preferably a tagged protein, in a target cell, or a tissue or an organ, isolating the protein complex which is attached to the protein, preferably the tagged protein, and optionally disassociating the protein complex and isolating the individual complex members.
10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.
12. Component of a protein complex obtainable by a process according to any of No. 9 - 11.
13. Protein selected from the group of proteins in table 1, sixth column of a given complex or a homologue or a variant of thereof, or a functionally active fragment or a functionally active derivative of said protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X

SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

14. Nucleic acid encoding a protein according to No. 13.
15. Construct, preferably a vector construct, comprising
 - (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or
 - (b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative thereof, or a homologue or a variant thereof, at least one of said proteins being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, being selected from the second group of proteins according to No. 1 (b) or
 - (c) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative thereof, or a homologue or a variant thereof, said proteins being selected from the proteins of complex (II) according to No. 1.
16. Host cell, containing a vector comprising at least one nucleic acid of No. 14 and /or a construct of No. 15 or containing several vectors each comprising at least one nucleic acid encoding at least one protein selected from the first group of proteins according to No. 1 (a) and at least one nucleic acid encoding at least one protein selected from the second group of proteins according to No. 1 (b).
17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody containing the binding domain thereof which binds to any of the proteins of the group of proteins according to No. 13.
18. A kit comprising in one or more containers:
 - (a) the complex of any of No. 1 - 8 and/or the proteins of No. 13 and/or
 - (b) an antibody according to No. 17 and/or

- (c) a nucleic acid encoding a protein of the complex of any of No. 1 – 8 and/or a protein of No. 13 and/or
- (d) cells expressing the complex of any of No. 1 – 8 and/or a protein of No. 13 and, optionally,
- (e) further components such as reagents, buffers and working instructions.

19. The kit according to No. 18 for processing a substrate of a complex of any one of No. 1 - 8.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as those as stated in column 2, table 4 of a given complex.

21. Array, preferably a microarray, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 13 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for modifying a substrate of a complex of any one of No. 1 - 8 comprising the step of bringing into contact a complex of any of No. 1 - 8 with said substrate, such that said substrate is modified.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or a protein according to No. 13.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders, preferentially for diseases or disorders such as those as stated in column 2, table 4 of a given complex.

25. A method for screening for a molecule that binds to a complex of any one of No. 1 - 8 and/or a protein of No. 13, comprising the following steps:
(a) exposing said complex or protein, or a cell or organism containing said complex or said protein, to one or more candidate molecules; and
(b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of a complex of any one of No. 1 - 8 comprising the steps of:
- (a) exposing said complex, or a cell or organism containing said complex to one or more candidate molecules; and
 - (b) determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent upon the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity, or composition of said complex.
27. The method of No. 26, wherein the amount of said complex is determined.
28. The method of No. 26, wherein the activity of said complex is determined.
29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
30. The method of No. 26, wherein the amount of the individual protein components of said complex is determined.

31. The method of No. 30, wherein said determining step comprises determining whether any of the proteins listed in table 1, third column of said complex, or a functionally active fragment or a functionally active derivative thereof, or a variant or a homologue thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low-stringency conditions, is present in the complex.
32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder, preferentially of a disease or disorder selected from the diseases or disorders such as those as stated in column 2, table 4 of a given complex.
33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as those as stated in column 2, table 4 of a given complex.
34. A method for the production of a pharmaceutical composition comprising carrying out the method of No. 26 - 31 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.
35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, component disposition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in a corresponding sample from a subject not having the disease or disorder or predisposition indicated the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.
37. The method of No. 35, wherein the activity of said complex is determined.
38. The method of No. 37, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.
40. The method of No. 39, wherein said determining step comprises determining whether any of the proteins according to No. 13 is present in the complex.
41. The complex of any one of No. 1 - 8, or a protein of No. 13 or an antibody or fragment thereof of No. 17, for use in a method of diagnosing a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as those as stated in column 2, table 4 of a given complex.
42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity of, component composition of or intracellular localization of, the complex of any one of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, activity of, or protein composition of, said complex.
43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.
45. Complex of No. 1 - 8 and/or a protein as listed in table 1, fifth column of said complex as a target for an active agent of a pharmaceutical, preferably a drug target, in the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as a neurodegenerative disease such as those as stated in column 2, table 4 of a given complex.

3.1 DEFINITIONS

The term "activity" as used herein, refers to the function of a molecule in its broadest sense. It generally includes, but is not limited to, biological, biochemical, physical or chemical functions of the molecule. It includes for example the enzymatic activity, the ability to interact with other molecules and ability to activate, facilitate, stabilize, inhibit, suppress or destabilize the function of other molecules, stability, ability to localize to certain subcellular locations. Where applicable, said term also relates to the function of a protein complex in its broadest sense.

The term "agonist" as used herein, means a molecule which modulates the formation of a protein complex or which, when bound to a complex or protein of the invention or a molecule in the protein complex, increases the amount of, or prolongs the duration of, the activity of the complex. The stimulation may be direct or indirect, including effects on the expression of a gene encoding a member of the protein complex, or by a competitive or non-competitive mechanism. Agonists may include proteins, nucleic acids, carbohydrates or any other organic or anorganic molecule or metals. Agonists also include a functional peptide or peptide fragment derived from a protein member of the complexes of the invention or a protein member itself of the complexes of the invention. Preferred activators are those which, when added to the complex and/or the protein of the invention under physiological conditions and/or in vitro assays, including diagnostic or prognostic assays, result in a change of the level of any of the activities of the protein complex and/or the proteins of the invention as exemplary illustrated above by at least 10%, at least 25%, at least 50%, at least 100%, at least, 200%, at least 500% or at least 1000% at a concentration of the activator $1\mu\text{g ml}^{-1}$, $10\mu\text{g ml}^{-1}$, $100\mu\text{g ml}^{-1}$, $500\mu\text{g ml}^{-1}$, 1mg ml^{-1} , 10mg ml^{-1} or 100mg ml^{-1} . Any combination of the

above mentioned degrees of percentages and concentration may be used to define an agonist of the invention, with greater effect at lower concentrations being preferred.

The term "amount" as used herein and as applicable to the embodiment described relates to the amount of the particular protein or protein complex described, including the value of null, i.e. where no protein or protein complex described in that particular embodiment is present under the or any of the conditions which might be specified in that particular embodiment.

The term "animal" as used herein includes, but is not limited to mammals, preferably mammals such as cows, pigs, horses, mice, rats, cats, dogs, sheep, goats and most preferably humans. Other animals used in agriculture, such as chickens, ducks etc. are also included in the definition as used herein.

The term "animal" as used herein does not include humans if being used in the context of genetic alterations to the germline.

The term "antagonist" as used herein, means a molecule which modulates the formation of a protein complex or which, when bound to a complex or protein of the invention or a molecule in the protein complex, decreases the amount of, or the duration or level of activity of the complex. The effect may be direct or indirect, including effects on the expression of a gene encoding a member of the protein complex, or by a competitive or non-competitive mechanism. Antagonists may include proteins, including antibodies, nucleic acids, carbohydrates or any other organic or inorganic molecule or metals. Antagonists also include a functional peptide or peptide fragment derived from a protein member of the complexes of the invention or a protein member itself of the complexes of the invention. Preferred antagonists are those which, when added to the complex and/or the protein of the invention under physiological conditions and/or in vitro assays, including diagnostic or prognostic assays, result in a change of the level of any of the activities of the protein complex and/or the proteins of the invention as exemplary illustrated above by at least 10%, at least 20%, at least 30%, at least 40% at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% or at least 99% at a concentration of the inhibitor of $1\mu\text{g ml}^{-1}$, $10\mu\text{g ml}^{-1}$, $100\mu\text{g ml}^{-1}$, $500\mu\text{g ml}^{-1}$, 1mg ml^{-1} , 10mg ml^{-1} or 100mg ml^{-1} .

Any combination of the above mentioned degrees of percentages and concentration may be used to define antagonist of the invention, with greater effect at lower concentrations being preferred.

The term "antibodies" as used herein, include include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments, and an Fab expression library.

The term "binding" as used herein means a stable or transient association between two molecules, including electrostatic, hydrophobic, ionic and/or hydrogen-bond interaction under physiological conditions and/or conditions being used in diagnostic or prognostic method or process or procedure.

The term "carrier" as used herein refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, including but not limited to peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered orally. Saline and aqueous dextrose are preferred carriers when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions are preferably employed as liquid carriers for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsions, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the therapeutic, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the mode of administration.

If not stated otherwise, the terms "complex" and "protein complex" are used interchangeably herein and refer to a complex of proteins that is able to perform one or more functions of the wild type protein complex. The protein complex may or may not include and/or be associated with other molecules such as nucleic acid, such as RNA or

DNA, or lipids or further cofactors or moieties selected from a metal ions, hormones, second messengers, phosphate, sugars.

A "complex" of the invention may also be part of or a unit of a larger physiological protein assembly.

The term "component of the APP processing pathway" as used herein refers to a protein and/or protein complex which is involved in mediating APP processing in a cell. Components of the APP processing pathway include the following protein complexes as provided herein and components thereof:

Aph1a-complex, APP-695SW-complex, APP-C99-complex, Fe65-complex, Nicastrin-complex, Psen-2-complex, Pen2-complex, Tau-complex, X11 β -complex

If not stated otherwise, the term "compound" as used herein are include but are not limited to peptides, nucleic acids, carbohydrates, natural product extract librariesorganic molecules, preferentially small organic molecules, anorganic molecules, including but not limited to chemicals, metals and organometallic molecules.

The terms "derivatives" or "analogs of component proteins" or "variants" as used herein include, but are not limited, to molecules comprising regions that are substantially homologous to the component proteins, in various embodiments, by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% identity over an amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to a sequence encoding the component protein under stringent, moderately stringent, or nonstringent conditions. It means a protein which is the outcome of a modification of the naturally occurring protein, by amino acid substitutions, deletions and additions, respectively, which derivatives still exhibit the biological function of the naturally occurring protein although not necessarily to the same degree. The biological function of such proteins can e.g. be examined by suitable available in vitro assays as provided in the invention.

The term "functionally active" as used herein refers to a polypeptide, namely a fragment or derivative, having structural, regulatory, or biochemical functions of the protein according to the embodiment of which this polypeptide, namely fragment or derivative is related to.

The term "fragment" as used herein refers to a polypeptide of at least 10, 20, 30, 40 or 50 amino acids of the component protein according to the embodiment. In specific embodiments, such fragments are not larger than 35, 100 or 200 amino acids.

The term "gene" as used herein refers to a nucleic acid comprising an open reading frame encoding a polypeptide of, if not stated otherwise, the present invention, including both exon and optionally intron sequences.

The terms "homologue" or "homologous gene products" as used herein mean a protein in another species, preferably mammals, which performs the same biological function as the a protein component of the complex further described herein. Such homologues are also termed "orthologous gene products". The algorithm for the detection of orthologue gene pairs from humans and mammals or other species uses the whole genome of these organisms. First, pairwise best hits are retrieved, using a full Smith-Waterman alignment of predicted proteins. To further improve reliability, these pairs are clustered with pairwise best hits involving *Drosophila melanogaster* and *C. elegans* proteins. Such analysis is given, e.g., in Nature, 2001, 409:860-921. The homologues of the proteins according to the invention can either be isolated based on the sequence homology of the genes encoding the proteins provided herein to the genes of other species by cloning the respective gene applying conventional technology and expressing the protein from such gene, or by isolating proteins of the other species by isolating the analogous complex according to the methods provided herein or to other suitable methods commonly known in the art.

The term "host cells" or, where applicable, "cells" or "hosts" as used herein is intended to be understood in a broadest sense and include, but are not limited to mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); microorganisms such as yeast containing yeast vectors; or bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used. It is understood that this term not only refers to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

The term "modification" as used herein refers to all modifications of a protein or protein complex of the invention including cleavage and addition or removal of a group.

The term "nucleic acid" as used herein refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). They may

also be polynucleotides which include within them synthetic or modified nucleotides. A number of different types of modification to polynucleotides are known in the art. These include methylphosphonate and phosphorothioate backbones, addition of acridine or polylysine chains at the 3' and/or 5' ends of the molecule. For the purposes of the present invention, it is to be understood that the polynucleotides described herein may be modified by any method available in the art. Such modifications may be carried out in order to enhance the in vivo activity or lifespan of polynucleotides of the invention. Polynucleotides according to the invention may be produced recombinantly, synthetically, or by any means available to those of skill in the art. They may also be cloned by standard techniques. The polynucleotides are typically provided in isolated and/or purified form. As applicable to the embodiment being described, they include both single stranded and double-stranded polynucleotides.

The term "percent identity", as used herein, means the number of identical residues as defined by an optimal alignment using the Smith-Waterman algorithm divided by the length of the overlap multiplied by 100. The alignment is performed by the search program (Pearson, 1991, Genomics 11:635-650) with the constraint to align the maximum of both sequences.

The terms "polypeptides" and "proteins" are, where applicable, used interchangeably herein. They may be chemically modified, e.g. post-translationally modified. For example, they may be glycosylated or comprise modified amino acid residues. They may also be modified by the addition of a signal sequence to promote their secretion from a cell where the polypeptide does not naturally contain such a sequence. They may be tagged with a tag. They may be tagged with different labels which may assist in identification of the proteins in a protein complex. Polypeptides/proteins for use in the invention may be in a substantially isolated form. It will be understood that the polypeptid/protein may be mixed with carriers or diluents which will not interfere with the intended purpose of the polypeptide and still be regarded as substantially isolated. A polypeptide/protein for use in the invention may also be in a substantially purified form, in which case it will generally comprise the polypeptide in a preparation in which more than 50%, e.g. more than 80%, 90%, 95% or 99%, by weight of the polypeptide in the preparation is a polypeptide of the invention.

"Target for therapeutic drug" means that the respective protein (target) can bind the active ingredient of a pharmaceutical composition and thereby changes its biological activity in response to the drug binding.

The term "tag" as used herein is meant to be understood in its broadest sense and to include, but is not limited to any suitable enzymatic, fluorescent, or radioactive labels and suitable epitopes, including but not limited to, HA-tag, Myc-tag, T7, His-tag, FLAG-tag, Calmodulin binding proteins, glutathione-S-transferase, strep-tag, KT3-epitope, EEF-epitopes, green-fluorescent protein and variants thereof.

The term "therapeutics" as used herein, includes, but is not limited to, a protein complex of the present invention, the individual component proteins, and analogs and derivatives (including fragments); antibodies thereto; nucleic acids encoding the component protein, and analogs or derivatives thereof; component protein antisense nucleic acids, and agents that modulate complex formation and/or activity (i.e., agonists and antagonists).

The term "vector" as used herein means a nucleic acid molecule capable of transporting another nucleic acid sequence to which it has been linked. Preferred vectors are those capable of autonomous replication and/or expression of nucleic acids to which they linked. The terms "plasmid" and "vector" are used interchangeably herein when applicable to the embodiment. However, vectors other than plasmids are also included herein. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

4. DETAILED DESCRIPTION OF THE INVENTION

Overview:

An object of the present invention was to identify protein complexes of the beta-amyloid precursor protein (APP) processing pathway, component proteins of the said complexes, fragments and derivatives of the component proteins, and antibodies specific to the complexes. The present invention also relates to methods for use of the protein complexes of the APP processing pathway and their interacting proteins in, inter alia, screening, diagnosis, and therapy, as well as to methods of preparing the complexes.

By applying the process according to the invention said protein complex were identified. The components are listed in table 1.

Said object is further achieved by the characterisation of component proteins. These proteins are listed in table 2.

The invention thus relates to the following embodiments:

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein, which first protein is selected from the group of proteins in table 1, fourth column of a given complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; and
 - (b) at least one second protein, which second protein is selected from the group of proteins in table 1, fifth column of said given complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said second protein, said variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
2. A protein complex comprising a first protein selected from the proteins listed in table 1, fourth column of a given complex or a homologue or variant thereof, or a functionally active fragment or functionally active derivative of said first protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said first protein under low stringency conditions, and at least one second protein selected from the group of proteins in table 1, fifth column of a given complex, or a variant or homologue thereof, or a functionally active fragment or a functionally active derivative of said second protein, the variant of said second protein being encoded by a nucleic acid that hybridizes to the nucleic acid of said second protein under low-

stringency conditions, and wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

3. A protein complex comprising all proteins selected from the proteins in table 1, third column of a given complex or at least one protein being a homologue thereof, or a variant thereof or functionally active fragment or functionally active derivative of said protein, said variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low stringency conditions; wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

4. A protein complex that comprises all proteins as listed in table 1, third column for a given complex or at least one protein being a homologue or a variant thereof, or a functionally active fragment or a functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins under low stringency conditions, except at least one protein of the proteins listed in table 5, third column, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C, with the proviso that the

complex comprises at least one protein selected from table 1, fifth column of a given complex.

5. The complex of any of No. 1 - 4 comprising at least one functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein.
6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.
7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of No. 1 - 7 that is involved in at least one biochemical activity as stated in table 3.
9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps:
expressing a protein of the complex, preferably a tagged protein, in a target cell, or a tissue or an organ, isolating the protein complex which is attached to the protein, preferably the tagged protein, and optionally disassociating the protein complex and isolating the individual complex members.
10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.
12. Component of a protein complex obtainable by a process according to any of No. 9 - 11.

13. Protein selected from the group of proteins in table 1, sixth column of a given complex or a homologue or a variant of thereof, or a functionally active fragment or a functionally active derivative of said protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
14. Nucleic acid encoding a protein according to No. 13.
15. Construct, preferably a vector construct, comprising
 - (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or
 - (b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative thereof, or a homologue or a variant thereof, at least one of said proteins being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, being selected from the second group of proteins according to No. 1 (b) or
 - (c) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative thereof, or a homologue or a variant thereof, said proteins being selected from the proteins of complex (II) according to No. 1.
16. Host cell, containing a vector comprising at least one nucleic acid of No. 14 and /or a construct of No. 15 or containing several vectors each comprising at least one nucleic acid encoding at least one protein selected from the first group of proteins according to No. 1 (a) and at least one nucleic acid encoding at least one protein selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody containing the binding domain thereof which binds to any of the proteins of the group of proteins according to No. 13.
18. A kit comprising in one or more containers:
- (a) the complex of any of No. 1 - 8 and/or the proteins of No. 13 and/or
 - (b) an antibody according to No. 17 and/or
 - (c) a nucleic acid encoding a protein of the complex of any of No. 1 - 8 and/or a protein of No. 13 and/or
 - (d) cells expressing the complex of any of No. 1 - 8 and/or a protein of No. 13 and, optionally,
 - (e) further components such as reagents, buffers and working instructions.
19. The kit according to No. 18 for processing a substrate of a complex of any one of No. 1 - 8.
20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as those as stated in column 2, table 4 of a given complex.
21. Array, preferably a microarray, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 13 and/or at least one antibody according to No. 17 is attached to a solid carrier.
22. A process for modifying a substrate of a complex of any one of No. 1 - 8 comprising the step of bringing into contact a complex of any of No. 1 - 8 with said substrate, such that said substrate is modified.
23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or a protein according to No. 13.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders, preferentially for diseases or disorders such as those as stated in column 2, table 4 of a given complex.
25. A method for screening for a molecule that binds to a complex of any one of No. 1 - 8 and/or a protein of No. 13, comprising the following steps:
- (a) exposing said complex or protein, or a cell or organism containing said complex or said protein, to one or more candidate molecules; and
 - (b) determining whether said candidate molecule is bound to the complex or protein.
26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of a complex of any one of No. 1 - 8 comprising the steps of:
- (a) exposing said complex, or a cell or organism containing said complex to one or more candidate molecules; and
 - (b) determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent upon the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity, or composition of said complex.
27. The method of No. 26, wherein the amount of said complex is determined.
28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
30. The method of No. 26, wherein the amount of the individual protein components of said complex is determined.
31. The method of No. 30, wherein said determining step comprises determining whether any of the proteins listed in table 1, third column of said complex, or a functionally active fragment or a functionally active derivative thereof, or a variant or a homologue thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low-stringency conditions, is present in the complex.
32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder, preferentially of a disease or disorder selected from the diseases or disorders such as those as stated in column 2, table 4 of a given complex.
33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as those as stated in column 2, table 4 of a given complex.
34. A method for the production of a pharmaceutical composition comprising carrying out the method of No. 26 - 31 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.
35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or

disorder is characterized by an aberrant amount of, component disposition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in a corresponding sample from a subject not having the disease or disorder or predisposition indicated the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.
37. The method of No. 35, wherein the activity of said complex is determined.
38. The method of No. 37, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.
40. The method of No. 39, wherein said determining step comprises determining whether any of the proteins according to No. 13 is present in the complex.
41. The complex of any one of No. 1 - 8, or a protein of No. 13 or an antibody or fragment thereof of No. 17, for use in a method of diagnosing a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as those as stated in column 2, table 4 of a given complex.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity of, component composition of or intracellular localization of, the complex of any one of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, activity of, or protein composition of, said complex.
43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.
44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.
45. Complex of No. 1 - 8 and/or a protein as listed in table 1, fifth column of said complex as a target for an active agent of a pharmaceutical, preferably a drug target, in the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as a neurodegenerative disease such as those as stated in column 2, table 4 of a given complex.

Animal models are also provided herein.

Preferably, the protein components of the complexes described herein are all mammalian proteins. The complexes can also consist only of the respective homologues from other mammals such as mouse, rat, pig, cow, dog, monkey, sheep or horse or other species such as *D. melanogaster*, *C. elegans* or chicken. In another preferred embodiment, the complexes are a mixture of proteins from two or more species.

TABLES:

Table 1: Composition of Complexes

First column ('Name of complex'): Lists the name of the protein complexes as used herein.

Second column ('Entry point'): Lists the bait proteins that have been chosen for the purification of the given complex.

Third column ('All interactors'): Lists all novel interactors which have been identified as members of the complex and all interactors which have been known to be associated with the bait so far.

Fourth column ('Known interactors'): Lists all interactors which have been known to be associated with the bait so far.

Fifth column ('Novel interactors of the complex'): Lists all novel interactors of the complex which have been identified in the experiments provided herein.

Sixth column: Separately lists the members of the newly identified complex which have not been annotated previously.

Table 2: Individual Proteins of the Complexes

First column ('Protein'): Lists in alphabetical order all proteins which have been identified as interactors of the complexes presented herein.

Second column ('SEQ ID'): Lists the SEQ ID (Sequence Identifications) of the proteins herein as used herein.

Third column ('IPI-Numbers'): Lists the IPI-Numbers of the proteins herein. The IPI-Numbers refer to the International Protein Index created by the European Bioinformatics Institute (EMBL-EBI), Hinxton, UK.

Fourth column ('Molecular Weight'): Lists the Molecular Weight of the proteins in Dalton.

Table 3: Biochemical Activities of the Complexes of the invention.

First column ('Name of complex'): Lists the name of the protein complexes as used herein.

Second column ('Biochemical Activity'): Lists biochemical activities of the complexes. Assays in order to test these activities are also provided herein (infra).

Table 4: Medical Applications of the Complexes of the invention

First column ('Name of complex'): Lists the name of the protein complexes as used herein

Second column ('Medical application'): lists disorder, diseases, disease areas etc. which are treatable and/or preventable and/or diagnosable etc. by therapeutics and methods interacting with/acting via the complex.

4.1 PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

The protein complexes of the present invention and their component proteins are described in the Tables 1-4. The protein complexes and component proteins can be obtained by methods well known in the art for protein purification and recombinant protein expression. For example, the protein complexes of the present invention can be isolated using the TAP method described in Section 5, *infra*, and in WO 00/09716 and Rigaut et al., 1999, *Nature Biotechnol.* 17:1030-1032, which are each incorporated by reference in their entirety. Additionally, the protein complexes can be isolated by immunoprecipitation of the component proteins and combining the immunoprecipitated proteins. The protein complexes can also be produced by recombinantly expressing the component proteins and combining the expressed proteins.

The nucleic and amino acid sequences of the component proteins of the protein complexes of the present invention are provided herein (SEQ ID NO 1 - 315), and can be obtained by any method known in the art, e.g., by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of each sequence, and/or by cloning from a cDNA or genomic library using an oligonucleotide specific for each nucleotide sequence.

Homologues (e.g., nucleic acids encoding component proteins from other species) or other related sequences (e.g., variants, paralogs) which are members of a native cellular protein complex can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular nucleic acid sequence as a probe, using methods well known in the art for nucleic acid hybridization and cloning.

Exemplary moderately stringent hybridization conditions are as follows: prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 hours at 65°C in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Washing of filters is done at 37°C for 1 hour in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA. This is followed by a wash in 0.1X SSC at 50 °C for 45 min before autoradiography. Alternatively, exemplary conditions of high stringency are as follows: e.g., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1xSSC/0.1% SDS at 68°C (Ausubel et al., eds., 1989, *Current Protocols in Molecular Biology*, Vol. 1, Green Publishing Associates, Inc., and John Wiley & sons, Inc., New York, at p. 2.10.3). Other conditions of high stringency which may be

used are well known in the art. Exemplary low stringency hybridization conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 μ g/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

For recombinant expression of one or more of the proteins, the nucleic acid containing all or a portion of the nucleotide sequence encoding the protein can be inserted into an appropriate expression vector, i.e., a vector that contains the necessary elements for the transcription and translation of the inserted protein coding sequence. The necessary transcriptional and translational signals can also be supplied by the native promoter of the component protein gene, and/or flanking regions.

A variety of host-vector systems may be utilized to express the protein coding sequence. These include but are not limited to mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); microorganisms such as yeast containing yeast vectors; or bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

In a preferred embodiment, a complex of the present invention is obtained by expressing the entire coding sequences of the component proteins in the same cell, either under the control of the same promoter or separate promoters. In yet another embodiment, a derivative, fragment or homologue of a component protein is recombinantly expressed. Preferably the derivative, fragment or homologue of the protein forms a complex with the other components of the complex, and more preferably forms a complex that binds to an anti-complex antibody. Such an antibody is further described *infra*.

Any method available in the art can be used for the insertion of DNA fragments into a vector to construct expression vectors containing a chimeric gene consisting of appropriate transcriptional/translational control signals and protein coding sequences. These methods may include *in vitro* recombinant DNA and synthetic techniques and *in vivo* recombinant techniques (genetic recombination). Expression of nucleic acid

sequences encoding a component protein, or a derivative, fragment or homologue thereof, may be regulated by a second nucleic acid sequence so that the gene or fragment thereof is expressed in a host transformed with the recombinant DNA molecule(s). For example, expression of the proteins may be controlled by any promoter/enhancer known in the art. In a specific embodiment, the promoter is not native to the gene for the component protein. Promoters that may be used can be selected from among the many known in the art, and are chosen so as to be operative in the selected host cell.

In a specific embodiment, a vector is used that comprises a promoter operably linked to nucleic acid sequences encoding a component protein, or a fragment, derivative or homologue thereof, one or more origins of replication, and optionally, one or more selectable markers (e.g., an antibiotic resistance gene).

In another specific embodiment, an expression vector containing the coding sequence, or a portion thereof, of a component protein, either together or separately, is made by subcloning the gene sequences into the EcoRI restriction site of each of the three pGEX vectors (glutathione S-transferase expression vectors; Smith and Johnson, 1988, Gene 7:31-40). This allows for the expression of products in the correct reading frame.

Expression vectors containing the sequences of interest can be identified by three general approaches: (a) nucleic acid hybridization, (b) presence or absence of "marker" gene function, and (c) expression of the inserted sequences. In the first approach, coding sequences can be detected by nucleic acid hybridization to probes comprising sequences homologous and complementary to the inserted sequences. In the second approach, the recombinant vector/host system can be identified and selected based upon the presence or absence of certain "marker" functions (e.g., resistance to antibiotics, occlusion body formation in baculovirus, etc.) caused by insertion of the sequences of interest in the vector. For example, if a component protein gene, or portion thereof, is inserted within the marker gene sequence of the vector, recombinants containing the encoded protein or portion will be identified by the absence of the marker gene function (e.g., loss of β -galactosidase activity). In the third approach, recombinant expression vectors can be identified by assaying for the component protein expressed by the recombinant vector. Such assays can be based, for example, on the physical or functional properties of the interacting species in in vitro assay systems, e.g., formation of a complex comprising the protein or binding to an anti-complex antibody.

Once recombinant component protein molecules are identified and the complexes or individual proteins isolated, several methods known in the art can be used to propagate them. Using a suitable host system and growth conditions, recombinant expression vectors can be propagated and amplified in quantity. As previously described, the expression vectors or derivatives which can be used include, but are not limited to, human or animal viruses such as vaccinia virus or adenovirus; insect viruses such as baculovirus, yeast vectors; bacteriophage vectors such as lambda phage; and plasmid and cosmid vectors.

In addition, a host cell strain may be chosen that modulates the expression of the inserted sequences, or modifies or processes the expressed proteins in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus expression of the genetically-engineered component proteins may be controlled. Furthermore, different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (e.g., glycosylation, phosphorylation, etc.) of proteins. Appropriate cell lines or host systems can be chosen to ensure that the desired modification and processing of the foreign protein is achieved. For example, expression in a bacterial system can be used to produce an unglycosylated core protein, while expression in mammalian cells ensures "native" glycosylation of a heterologous protein. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

In other specific embodiments, a component protein or a fragment, homologue or derivative thereof, may be expressed as fusion or chimeric protein product comprising the protein, fragment, homologue, or derivative joined via a peptide bond to a heterologous protein sequence of a different protein. Such chimeric products can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acids to each other by methods known in the art, in the proper coding frame, and expressing the chimeric products in a suitable host by methods commonly known in the art. Alternatively, such a chimeric product can be made by protein synthetic techniques, e.g., by use of a peptide synthesizer. Chimeric genes comprising a portion of a component protein fused to any heterologous protein-encoding sequences may be constructed.

In particular, protein component derivatives can be made by altering their sequences by substitutions, additions or deletions that provide for functionally equivalent molecules. Due to the degeneracy of nucleotide coding sequences, other DNA

sequences that encode substantially the same amino acid sequence as a component gene or cDNA can be used in the practice of the present invention. These include but are not limited to nucleotide sequences comprising all or portions of the component protein gene that are altered by the substitution of different codons that encode a functionally equivalent amino acid residue within the sequence, thus producing a silent change. Likewise, the derivatives of the invention include, but are not limited to, those containing, as a primary amino acid sequence, all or part of the amino acid sequence of a component protein, including altered sequences in which functionally equivalent amino acid residues are substituted for residues within the sequence resulting in a silent change. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity that acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid.

In a specific embodiment, up to 1%, 2%, 5%, 10%, 15% or 20% of the total number of amino acids in the wild type protein are substituted or deleted; or 1, 2, 3, 4, 5, or 6 or up to 10 or up to 20 amino acids are inserted, substituted or deleted relative to the wild type protein.

In a specific embodiment of the invention, the nucleic acids encoding a protein component and protein components consisting of or comprising a fragment of or consisting of at least 6 (continuous) amino acids of the protein are provided. In other embodiments, the fragment consists of at least 10, 20, 30, 40, or 50 amino acids of the component protein. In specific embodiments, such fragments are not larger than 35, 100 or 200 amino acids. Derivatives or analogs of component proteins include, but are not limited, to molecules comprising regions that are substantially homologous to the component proteins, in various embodiments, by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% identity over an amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of

hybridizing to a sequence encoding the component protein under stringent, moderately stringent, or nonstringent conditions.

In a specific embodiment, proteins are provided herein, which share an identical region of 20, 30, 40, 50 or 60 contiguous amino acids of the proteins listed in table 2.

The protein component derivatives and analogs of the invention can be produced by various methods known in the art. The manipulations which result in their production can occur at the gene or protein level. For example, the cloned gene sequences can be modified by any of numerous strategies known in the art (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York). The sequences can be cleaved at appropriate sites with restriction endonuclease(s), followed by further enzymatic modification if desired, isolated, and ligated in vitro. In the production of the gene encoding a derivative, homologue or analog of a component protein, care should be taken to ensure that the modified gene retains the original translational reading frame, uninterrupted by translational stop signals, in the gene region where the desired activity is encoded.

Additionally, the encoding nucleic acid sequence can be mutated in vitro or in vivo, to create and/or destroy translation, initiation, and/or termination sequences, or to create variations in coding regions and/or form new restriction endonuclease sites or destroy pre-existing ones, to facilitate further in vitro modification. Any technique for mutagenesis known in the art can be used, including but not limited to, chemical mutagenesis and in vitro site-directed mutagenesis (Hutchinson et al., 1978, *J. Biol. Chem.* 253:6551-6558), amplification with PCR primers containing a mutation, etc.

Once a recombinant cell expressing a component protein, or fragment or derivative thereof, is identified, the individual gene product or complex can be isolated and analyzed. This is achieved by assays based on the physical and/or functional properties of the protein or complex, including, but not limited to, radioactive labeling of the product followed by analysis by gel electrophoresis, immunoassay, cross-linking to marker-labeled product, etc.

The component proteins and complexes may be isolated and purified by standard methods known in the art (either from natural sources or recombinant host cells expressing the complexes or proteins), including but not restricted to column chromatography (e.g., ion exchange, affinity, gel exclusion, reversed-phase high pressure, fast protein liquid, etc.), differential centrifugation, differential solubility, or by

any other standard technique used for the purification of proteins. Functional properties may be evaluated using any suitable assay known in the art.

Alternatively, once a component protein or its derivative, is identified, the amino acid sequence of the protein can be deduced from the nucleic acid sequence of the chimeric gene from which it was encoded. As a result, the protein or its derivative can be synthesized by standard chemical methods known in the art (e.g., Hunkapiller et al., 1984, *Nature* 310:105-111).

Manipulations of component protein sequences may be made at the protein level. Included within the scope of the invention is a complex in which the component proteins or derivatives and analogs that are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH_4 , acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, etc.

In specific embodiments, the amino acid sequences are modified to include a fluorescent label. In another specific embodiment, the protein sequences are modified to have a heterofunctional reagent; such heterofunctional reagents can be used to crosslink the members of the complex.

In addition, complexes of analogs and derivatives of component proteins can be chemically synthesized. For example, a peptide corresponding to a portion of a component protein, which comprises the desired domain or mediates the desired activity *in vitro* (e.g., complex formation) can be synthesized by use of a peptide synthesizer. Furthermore, if desired, non-classical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the protein sequence.

In cases where natural products are suspected of being mutant or are isolated from new species, the amino acid sequence of a component protein isolated from the natural source, as well as those expressed *in vitro*, or from synthesized expression vectors *in vivo* or *in vitro*, can be determined from analysis of the DNA sequence, or alternatively, by direct sequencing of the isolated protein. Such analysis can be performed by manual sequencing or through use of an automated amino acid sequenator.

The complexes can also be analyzed by hydrophilicity analysis (Hopp and Woods, 1981, Proc. Natl. Acad. Sci. USA 78:3824-3828). A hydrophilicity profile can be used to identify the hydrophobic and hydrophilic regions of the proteins, and help predict their orientation in designing substrates for experimental manipulation, such as in binding experiments, antibody synthesis, etc. Secondary structural analysis can also be done to identify regions of the component proteins, or their derivatives, that assume specific structures (Chou and Fasman, 1974, Biochemistry 13:222-23). Manipulation, translation, secondary structure prediction, hydrophilicity and hydrophobicity profile predictions, open reading frame prediction and plotting, and determination of sequence homologies, etc., can be accomplished using computer software programs available in the art.

Other methods of structural analysis including but not limited to X-ray crystallography (Engstrom, 1974, Biochem. Exp. Biol. 11:7-13), mass spectroscopy and gas chromatography (Methods in Protein Science, J. Wiley and Sons, New York, 1997), and computer modeling (Fletterick and Zoller, eds., 1986, Computer Graphics and Molecular Modeling, In: Current Communications in Molecular Biology, Cold Spring Harbor Laboratory, Cold Spring Harbor Press, New York) can also be employed.

4.2 ANTIBODIES TO PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

According to the present invention, a protein complex of the present invention comprising a first protein, or a functionally active fragment or functionally active derivative thereof, selected from the group consisting of proteins listed in fourth column of table 1; and a second protein, or a functionally active fragment or functionally active derivative thereof, selected from the group consisting of proteins listed in fifth column of table 1, or a functionally active fragment or functionally active derivative thereof, can be used as an immunogen to generate antibodies which immunospecifically bind such immunogen. According to the present invention, also a protein complex of the present invention can be used as an immunogen to generate antibodies which immunospecifically bind to such immunogen comprising all proteins listed in fifth column of table 1.

Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments, and an Fab expression library. In a specific embodiment, antibodies to a complex comprising human protein components are

produced. In another embodiment, a complex formed from a fragment of said first protein and a fragment of said second protein, which fragments contain the protein domain that interacts with the other member of the complex, are used as an immunogen for antibody production. In a preferred embodiment, the antibody specific for the complex in that the antibody does not bind the individual protein components of the complex.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a polypeptide of the invention as an immunogen. Preferred polyclonal antibody compositions are ones that have been selected for antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred polyclonal antibody preparations are ones that contain only antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred immunogen compositions are those that contain no other human proteins such as, for example, immunogen compositions made using a non-human host cell for recombinant expression of a polypeptide of the invention. In such a manner, the only human epitope or epitopes recognized by the resulting antibody compositions raised against this immunogen will be present as part of a polypeptide or polypeptides of the invention.

The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules can be isolated from the mammal (e.g., from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. Alternatively, antibodies specific for a protein or polypeptide of the invention can be selected for (e.g., partially purified) or purified by, e.g., affinity chromatography. For example, a recombinantly expressed and purified (or partially purified) protein of the invention is produced as described herein, and covalently or non-covalently coupled to a solid support such as, for example, a chromatography column. The column can then be used to affinity purify antibodies specific for the proteins of the invention from a sample containing antibodies directed against a large number of different epitopes, thereby generating a substantially purified antibody composition, i.e., one that is substantially free of contaminating antibodies. By a substantially purified antibody composition is meant, in this context, that the antibody sample contains at most only 30% (by dry weight) of contaminating antibodies directed against epitopes other than those on the desired protein or polypeptide of the invention, and preferably at most 20%, yet more preferably at most 10%, and most preferably at

most 5% (by dry weight) of the sample is contaminating antibodies. A purified antibody composition means that at least 99% of the antibodies in the composition are directed against the desired protein or polypeptide of the invention.

At an appropriate time after immunization, e.g., when the specific antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, 1975, *Nature* 256:495-497, the human B cell hybridoma technique (Kozbor et al., 1983, *Immunol. Today* 4:72), the EBV-hybridoma technique (Cole et al., 1985, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* 1994, Coligan et al. (eds.) John Wiley & Sons, Inc., New York, NY). Hybridoma cells producing a monoclonal antibody of the invention are detected by screening the hybridoma culture supernatants for antibodies that bind the polypeptide of interest, e.g., using a standard ELISA assay.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody directed against a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with the polypeptide of interest. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia Recombinant Phage Antibody System, Catalog No. 27-9400-01; and the Stratagene SurfZAP Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs et al., 1991, *Bio/Technology* 9:1370-1372; Hay et al., 1992, *Hum. Antibod. Hybridomas* 3:81-85; Huse et al., 1989, *Science* 246:1275-1281; Griffiths et al., 1993, *EMBO J.* 12:725-734.

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. A chimeric antibody is a molecule in which different portions are derived from different

animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, e.g., Cabilly et al., U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.) Humanized antibodies are antibody molecules from non-human species having one or more complementarily determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. (See, e.g., Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better et al., 1988, *Science* 240:1041-1043; Liu et al., 1987, *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu et al., 1987, *J. Immunol.* 139:3521-3526; Sun et al., 1987, *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura et al., 1987, *Canc. Res.* 47:999-1005; Wood et al., 1985, *Nature* 314:446-449; and Shaw et al., 1988, *J. Natl. Cancer Inst.* 80:1553-1559; Morrison, 1985, *Science* 229:1202-1207; Oi et al., 1986, *Bio/Techniques* 4:214; U.S. Patent 5,225,539; Jones et al., 1986, *Nature* 321:552-525; Verhoeyan et al., 1988, *Science* 239:1534; and Beidler et al., 1988, *J. Immunol.* 141:4053-4060.

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Such antibodies can be produced, for example, using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar, 1995, *Int. Rev. Immunol.* 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In

addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al., 1994, *Bio/technology* 12:899-903).

Antibody fragments that contain the idiotypes of the complex can be generated by techniques known in the art. For example, such fragments include, but are not limited to, the F(ab')₂ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragment that can be generated by reducing the disulfide bridges of the F(ab')₂ fragment; the Fab fragment that can be generated by treating the antibody molecular with papain and a reducing agent; and Fv fragments.

In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, e.g., ELISA (enzyme-linked immunosorbent assay). To select antibodies specific to a particular domain of the complex, or a derivative thereof, one may assay generated hybridomas for a product that binds to the fragment of the complex, or a derivative thereof, that contains such a domain. For selection of an antibody that specifically binds a complex of the present, or a derivative, or homologue thereof, but which does not specifically bind to the individual proteins of the complex, or a derivative, or homologue thereof, one can select on the basis of positive binding to the complex and a lack of binding to the individual protein components.

Antibodies specific to a domain of the complex, or a derivative, or homologue thereof, are also provided.

The foregoing antibodies can be used in methods known in the art relating to the localization and/or quantification of the complexes of the invention, e.g., for imaging these proteins, measuring levels thereof in appropriate physiological samples (by immunoassay), in diagnostic methods, etc. This hold true also for a derivative, or homologue thereof of a complex.

In another embodiment of the invention (see *infra*), an antibody to a complex or a fragment of such antibodies containing the antibody binding domain, is a therapeutic.

4.3 DIAGNOSTIC, PROGNOSTIC, AND SCREENING USES OF THE PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

The particular protein complexes and proteins of the present invention may be markers of normal physiological processes, and thus have diagnostic utility. Further, definition of particular groups of patients with elevations or deficiencies of a protein complex of the present invention, or wherein the protein complex has a change in protein component composition, can lead to new nosological classifications of diseases, furthering diagnostic ability.

Examples for diseases or disorders are those as listed in table 4

Detecting levels of protein complexes, or individual component proteins that form the complexes, or detecting levels of the mRNAs encoding the components of the complex, may be used in diagnosis, prognosis, and/or staging to follow the course of a disease state, to follow a therapeutic response, etc.

A protein complex of the present invention and the individual components of the complex and a derivative, analog or subsequence thereof, encoding nucleic acids (and sequences complementary thereto), and anti-complex antibodies and antibodies directed against individual components that can form the complex, are useful in diagnostics. The foregoing molecules can be used in assays, such as immunoassays, to detect, prognose, diagnose, or monitor various conditions, diseases, and disorders characterized by aberrant levels of a complex or aberrant component composition of a complex, or monitor the treatment of such various conditions, diseases, and disorders.

In particular, such an immunoassay is carried out by a method comprising contacting a sample derived from a patient with an anti-complex antibody under conditions such that immunospecific binding can occur, and detecting or measuring the amount of any immunospecific binding by the antibody. In a specific aspect, such binding of antibody, in tissue sections, can be used to detect aberrant complex localization, or aberrant (e.g., high, low or absent) levels of a protein complex or complexes. In a specific embodiment, an antibody to the complex can be used to assay a patient tissue or serum sample for the presence of the complex, where an aberrant level of the complex is an indication of a diseased condition. By "aberrant levels" is meant increased or decreased levels relative to that present, or a standard level

representing that present, in an analogous sample from a portion or fluid of the body, or from a subject not having the disorder.

The immunoassays which can be used include but are not limited to competitive and non-competitive assay systems using techniques such as Western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few known in the art.

Nucleic acids encoding the components of the protein complex and related nucleic acid sequences and subsequences, including complementary sequences, can be used in hybridization assays. The nucleic acid sequences, or subsequences thereof, comprising about at least 8 nucleotides, can be used as hybridization probes. Hybridization assays can be used to detect, prognose, diagnose, or monitor conditions, disorders, or disease states associated with aberrant levels of the mRNAs encoding the components of a complex as described, supra. In particular, such a hybridization assay is carried out by a method comprising contacting a sample containing nucleic acid with a nucleic acid probe capable of hybridizing to component protein coding DNA or RNA, under conditions such that hybridization can occur, and detecting or measuring any resulting hybridization.

In specific embodiments, diseases and disorders involving or characterized by aberrant levels of a protein complex or aberrant complex composition can be diagnosed, or its suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by determining the component protein composition of the complex, or detecting aberrant levels of a member of the complex or un-complexed component proteins or encoding nucleic acids, or functional activity including, but not restricted to, binding to an interacting partner, or by detecting mutations in component protein RNA, DNA or protein (e.g., mutations such as translocations, truncations, changes in nucleotide or amino acid sequence relative to wild-type that cause increased or decreased expression or activity of a complex, and/or component protein).

Such diseases and disorders include, but are not limited to neurodegenerative disease such as listed in table 4.

By way of example, levels of a protein complex and the individual components of a complex can be detected by immunoassay, levels of component protein RNA or DNA

can be detected by hybridization assays (e.g., Northern blots, dot blots, RNase protection assays), and binding of component proteins to each other (e.g., complex formation) can be measured by binding assays commonly known in the art. Translocations and point mutations in component protein genes can be detected by Southern blotting, RFLP analysis, PCR using primers that preferably generate a fragment spanning at least most of the gene by sequencing of genomic DNA or cDNA obtained from the patient, etc.

Assays well known in the art (e.g., assays described above such as immunoassays, nucleic acid hybridization assays, activity assays, etc.) can be used to determine whether one or more particular protein complexes are present at either increased or decreased levels, or are absent, in samples from patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, as compared to the levels in samples from subjects not having such a disease or disorder, or having a predisposition to develop such a disease or disorder. Additionally, these assays can be used to determine whether the ratio of the complex to the un-complexed components of the complex, is increased or decreased in samples from patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, as compared to the ratio in samples from subjects not having such a disease or disorder.

In the event that levels of one or more particular protein complexes (i.e., complexes formed from component protein derivatives, homologs, fragments, or analogs) are determined to be increased in patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, then the particular disease or disorder, or predisposition for a disease or disorder, can be diagnosed, have prognosis defined for, be screened for, or be monitored by detecting increased levels of the one or more protein complexes, increased levels of the mRNA that encodes one or more members of the one or more particular protein complexes, or by detecting increased complex functional activity.

Accordingly, in a specific embodiment of the present invention, diseases and disorders involving increased levels of one or more protein complexes can be diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting increased levels of the one or more protein complexes, the mRNA encoding both members of the complex, or complex functional activity, or by detecting mutations in the component proteins that stabilize or enhance

complex formation, e.g., mutations such as translocations in nucleic acids, truncations in the gene or protein, changes in nucleotide or amino acid sequence relative to wild-type, that stabilize or enhance complex formation.

In the event that levels of one or more particular protein complexes are determined to be decreased in patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, then the particular disease or disorder or predisposition for a disease or disorder can be diagnosed, have its prognosis determined, be screened for, or be monitored by detecting decreased levels of the one or more protein complexes, the mRNA that encodes one or more members of the particular one or more protein complexes, or by detecting decreased protein complex functional activity.

Accordingly, in a specific embodiment of the invention, diseases and disorders involving decreased levels of one or more protein complexes can be diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting decreased levels of the one or more protein complexes, the mRNA encoding one or more members of the one or more complexes, or complex functional activity, or by detecting mutations in the component proteins that decrease complex formation, e.g., mutations such as translocations in nucleic acids, truncations in the gene or protein, changes in nucleotide or amino acid sequence relative to wild-type, that decrease complex formation.

Accordingly, in a specific embodiment of the invention, diseases and disorders involving aberrant compositions of the complexes can be diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting the component proteins of one or more complexes, or the mRNA encoding the members of the one or more complexes.

The use of detection techniques, especially those involving antibodies against a protein complex, provides a method of detecting specific cells that express the complex or component proteins. Using such assays, specific cell types can be defined in which one or more particular protein complexes are expressed, and the presence of the complex or component proteins can be correlated with cell viability, state, health, etc.

Also embodied are methods to detect a protein complex of the present invention in cell culture models that express particular protein complexes or derivatives thereof, for the purpose of characterizing or preparing the complexes for harvest. This embodiment includes cell sorting of prokaryotes such as but not restricted to bacteria (Davey and Kell,

1996, *Microbiol. Rev.* 60:641-696), primary cultures and tissue specimens from eukaryotes, including mammalian species such as human (Steele et al., 1996, *Clin. Obstet. Gynecol.* 39:801-813), and continuous cell cultures (Orfao and Ruiz-Arguelles, 1996, *Clin. Biochem.* 29:5-9). Such isolations can be used as methods of diagnosis, described, *supra*.

In a further specific embodiment, a modulation of the formation process of a complex can be determined.

Such a modulation can either be a change in the typical time course of its formation or a change in the typical steps leading to the formation of the complete complex.

Such changes can for example be detected by analysing and comparing the process of complex formation in untreated wild type cells of a particular type and/or cells showing or having the predisposition to develop a certain disease phenotype and/or cells which have been treated with particular conditions and/or particular agents in a particular situation.

Methods to study such changes in time course are well known in the art and include for example Western-blot analysis of the proteins in the complex isolated at different steps of its formation.

Furthermore an aberrant intracellular localization of the protein complex and/or an aberrant transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or a gene dependent on the complex can serve as a marker for a disease and thus have diagnostic utility for any disease which is caused by an aberrant activity, function, composition or formation of the complex of the invention.

Methods to study the intracellular localization are well known in the art and include, but are not limited to immunofluorescence analysis using antibodies specific for components of the protein. Preferentially, double-stainings including staining of other cellular structures are being used to facilitate the detection of the intracellular localization. Methods to analyse the transcription levels of a gene dependent on the complex are also well known in the art and include Northern blot analysis, quantitative PCR etc. The abundance of proteins dependent on the protein can be analyzed as described *supra*. Methods to study changes in the activity of proteins dependent on complex depend on the protein. The choice of such methods will be apparent to any person skilled in the art.

4.4 THERAPEUTIC USES OF PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

The present invention is directed to a method for treatment or prevention of various diseases and disorders by administration of a therapeutic compound (termed herein "therapeutic"). Such "therapeutics" include, but are not limited to, a protein complex of the present invention, the individual component proteins, and analogs and derivatives (including fragments) of the foregoing (e.g., as described hereinabove); antibodies thereto (as described hereinabove); nucleic acids encoding the component protein, and analogs or derivatives, thereof (e.g., as described hereinabove); component protein antisense nucleic acids, and agents that modulate complex formation and/or activity (i.e., agonists and antagonists).

The protein complexes as identified herein can be implicated in processes which are implicated in or associated with pathological conditions.

Diseases and disorders which can be treated and/or prevented and/or diagnosed by therapeutics interacting with any of the complexes provided herein are for example those listed in table 4.

These disorders are treated or prevented by administration of a therapeutic that modulates (i.e. inhibits or promotes) protein complex activity or formation or modulates its function or composition. Diseases or disorders associated with aberrant levels of complex activity or formation, or aberrant levels or activity of the component proteins, or aberrant complex composition or a change in the function, may be treated by administration of a therapeutic that modulates complex formation or activity or by the administration of a protein complex.

Therapeutics may also be administered to modulate complex formation or activity or level thereof in a microbial organism such as yeast, fungi such as candida albicans causing an infectious disease in animals or humans.

Diseases and disorders characterized by increased (relative to a subject not suffering from the disease or disorder) complex levels or activity can be treated with therapeutics that antagonize (i.e., reduce or inhibit) complex formation or activity. Therapeutics that can be used include, but are not limited to, the component proteins or an analog, derivative or fragment of the component protein; anti-complex antibodies (e.g., antibodies specific for the protein complex, or a fragment or derivative of the

antibody containing the binding region thereof; nucleic acids encoding the component proteins; antisense nucleic acids complementary to nucleic acids encoding the component proteins; and nucleic acids encoding the component protein that are dysfunctional due to, e.g., a heterologous insertion within the protein coding sequence, that are used to "knockout" endogenous protein function by homologous recombination, see, e.g., Capecchi, 1989, *Science* 244:1288-1292. In one embodiment, a therapeutic is 1, 2 or more antisense nucleic acids which are complementary to 1, 2, or more nucleic acids, respectfully, that encode component proteins of a complex.

In a specific embodiment of the present invention, a nucleic acid containing a portion of a component protein gene in which gene sequences flank (are both 5' and 3' to) a different gene sequence, is used as a component protein antagonist, or to promote component protein inactivation by homologous recombination (see also, Koller and Smithies, 1989, *Proc. Natl. Acad. Sci. USA* 86:8932-8935; Zijlstra et al., 1989, *Nature* 342: 435-438). Additionally, mutants or derivatives of a component protein that has greater affinity for another component protein or the complex than wild type may be administered to compete with wild type protein for binding, thereby reducing the levels of complexes containing the wild type protein. Other therapeutics that inhibit complex function can be identified by use of known convenient *in vitro* assays, e.g., based on their ability to inhibit complex formation, or as described in Section 4.5, *infra*.

In specific embodiments, therapeutics that antagonize complex formation or activity are administered therapeutically, including prophylactically, (1) in diseases or disorders involving an increased (relative to normal or desired) level of a complex, for example, in patients where complexes are overactive or overexpressed; or (2) in diseases or disorders where an *in vitro* (or *in vivo*) assay (see *infra*) indicates the utility of antagonist administration. Increased levels of a complex can be readily detected, e.g., by quantifying protein and/or RNA, by obtaining a patient tissue sample (e.g., from biopsy tissue) and assaying it *in vitro* for RNA or protein levels, or structure and/or activity of the expressed complex (or the encoding mRNA). Many methods standard in the art can be thus employed including, but not limited to, immunoassays to detect complexes and/or visualize complexes (e.g., Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate polyacrylamide gel electrophoresis [SDS-PAGE], immunocytochemistry, etc.), and/or hybridization assays to detect concurrent expression of component protein mRNA (e.g., Northern assays, dot blot analysis, *in situ* hybridization, etc.).

A more specific embodiment of the present invention is directed to a method of reducing complex expression (i.e., expression of the protein components of the complex and/or formation of the complex) by targeting mRNAs that express the protein moieties. RNA therapeutics currently fall within three classes, antisense species, ribozymes, or RNA aptamers (Good et al., 1997, *Gene Therapy* 4:45-54).

Antisense oligonucleotides have been the most widely used. By way of example, but not limitation, antisense oligonucleotide methodology to reduce complex formation is presented below, *infra*. Ribozyme therapy involves the administration, induced expression, etc. of small RNA molecules with enzymatic ability to cleave, bind, or otherwise inactivate specific RNAs, to reduce or eliminate expression of particular proteins (Grassi and Marini, 1996, *Annals of Medicine* 28:499-510; Gibson, 1996, *Cancer and Metastasis Reviews* 15:287-299). RNA aptamers are specific RNA ligand proteins, such as for Tat and Rev RNA (Good et al., 1997, *Gene Therapy* 4:45-54) that can specifically inhibit their translation. Aptamers specific for component proteins can be identified by many methods well known in the art, for example, by affecting the formation of a complex in the protein-protein interaction assay described, *infra*.

In another embodiment, the activity or levels of a component protein are reduced by administration of another component protein, or the encoding nucleic acid, or an antibody that immunospecifically binds to the component protein, or a fragment or a derivative of the antibody containing the binding domain thereof.

In another aspect of the invention, diseases or disorders associated with increased levels of a component protein of the complex may be treated or prevented by administration of a therapeutic that increases complex formation if the complex formation acts to reduce or inactivate the component protein through complex formation. Such diseases or disorders can be treated or prevented by administration of one component member of the complex, administration of antibodies or other molecules that stabilize the complex, etc.

Diseases and disorders associated with underexpression of a complex, or a component protein, are treated or prevented by administration of a therapeutic that promotes (i.e., increases or supplies) complex levels and/or function, or individual component protein function. Examples of such a therapeutic include but are not limited to a complex or a derivative, analog or fragment of the complex that are functionally active (e.g., able to form a complex), un-complexed component proteins and derivatives, analogs, and fragments of un-complexed component proteins, and nucleic acids

encoding the members of a complex or functionally active derivatives or fragments of the members of the complex, e.g., for use in gene therapy. In a specific embodiment, a therapeutic includes derivatives, homologs or fragments of a component protein that increase and/or stabilize complex formation. Examples of other agonists can be identified using in vitro assays or animal models, examples of which are described, *infra*.

In yet other specific embodiments of the present invention, therapeutics that promote complex function are administered therapeutically, including prophylactically, (1) in diseases or disorders involving an absence or decreased (relative to normal or desired) level of a complex, for example, in patients where a complex, or the individual components necessary to form the complex, is lacking, genetically defective, biologically inactive or underactive, or under-expressed; or (2) in diseases or disorders wherein an in vitro or in vivo assay (see, *infra*) indicates the utility of complex agonist administration. The absence or decreased level of a complex, component protein or function can be readily detected, e.g., by obtaining a patient tissue sample (e.g., from biopsy tissue) and assaying it in vitro for RNA or protein levels, structure and/or activity of the expressed complex and/or the concurrent expression of mRNA encoding the two components of the complex. Many methods standard in the art can be thus employed, including but not limited to immunoassays to detect and/or visualize a complex, or the individual components of a complex (e.g., Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate polyacrylamide gel electrophoresis [SDS-PAGE], immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs encoding the individual protein components of a complex by detecting and/or visualizing component mRNA concurrently or separately using, e.g., Northern assays, dot blot analysis, in situ hybridization, etc.

In specific embodiments, the activity or levels of a component protein are increased by administration of another component protein of the same complex, or a derivative, homolog or analog thereof, a nucleic acid encoding the other component, or an agent that stabilizes or enhances the other component, or a fragment or derivative of such an agent.

Generally, administration of products of species origin or species reactivity (in the case of antibodies) that is the same species as that of the patient is preferred. Thus, in a preferred embodiment, a human complex, or derivative, homolog or analog thereof; nucleic acids encoding the members of the human complex or a derivative, homolog or analog thereof; an antibody to a human complex, or a derivative thereof; or other human

agents that affect component proteins or the complex, are therapeutically or prophylactically administered to a human patient.

Preferably, suitable in vitro or in vivo assays are utilized to determine the effect of a specific therapeutic and whether its administration is indicated for treatment of the affected tissue or individual.

In various specific embodiments, in vitro assays can be carried out with representative cells of cell types involved in a patient's disorder, to determine if a therapeutic has a desired effect upon such cell types.

Compounds for use in therapy can be tested in suitable animal model systems prior to testing in humans, including, but not limited to, rats, mice, chicken, cows, monkeys, rabbits, etc. For in vivo testing, prior to administration to humans, any animal model system known in the art may be used. Additional descriptions and sources of therapeutics that can be used according to the invention are found in Sections 4.1 to 4.3 and 4.7 herein.

4.4.1 GENE THERAPY

In a specific embodiment of the present invention, nucleic acids comprising a sequence encoding the component proteins, or a functional derivative thereof, are administered to modulate complex activity or formation by way of gene therapy. Gene therapy refers to therapy performed by the administration of a nucleic acid to a subject. In this embodiment of the present invention, the nucleic acid expresses its encoded protein(s) that mediates a therapeutic effect by modulating complex activity or formation. Any of the methods for gene therapy available in the art can be used according to the present invention. Exemplary methods are described below.

For general reviews of the methods of gene therapy, see Goldspiel et al., 1993, *Clinical Pharmacy* 12:488-505; Wu and Wu, 1991, *Biotherapy* 3:87-95; Tolstoshev, 1993, *Ann. Rev. Pharmacol. Toxicol.* 32:573-596; Mulligan, 1993, *Science* 260:926-932; Morgan and Anderson, 1993, *Ann. Rev. Biochem.* 62:191-217; and May, 1993, *TIBTECH* 11:155-215. Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al., eds., 1993, *Current Protocols in Molecular Biology*, John Wiley & Sons, NY; and Kriegler, 1990, *Gene Transfer and Expression, A Laboratory Manual*, Stockton Press, NY.

In a preferred aspect, the therapeutic comprises a nucleic acid that is part of an expression vector that expresses one or more of the component proteins, or fragments or chimeric proteins thereof, in a suitable host. In particular, such a nucleic acid has a promoter operably linked to the protein coding region(s) (or, less preferably separate promoters linked to the separate coding regions separately), said promoter being inducible or constitutive, and optionally, tissue-specific. In another particular embodiment, a nucleic acid molecule is used in which the coding sequences, and any other desired sequences, are flanked by regions that promote homologous recombination at a desired site in the genome, thus providing for intra-chromosomal expression of the component protein nucleic acids (Koller and Smithies, 1989, *Proc. Natl. Acad. Sci. USA* 86:8932-8935; Zijlstra et al., 1989, *Nature* 342:435-438).

Delivery of the nucleic acid into a patient may be either direct, in which case the patient is directly exposed to the nucleic acid or nucleic acid-carrying vector, or indirect, in which case, cells are first transformed with the nucleic acid in vitro, then transplanted into the patient. These two approaches are known, respectively, as in vivo or ex vivo gene therapy.

In a specific embodiment, the nucleic acid is directly administered in vivo, where it is expressed to produce the encoded product. This can be accomplished by any of numerous methods known in the art, e.g., by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by infection using a defective or attenuated retroviral or other viral vector (U.S. Patent No. 4,980,286), or by direct injection of naked DNA, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors, or through use of transfecting agents, by encapsulation in liposomes, microparticles, or microcapsules, or by administering it in linkage to a peptide that is known to enter the nucleus, or by administering it in linkage to a ligand subject to receptor-mediated endocytosis that can be used to target cell types specifically expressing the receptors (e.g., Wu and Wu, 1987, *J. Biol. Chem.* 262:4429-4432), etc. In another embodiment, a nucleic acid-ligand complex can be formed in which the ligand comprises a fusogenic viral peptide that disrupts endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted in vivo for cell specific uptake and expression, by targeting a specific receptor (see, e.g., International Patent Publications WO 92/06180; WO 92/22635; WO 92/20316; WO 93/14188; and WO 93/20221. Alternatively, the nucleic acid can be introduced

intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, 1989, *Proc. Natl. Acad. Sci. USA* 86:8932-8935; Zijlstra et al., 1989, *Nature* 342:435-438).

In a specific embodiment, a viral vector that contains the component protein encoding nucleic acids is used. For example, a retroviral vector can be used (Miller et al., 1993, *Meth. Enzymol.* 217:581-599). These retroviral vectors have been modified to delete retroviral sequences that are not necessary for packaging of the viral genome and integration into host cell DNA. The encoding nucleic acids to be used in gene therapy is/are cloned into the vector, which facilitates delivery of the gene into a patient. More detail about retroviral vectors can be found in Boesen et al., 1994, *Biotherapy* 6:291-302, which describes the use of a retroviral vector to deliver the *mdr1* gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are Clowes et al., 1994, *J. Clin. Invest.* 93:644-651; Kiem et al., 1994, *Blood* 83:1467-1473; Salmons and Gunzberg, 1993, *Human Gene Therapy* 4:129-141; and Grossman and Wilson, 1993, *Curr. Opin. in Genetics and Devel.* 3:110-114.

Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are the liver, the central nervous system, endothelial cells and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Kozarsky and Wilson, 1993, *Curr. Opin. Genet. Devel.* 3:499-503, discuss adenovirus-based gene therapy. The use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys has been demonstrated by Bout et al., 1994, *Human Gene Therapy* 5:3-10. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., 1991, *Science* 252:431-434; Rosenfeld et al., 1992, *Cell* 68:143-155; and Mastrangeli et al., 1993, *J. Clin. Invest.* 91:225-234.

Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., 1993, *Proc. Soc. Exp. Biol. Med.* 204:289-300).

Another approach to gene therapy involves transferring a gene into cells in tissue culture by methods such as electroporation, lipofection, calcium phosphate-mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection to isolate those

cells that have taken up and are expressing the transferred gene from these that have not. Those cells are then delivered to a patient.

In this embodiment, the nucleic acid is introduced into a cell prior to administration in vivo of the resulting recombinant cell. Such introduction can be carried out by any method known in the art including, but not limited to, transfection by electroporation, microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosome-mediated gene transfer, microcell-mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the introduction of foreign genes into cells (see, e.g., Loeffler and Behr, 1993, *Meth. Enzymol.* 217:599-618; Cohen et al., 1993, *Meth. Enzymol.* 217:618-644; Cline, 1985, *Pharmac. Ther.* 29:69-92) and may be used in accordance with the present invention, provided that the necessary developmental and physiological functions of the recipient cells are not disrupted. The technique should provide for the stable transfer of the nucleic acid to the cell, so that the nucleic acid is expressible by the cell and preferably, is heritable and expressible by its cell progeny.

The resulting recombinant cells can be delivered to a patient by various methods known in the art. In a preferred embodiment, epithelial cells are injected, e.g., subcutaneously. In another embodiment, recombinant skin cells may be applied as a skin graft onto the patient. Recombinant blood cells (e.g., hematopoietic stem or progenitor cells) are preferably administered intravenously. The amount of cells envisioned for use depends on the desired effect, patient state, etc., and can be determined by one skilled in the art.

Cells into which a nucleic acid can be introduced for purposes of gene therapy encompass any desired, available cell type, and include but are not limited to epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes, blood cells such as T lymphocytes, B lymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryocytes, and granulocytes, various stem or progenitor cells, in particular hematopoietic stem or progenitor cells, e.g., as obtained from bone marrow, umbilical cord blood, peripheral blood, fetal liver, etc.

In a preferred embodiment, the cell used for gene therapy is autologous to the patient.

In an embodiment in which recombinant cells are used in gene therapy, a component protein encoding nucleic acid is/are introduced into the cells such that the gene or genes are expressible by the cells or their progeny, and the recombinant cells

are then administered *in vivo* for therapeutic effect. In a specific embodiment, stem or progenitor cells are used. Any stem and/or progenitor cells which can be isolated and maintained *in vitro* can potentially be used in accordance with this embodiment of the present invention. Such stem cells include but are not limited to hematopoietic stem cells (HSCs), stem cells of epithelial tissues such as the skin and the lining of the gut, embryonic heart muscle cells, liver stem cells (International Patent Publication WO 94/08598), and neural stem cells (Stemple and Anderson, 1992, Cell 71:973-985).

Epithelial stem cells (ESCs), or keratinocytes, can be obtained from tissues such as the skin and the lining of the gut by known procedures (Rheinwald, 1980, Meth. Cell Biol. 2A:229). In stratified epithelial tissue such as the skin, renewal occurs by mitosis of stem cells within the germinal layer, the layer closest to the basal lamina. Similarly, stem cells within the lining of the gut provide for a rapid renewal rate of this tissue. ESCs or keratinocytes obtained from the skin or lining of the gut of a patient or donor can be grown in tissue culture (Rheinwald, 1980, Meth. Cell Bio. 2A:229; Pittelkow and Scott, 1986, Mayo Clinic Proc. 61:771). If the ESCs are provided by a donor, a method for suppression of host versus graft reactivity (e.g., irradiation, or drug or antibody administration to promote moderate immunosuppression) can also be used.

With respect to hematopoietic stem cells (HSCs), any technique that provides for the isolation, propagation, and maintenance *in vitro* of HSCs can be used in this embodiment of the invention. Techniques by which this may be accomplished include (a) the isolation and establishment of HSC cultures from bone marrow cells isolated from the future host, or a donor, or (b) the use of previously established long-term HSC cultures, which may be allogeneic or xenogeneic. Non-autologous HSCs are used preferably in conjunction with a method of suppressing transplantation immune reactions between the future host and patient. In a particular embodiment of the present invention, human bone marrow cells can be obtained from the posterior iliac crest by needle aspiration (see, e.g., Kodo et al., 1984, J. Clin. Invest. 73: 1377-1384). In a preferred embodiment of the present invention, the HSCs can be made highly enriched or in substantially pure form. This enrichment can be accomplished before, during, or after long-term culturing, and can be done by any technique known in the art. Long-term cultures of bone marrow cells can be established and maintained by using, for example, modified Dexter cell culture techniques (Dexter et al., 1977, J. Cell Physiol. 91:335) or Witlock-Witte culture techniques (Witlock and Witte, 1982, Proc. Natl. Acad. Sci. USA 79:3608-3612).

In a specific embodiment, the nucleic acid to be introduced for purposes of gene therapy comprises an inducible promoter operably linked to the coding region, such that expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription.

Additional methods can be adapted for use to deliver a nucleic acid encoding the component proteins, or functional derivatives thereof, e.g., as described in Section 4.1, *supra*.

4.4.2 USE OF ANTISENSE OLIGONUCLEOTIDES FOR SUPPRESSION OF PROTEIN COMPLEX FORMATION OR PROTEIN COMPLEX/PROTEIN ACTIVITY

In a specific embodiment of the present invention, protein complex activity and formation and protein activity is inhibited by use of antisense nucleic acids for the component proteins of the complex, that inhibit transcription and/or translation of their complementary sequence. The present invention provides the therapeutic or prophylactic use of nucleic acids of at least six nucleotides that are antisense to a gene or cDNA encoding a component protein, or a portion thereof. An "antisense" nucleic acid as used herein refers to a nucleic acid capable of hybridizing to a sequence-specific portion of a component protein RNA (preferably mRNA) by virtue of some sequence complementarity. The antisense nucleic acid may be complementary to a coding and/or noncoding region of a component protein mRNA. Such antisense nucleic acids that inhibit complex formation or activity have utility as therapeutics, and can be used in the treatment or prevention of disorders as described *supra*.

The antisense nucleic acids of the invention can be oligonucleotides that are double-stranded or single-stranded, RNA or DNA, or a modification or derivative thereof, which can be directly administered to a cell, or which can be produced intracellularly by transcription of exogenous, introduced sequences.

In another embodiment, the present invention is directed to a method for inhibiting the expression of component protein nucleic acid sequences, in a prokaryotic or eukaryotic cell, comprising providing the cell with an effective amount of a composition comprising an antisense nucleic acid of the component protein, or a derivative thereof, of the invention.

The antisense nucleic acids are of at least six nucleotides and are preferably oligonucleotides, ranging from 6 to about 200 nucleotides. In specific aspects, the oligonucleotide is at least 10 nucleotides, at least 15 nucleotides, at least 100 nucleotides, or at least 200 nucleotides. The oligonucleotides can be DNA or RNA or chimeric mixtures, or derivatives or modified versions thereof, and either single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone. The oligonucleotide may include other appending groups such as peptides, agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. USA 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. USA 84:648-652; International Patent Publication No. WO 88/09810) or blood-brain barrier (see, e.g., International Patent Publication No. WO 89/10134), hybridization-triggered cleavage agents (see, e.g., Krol et al., 1988, BioTechniques 6:958-976), or intercalating agents (see, e.g., Zon, 1988, Pharm. Res. 5:539-549).

In a preferred aspect of the invention, an antisense oligonucleotide is provided, preferably as single-stranded DNA. The oligonucleotide may be modified at any position in its structure with constituents generally known in the art.

The antisense oligonucleotides may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl)uracil, 5-carboxymethylaminomethyl-2-thio-uridine, 5-carboxymethylaminomethyluracil, dihydrouracil, β -D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, β -D-mannosylqueosine, 5N-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

In another embodiment, the oligonucleotide comprises at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal, or an analog of the foregoing.

In yet another embodiment, the oligonucleotide is a 2'-anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641).

The oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization-triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. USA 85:7448-7451), etc.

In a specific embodiment, the antisense oligonucleotides comprise catalytic RNAs, or ribozymes (see, e.g., International Patent Publication No. WO 90/11364; Sarver et al., 1990, Science 247:1222-1225). In another embodiment, the oligonucleotide is a 2'-O-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analog (Inoue et al., 1987, FEBS Lett. 215:327-330).

In an alternative embodiment, the antisense nucleic acids of the invention are produced intracellularly by transcription from an exogenous sequence. For example, a vector can be introduced in vivo such that it is taken up by a cell, within which cell the vector or a portion thereof is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would contain a sequence encoding the component protein. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art to be capable of replication and expression in

mammalian cells. Expression of the sequences encoding the antisense RNAs can be by any promoter known in the art to act in mammalian, preferably human, cells. Such promoters can be inducible or constitutive. Such promoters include, but are not limited to, the SV40 early promoter region (Bernoist and Chambon, 1981, *Nature* 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., 1980, *Cell* 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, *Proc. Natl. Acad. Sci. USA* 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, *Nature* 296:39-42), etc.

The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a component protein gene, preferably a human gene. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with a component protein RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

The component protein antisense nucleic acids can be used to treat (or prevent) disorders of a cell type that expresses, or preferably overexpresses, a protein complex.

Cell types that express or overexpress component protein RNA can be identified by various methods known in the art. Such methods include, but are not limited to, hybridization with component protein-specific nucleic acids (e.g., by Northern blot hybridization, dot blot hybridization, or in situ hybridization), or by observing the ability of RNA from the cell type to be translated in vitro into the component protein by immunohistochemistry, Western blot analysis, ELISA, etc. In a preferred aspect, primary tissue from a patient can be assayed for protein expression prior to treatment, e.g., by immunocytochemistry, in situ hybridization, or any number of methods to detect protein or mRNA expression.

Pharmaceutical compositions of the invention (see Section 4.7, *infra*), comprising an effective amount of a protein component antisense nucleic acid in a pharmaceutically

acceptable carrier can be administered to a patient having a disease or disorder that is of a type that expresses or overexpresses a protein complex of the present invention.

The amount of antisense nucleic acid that will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. Where possible, it is desirable to determine the antisense cytotoxicity in vitro, and then in useful animal model systems, prior to testing and use in humans.

In a specific embodiment, pharmaceutical compositions comprising antisense nucleic acids are administered via liposomes, microparticles, or microcapsules. In various embodiments of the invention, it may be useful to use such compositions to achieve sustained release of the antisense nucleic acids. In a specific embodiment, it may be desirable to utilize liposomes targeted via antibodies to specific identifiable central nervous system cell types (Leonetti et al., 1990, Proc. Natl. Acad. Sci. U.S.A. 87:2448-2451; Renneisen et al., 1990, J. Biol. Chem. 265:16337-16342).

4.5 ASSAYS OF PROTEIN COMPLEXES/PROTEINS OF THE INVENTION AND DERIVATIVES AND ANALOGS THEREOF

The functional activity of a protein complex of the present invention, or a derivative, fragment or analog thereof or protein component thereof, can be assayed by various methods. Potential modulators (e.g., agonists and antagonists) of complex activity or formation, e.g., anti-complex antibodies and antisense nucleic acids, can be assayed for the ability to modulate complex activity or formation.

In one embodiment of the present invention, where one is assaying for the ability to bind or compete with a wild-type complex for binding to an anti-complex antibody, various immunoassays known in the art can be used, including but not limited to competitive and non-competitive assay systems using techniques such as radioimmunoassay, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels), western blot analysis, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, immunoelectrophoresis assays, etc. In

one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

The expression of the component protein genes (both endogenous and those expressed from cloned DNA containing the genes) can be detected using techniques known in the art, including but not limited to Southern hybridization (Southern, 1975, J. Mol. Biol. 98:503-517), northern hybridization (see, e.g., Freeman et al., 1983, Proc. Natl. Acad. Sci. USA 80:4094-4098), restriction endonuclease mapping (Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2nd Ed. Cold Spring Harbor Laboratory Press, New York), RNase protection assays (Current Protocols in Molecular Biology, John Wiley and Sons, New York, 1997), DNA sequence analysis, and polymerase chain reaction amplification (PCR; U.S. Patent Nos. 4,683,202, 4,683,195, and 4,889,818; Gyllenstein et al., 1988, Proc. Natl. Acad. Sci. USA 85:7652-7657; Ochman et al., 1988, Genetics 120:621-623; Loh et al., 1989, Science 243:217-220) followed by Southern hybridization with probes specific for the component protein genes, in various cell types. Methods of amplification other than PCR commonly known in the art can be employed. In one embodiment, Southern hybridization can be used to detect genetic linkage of component protein gene mutations to physiological or pathological states. Various cell types, at various stages of development, can be characterized for their expression of component proteins at the same time and in the same cells. The stringency of the hybridization conditions for northern or Southern blot analysis can be manipulated to ensure detection of nucleic acids with the desired degree of relatedness to the specific probes used. Modifications to these methods and other methods commonly known in the art can be used.

Derivatives (e.g., fragments), homologs and analogs of one component protein can be assayed for binding to another component protein in the same complex by any method known in the art, for example the modified yeast matrix mating test described in Section 4.6.1 *infra*, immunoprecipitation with an antibody that binds to the component protein complexed with other component proteins in the same complex, followed by size fractionation of the immunoprecipitated proteins (e.g., by denaturing or nondenaturing polyacrylamide gel electrophoresis), Western blot analysis, etc.

One embodiment of the invention provides a method for screening a derivative, homolog or analog of a component protein for biological activity comprising contacting said derivative, homolog or analog of the component protein with the other component proteins in the same complex; and detecting the formation of a complex between said derivative, homolog or analog of the component protein and the other component proteins; wherein detecting formation of said complex indicates that said derivative, homolog or analog of has biological (e.g., binding) activity.

The invention also provides methods of modulating the activity of a component protein that can participate in a protein complex by administration of a binding partner of that protein or derivative, homolog or analog thereof.

In a specific embodiment of the present invention, a protein complex of the present invention is administered to treat or prevent a disease or disorder, since the complex and/or component proteins have been implicated in the disease and disorder. Accordingly, a protein complex or a derivative, homolog, analog or fragment thereof, nucleic acids encoding the component proteins, anti-complex antibodies, and other modulators of protein complex activity, can be tested for activity in treating or preventing a disease or disorder in in vitro and in vivo assays.

In one embodiment, a therapeutic of the invention can be assayed for activity in treating or preventing a disease by contacting cultured cells that exhibit an indicator of the disease in vitro, with the therapeutic, and comparing the level of said indicator in the cells contacted with the therapeutic, with said level of said indicator in cells not so contacted, wherein a lower level in said contacted cells indicates that the therapeutic has activity in treating or preventing the disease.

In another embodiment of the invention, a therapeutic of the invention can be assayed for activity in treating or preventing a disease by administering the therapeutic to a test animal that is predisposed to develop symptoms of a disease, and measuring the change in said symptoms of the disease after administration of said therapeutic, wherein a reduction in the severity of the symptoms of the disease or prevention of the symptoms of the disease indicates that the therapeutic has activity in treating or preventing the disease. Such a test animal can be any one of a number of animal models known in the art for disease. These animal models are well known in the art. These animal models include, but are not limited to those which are listed in the section 4.6 (supra) as exemplary animal models to study any of the complexes provided in the invention.

4.6 SCREENING FOR MODULATORS OF THE PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

A complex of the present invention, the component proteins of the complex and nucleic acids encoding the component proteins, as well as derivatives and fragments of the amino and nucleic acids, can be used to screen for compounds that bind to, or modulate the amount of, activity of, or protein component composition of, said complex, and thus, have potential use as modulators, i.e., agonists or antagonists, of complex activity, and/or complex formation, i.e., the amount of complex formed, and/or protein component composition of the complex.

Thus, the present invention is also directed to methods for screening for molecules that bind to, or modulate the function of, amount of, activity of, formation of or protein component composition of, a complex of the present invention. In one embodiment of the invention, the method for screening for a molecule that modulates directly or indirectly the function, activity or formation of a complex of the present invention comprises exposing said complex, or a cell or organism containing the complex machinery, to one or more candidate molecules under conditions conducive to modulation; and determining the amount of, the biochemical activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

In a further specific embodiment, a modulation of the formation process of a complex can be determined.

Such a modulation can either be a change in the typical time course of its formation or a change in the typical steps leading to the formation of the complete complex.

Such changes can for example be detected by analysing and comparing the process of complex formation in untreated wild type cells of a particular type and/or cells showing or having the predisposition to develop a certain disease phenotype and/or cells which have been treated with particular conditions and/or particular agents in a particular situation. Methods to study such changes in time course are well known in the art and include for example Western-blot analysis of the proteins in the complex isolated at different steps of its formation.

Furthermore an aberrant intracellular localization of the protein complex and/or an aberrant transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or a gene dependent on the complex can serve as a marker for a disease and thus have diagnostic utility for any disease which is caused by an aberrant activity, function, composition or formation of the complex of the invention.

Methods to study the intracellular localization are well known in the art and include, but are not limited to immunofluorescence analysis using antibodies specific for components of the protein. Preferentially, double-stainings including staining of other cellular structures are being used to facilitate the detection of the intracellular localization. Methods to analyse the transcription levels of a gene dependent on the complex are also well known in the art and include Northern blot analysis, quantitative PCR etc. The abundance of proteins dependent on the protein can be analyzed as described supra. Methods to study changes in the activity of proteins dependent on complex depend on the protein. The choice of such methods will be apparent to any person skilled in the art.

In another embodiment, the present invention further relates to a process for the identification and/or preparation of an effector of the complex comprising the step of bringing into contact a product of any of claims 1 to 8 with a compound, a mixture or a library of compounds and determining whether the compound or a certain compound of the mixture or library binds to the product and/or effects the products biological activity and optionally further purifying the compound positively tested as effector.

In another embodiment, the present invention is directed to a method for screening for a molecule that binds a protein complex of the present invention comprising exposing said complex, or a cell or organism containing the complex

machinery, to one or more candidate molecules; and determining whether said complex is bound by any of said candidate molecules. Such screening assays can be carried out using cell-free and cell-based methods that are commonly known in the art in vitro, in vivo or ex vivo. For example, an isolated complex can be employed, or a cell can be contacted with the candidate molecule and the complex can be isolated from such contacted cells and the isolated complex can be assayed for activity or component composition. In another example, a cell containing the complex can be contacted with the candidate molecule and the levels of the complex in the contacted cell can be measured. Additionally, such assays can be carried out in cells recombinantly expressing a component protein from the fourth column of table 1, or a functionally active fragment or functionally active derivative thereof, and a component protein from fifth column of table 1, or a functionally active fragment or functionally active derivative thereof. Additionally, such assays can also be carried out in cells recombinantly expressing all component proteins from the group of proteins in the fifth column of table 1.

For example, assays can be carried out using recombinant cells expressing the protein components of a complex, to screen for molecules that bind to, or interfere with, or promote complex activity or formation. In preferred embodiments, polypeptide derivatives that have superior stabilities but retain the ability to form a complex (e.g., one or more component proteins modified to be resistant to proteolytic degradation in the binding assay buffers, or to be resistant to oxidative degradation), are used to screen for modulators of complex activity or formation. Such resistant molecules can be generated, e.g., by substitution of amino acids at proteolytic cleavage sites, the use of chemically derivatized amino acids at proteolytic susceptible sites, and the replacement of amino acid residues subject to oxidation, i.e. methionine and cysteine.

A particular aspect of the present invention relates to identifying molecules that inhibit or promote formation or degradation of a complex of the present invention, e.g., using the method described for isolating the complex and identifying members of the complex using the TAP assay described in Section 4, *infra*, and in WO 00/09716 and Rigaut et al., 1999, *Nature Biotechnol.* 17:1030-1032, which are each incorporated by reference in their entirety. TNRF1

In another embodiment of the invention, a modulator is identified by administering a candidate molecule to a transgenic non-human animal expressing the complex component proteins from promoters that are not the native promoters of the respective

proteins, more preferably where the candidate molecule is also recombinantly expressed in the transgenic non-human animal. Alternatively, the method for identifying such a modulator can be carried out in vitro, preferably with a purified complex, and a purified candidate molecule.

Agents/molecules (candidate molecules) to be screened can be provided as mixtures of a limited number of specified compounds, or as compound libraries, peptide libraries and the like. Agents/molecules to be screened may also include all forms of antisera, antisense nucleic acids, etc., that can modulate complex activity or formation. Exemplary candidate molecules and libraries for screening are set forth in Section 4.6.1, *infra*.

Screening the libraries can be accomplished by any of a variety of commonly known methods. See, e.g., the following references, which disclose screening of peptide libraries: Parmley and Smith, 1989, *Adv. Exp. Med. Biol.* 251:215-218; Scott and Smith, 1990, *Science* 249:386-390; Fowlkes et al., 1992, *BioTechniques* 13:422-427; Oldenburg et al., 1992, *Proc. Natl. Acad. Sci. USA* 89:5393-5397; Yu et al., 1994, *Cell* 76:933-945; Staudt et al., 1988, *Science* 241:577-580; Bock et al., 1992, *Nature* 355:564-566; Tuerk et al., 1992, *Proc. Natl. Acad. Sci. USA* 89:6988-6992; Ellington et al., 1992, *Nature* 355:850-852; U.S. Patent No. 5,096,815, U.S. Patent No. 5,223,409, and U.S. Patent No. 5,198,346, all to Ladner et al.; Rebar and Pabo, 1993, *Science* 263:671-673; and International Patent Publication No. WO 94/18318.

In a specific embodiment, screening can be carried out by contacting the library members with a complex immobilized on a solid phase, and harvesting those library members that bind to the protein (or encoding nucleic acid or derivative). Examples of such screening methods, termed "panning" techniques, are described by way of example in Parmley and Smith, 1988, *Gene* 73:305-318; Fowlkes et al., 1992, *BioTechniques* 13:422-427; International Patent Publication No. WO 94/18318; and in references cited hereinabove.

In a specific embodiment, fragments and/or analogs of protein components of a complex, especially peptidomimetics, are screened for activity as competitive or non-competitive inhibitors of complex formation (amount of complex or composition of complex) or activity in the cell, which thereby inhibit complex activity or formation in the cell.

In one embodiment, agents that modulate (i.e., antagonize or agonize) complex activity or formation can be screened for using a binding inhibition assay, wherein agents

are screened for their ability to modulate formation of a complex under aqueous, or physiological, binding conditions in which complex formation occurs in the absence of the agent to be tested. Agents that interfere with the formation of complexes of the invention are identified as antagonists of complex formation. Agents that promote the formation of complexes are identified as agonists of complex formation. Agents that completely block the formation of complexes are identified as inhibitors of complex formation.

Methods for screening may involve labeling the component proteins of the complex with radioligands (e.g., ^{125}I or ^3H), magnetic ligands (e.g., paramagnetic beads covalently attached to photobiotin acetate), fluorescent ligands (e.g., fluorescein or rhodamine), or enzyme ligands (e.g., luciferase or β -galactosidase). The reactants that bind in solution can then be isolated by one of many techniques known in the art, including but not restricted to, co-immunoprecipitation of the labeled complex moiety using antisera against the unlabeled binding partner (or labeled binding partner with a distinguishable marker from that used on the second labeled complex moiety), immunoaffinity chromatography, size exclusion chromatography, and gradient density centrifugation. In a preferred embodiment, the labeled binding partner is a small fragment or peptidomimetic that is not retained by a commercially available filter. Upon binding, the labeled species is then unable to pass through the filter, providing for a simple assay of complex formation.

Methods commonly known in the art are used to label at least one of the component members of the complex. Suitable labeling methods include, but are not limited to, radiolabeling by incorporation of radiolabeled amino acids, e.g., ^3H -leucine or ^{35}S -methionine, radiolabeling by post-translational iodination with ^{125}I or ^{131}I using the chloramine T method, Bolton-Hunter reagents, etc., or labeling with ^{32}P using phosphorylase and inorganic radiolabeled phosphorous, biotin labeling with photobiotin-acetate and sunlamp exposure, etc. In cases where one of the members of the complex is immobilized, e.g., as described *infra*, the free species is labeled. Where neither of the interacting species is immobilized, each can be labeled with a distinguishable marker such that isolation of both moieties can be followed to provide for more accurate quantification, and to distinguish the formation of homomeric from heteromeric complexes. Methods that utilize accessory proteins that bind to one of the modified interactants to improve the sensitivity of detection, increase the stability of the complex, etc., are provided.

Typical binding conditions are, for example, but not by way of limitation, in an aqueous salt solution of 10-250 mM NaCl, 5-50 mM Tris-HCl, pH 5-8, and 0.5% Triton X-100 or other detergent that improves specificity of interaction. Metal chelators and/or divalent cations may be added to improve binding and/or reduce proteolysis. Reaction temperatures may include 4, 10, 15, 22, 25, 35, or 42 degrees Celsius, and time of incubation is typically at least 15 seconds, but longer times are preferred to allow binding equilibrium to occur. Particular complexes can be assayed using routine protein binding assays to determine optimal binding conditions for reproducible binding.

The physical parameters of complex formation can be analyzed by quantification of complex formation using assay methods specific for the label used, e.g., liquid scintillation counting for radioactivity detection, enzyme activity for enzyme-labeled moieties, etc. The reaction results are then analyzed utilizing Scatchard analysis, Hill analysis, and other methods commonly known in the arts (see, e.g., *Proteins, Structures, and Molecular Principles*, 2nd Edition (1993) Creighton, Ed., W.H. Freeman and Company, New York).

In a second common approach to binding assays, one of the binding species is immobilized on a filter, in a microtiter plate well, in a test tube, to a chromatography matrix, etc., either covalently or non-covalently. Proteins can be covalently immobilized using any method well known in the art, for example, but not limited to the method of Kadonaga and Tjian, 1986, *Proc. Natl. Acad. Sci. USA* 83:5889-5893, i.e., linkage to a cyanogen-bromide derivatized substrate such as CNBr-Sepharose 4B (Pharmacia). Where needed, the use of spacers can reduce steric hindrance by the substrate. Non-covalent attachment of proteins to a substrate include, but are not limited to, attachment of a protein to a charged surface, binding with specific antibodies, binding to a third unrelated interacting protein, etc.

Assays of agents (including cell extracts or a library pool) for competition for binding of one member of a complex (or derivatives thereof) with another member of the complex labeled by any means (e.g., those means described above) are provided to screen for competitors or enhancers of complex formation.

In specific embodiments, blocking agents to inhibit non-specific binding of reagents to other protein components, or absorptive losses of reagents to plastics, immobilization matrices, etc., are included in the assay mixture. Blocking agents include, but are not restricted to bovine serum albumin, β -casein, nonfat dried milk, Denhardt's reagent, Ficoll, polyvinylpyrrolidone, nonionic detergents (NP40, Triton X-100, Tween 20,

Tween 80, etc.), ionic detergents (e.g., SDS, LDS, etc.), polyethylene glycol, etc. Appropriate blocking agent concentrations allow complex formation.

After binding is performed, unbound, labeled protein is removed in the supernatant, and the immobilized protein retaining any bound, labeled protein is washed extensively. The amount of bound label is then quantified using standard methods in the art to detect the label as described, *supra*.

In another specific embodiments screening for modulators of the protein complexes/protein as provided herein can be carried out by attaching those and/or the antibodies as provided herein to a solid carrier. In a further specific embodiment, the invention relates to an array of said molecules.

The preparation of such an array containing different types of proteins, including antibodies) is well known in the art and is apparent to a person skilled in the art (see e.g. Ekins et al., 1989, *J. Pharm. Biomed. Anal.* 7:155-168; Mitchell et al. 2002, *Nature Biotechnol.* 20:225-229; Petricoin et al., 2002, *Lancet* 359:572-577; Templin et al., 2001, *Trends Biotechnol.* 20:160-166; Wilson and Nock, 2001, *Curr. Opin. Chem. Biol.* 6:81-85; Lee et al., 2002 *Science* 295:1702-1705; MacBeath and Schreiber, 2000, *Science* 289:1760; Blawas and Reichert, 1998, *Biomaterials* 19:595; Kane et al., 1999, *Biomaterials* 20:2363; Chen et al., 1997, *Science* 276:1425; Vaugham et al., 1996, *Nature Biotechnol.* 14:309-314; Mahler et al., 1997, *Immunotechnology* 3:31-43; Roberts et al., 1999, *Curr. Opin. Chem. Biol.* 3:268-273; Nord et al., 1997, *Nature Biotechnol.* 15:772-777; Nord et al., 2001, *Eur. J. Biochem.* 268:4269-4277; Brody and Gold, 2000, *Rev. Mol. Biotechnol.* 74:5-13; Karlstroem and Nygren, 2001, *Anal. Biochem.* 295:22-30; Nelson et al., 2000, *Electrophoresis* 21:1155-1163; Honore et al., 2001, *Expert Rev. Mol. Diagn.* 3:265-274; Albala, 2001, *Expert Rev. Mol. Diagn.* 2:145-152, Figeys and Pinto, 2001, *Electrophoresis* 2:208-216 and references in the publications listed here).

Complexes can be attached to an array by different means as will be apparent to a person skilled in the art. Complexes can for example be added to the array via a TAP-tag (as described in WO/0009716 and in Rigaut et al., 1999, *Nature Biotechnol.* 10:1030-1032) after the purification step or by another suitable purification scheme as will be apparent to a person skilled in the art.

Optionally, the proteins of the complex can be cross-linked to enhance the stability of the complex. Different methods to cross-link proteins are well known in the art. Reactive end-groups of cross-linking agents include but are not limited to -COOH, -SH, -NH₂ or N-oxy-succinamate.

The spacer of the cross-linking agent should be chosen with respect to the size of the complex to be cross-linked. For small protein complexes, comprising only a few proteins, relatively short spacers are preferable in order to reduce the likelihood of cross-linking separate complexes in the reaction mixture. For larger protein complexes, additional use of larger spacers is preferable in order to facilitate cross-linking between proteins within the complex.

It is preferable to check the success-rate of cross-linking before linking the complex to the carrier.

As will be apparent to a person skilled in the art, the optimal rate of cross-linking need to be determined on a case by case basis. This can be achieved by methods well known in the art, some of which are exemplary described below.

A sufficient rate of cross-linking can be checked f.e. by analysing the cross-linked complex vs. a non-cross-linked complex on a denaturing protein gel.

If cross-linking has been performed successfully, the proteins of the complex are expected to be found in the same lane, whereas the proteins of the non-cross-linked complex are expected to be separated according to their individual characteristics. Optionally the presence of all proteins of the complex can be further checked by peptide-sequencing of proteins in the respective bands using methods well known in the art such as mass spectrometry and/or Edman degradation.

In addition, a rate of crosslinking which is too high should also be avoided. If cross-linking has been carried out too extensively, there will be an increasing amount of cross-linking of the individual protein complex, which potentially interferes with a screening for potential binding partners and/or modulators etc. using the arrays.

The presence of such structures can be determined by methods well known in the art and include e.g. gel-filtration experiments comparing the gel filtration profile solutions containing cross-linked complexes vs. uncross-linked complexes.

Optionally, functional assays as will be apparent to a person skilled in the art, some of which are exemplarily provided herein, can be performed to check the integrity of the complex.

Alternatively, members of the protein complex can be expressed as a single fusion protein and coupled to the matrix as will be apparent to a person skilled in the art.

Optionally, the attachment of the complex or proteins or antibody as outlined above can be further monitored by various methods apparent to a person skilled in the art. Those include, but are not limited to surface plasmon resonance (see e.g. McDonnel, 2001, *Curr. Opin. Chem. Biol.* 5:572-577; Lee, 2001, *Trends Biotechnol.* 19:217-222; Weinberger et al., 2000, 1:395-416; Pearson et al., 2000, *Ann. Clin. Biochem.* 37:119-145; Vely et al., 2000, *Methods Mol. Biol.* 121:313-321; Slepak, 2000, *J. Mol. Recognit.* 13:20-26.

Exemplary assays useful for measuring transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Fe65-complex include but are not limited to those described in Cao X et al., 2001, *Science*, 293:115-20.

Exemplary assays useful for measuring the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Fe65-complex include but are not limited to those described in Vassar R et al., 1999, *Science*, 286:735-41.

Exemplary assays useful for measuring the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Fe65-complex include but are not limited to those described in Yan R et al., 1999, *Nature*, 402:533-7.

Exemplary assays useful for measuring the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting of the Fe65-complex include but are not limited to those described in Tian Gaochao et al., 2002, *J Biol Chem*, 277:31499-505.

Exemplary assays useful for measuring the transactivation of reporter genes by APP-Gal4/VP16 (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the X11b-complex include but are not limited to those described in Biederer Thomas et al., 2002, *J Neurosci*, 22:7340-51.

Exemplary assays useful for measuring the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the X11b-complex include but are not limited to those described in Vassar R et al., 1999, *Science*, 286:735-41.

Exemplary assays useful for measuring the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the X11b-complex include but are not limited to those described in Yan R et al., 1999, *Nature*, 402:533-7.

Exemplary assays useful for measuring the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the X11b-complex include but are not limited to those described in Tian Gaochao et al., 2002, *J Biol Chem*, 277:31499-505.

Exemplary assays useful for measuring the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the PSEN2 -complex include but are not limited to those described in Vassar R et al., 1999, *Science*, 286:735-41.

Exemplary assays useful for measuring the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the PSEN2 -complex include but are not limited to those described in Yan R et al., 1999, *Nature*, 402:533-7.

Exemplary assays useful for measuring the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting of the PSEN2 -complex include but are not limited to those described in Tian Gaochao et al., 2002, *J Biol Chem*, 277:31499-505.

Exemplary assays useful for measuring transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the

PSEN2 -complex include but are not limited to those described in Cao X et al., 2001, Science, 293:115-20.

Exemplary assays useful for measuring the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Nicastrin-complex include but are not limited to those described in Vassar R et al., 1999, Science, 286:735-41.

Exemplary assays useful for measuring the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Nicastrin-complex include but are not limited to those described in Yan R et al., 1999, Nature, 402:533-7.

Exemplary assays useful for measuring the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting of the Nicastrin-complex include but are not limited to those described in Tian Gaochao et al., 2002, J Biol Chem, 277:31499-505.

Exemplary assays useful for measuring transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Nicastrin-complex include but are not limited to those described in Cao X et al., 2001, Science, 293:115-20.

Exemplary assays useful for measuring the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Aph-1a-complex include but are not limited to those described in Vassar R et al., 1999, Science, 286:735-41.

Exemplary assays useful for measuring the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Aph-1a-complex include but are not limited to those described in Yan R et al., 1999, Nature, 402:533-7.

Exemplary assays useful for measuring the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the

expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting of the Aph-1a-complex include but are not limited to those described in Tian Gaochao et al., 2002, J Biol Chem, 277:31499-505.

Exemplary assays useful for measuring transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Aph-1a-complex include but are not limited to those described in Cao X et al., 2001, Science, 293:115-20.

Exemplary assays useful for measuring the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Pen-2-complex include but are not limited to those described in Vassar R et al., 1999, Science, 286:735-41.

Exemplary assays useful for measuring the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Pen-2-complex include but are not limited to those described in Yan R et al., 1999, Nature, 402:533-7.

Exemplary assays useful for measuring the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting of the Pen-2-complex include but are not limited to those described in Tian Gaochao et al., 2002, J Biol Chem, 277:31499-505.

Exemplary assays useful for measuring transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Pen-2-complex include but are not limited to those described in Cao X et al., 2001, Science, 293:115-20.

Exemplary assays useful for measuring the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the APP695SW-complex include but are not limited to those described in Vassar R et al., 1999, Science, 286:735-41.

Exemplary assays useful for measuring the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the APP695SW-complex include but are not limited to those described in Yan R et al., 1999, *Nature*, 402:533-7.

Exemplary assays useful for measuring the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting of the APP695SW-complex include but are not limited to those described in Tian Gaochao et al., 2002, *J Biol Chem*, 277:31499-505.

Exemplary assays useful for measuring transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the APP695SW-complex include but are not limited to those described in Cao X et al., 2001, *Science*, 293:115-20.

Exemplary assays useful for measuring the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the APP-C99 -complex include but are not limited to those described in Vassar R et al., 1999, *Science*, 286:735-41.

Exemplary assays useful for measuring the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the APP-C99 -complex include but are not limited to those described in Yan R et al., 1999, *Nature*, 402:533-7.

Exemplary assays useful for measuring the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting of the APP-C99 -complex include but are not limited to those described in Tian Gaochao et al., 2002, *J Biol Chem*, 277:31499-505.

Exemplary assays useful for measuring transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the APP-

C99 -complex include but are not limited to those described in Cao X et al., 2001, Science, 293:115-20.

Exemplary assays useful for measuring the phosphorylation of tau proteins in vitro or in cells (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Tau-complex include but are not limited to those described in Drewes G et al., 1997, Cell, 89:297-308.

Exemplary assays useful for measuring the aggregation of tau proteins into filaments or tangles in vitro or in cells (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Tau-complex include but are not limited to those described in Barghorn S et al., 2000, Biochemistry, 39:11714-21.

4.6.1 CANDIDATE MOLECULES

Any molecule known in the art can be tested for its ability to modulate (increase or decrease) the amount of, activity of, or protein component composition of a complex of the present invention as detected by a change in the amount of, activity of, or protein component composition of, said complex. By way of example, a change in the amount of the complex can be detected by detecting a change in the amount of the complex that can be isolated from a cell expressing the complex machinery. For identifying a molecule that modulates complex activity, candidate molecules can be directly provided to a cell expressing the complex machinery, or, in the case of candidate proteins, can be provided by providing their encoding nucleic acids under conditions in which the nucleic acids are recombinantly expressed to produce the candidate proteins within the cell expressing the complex machinery, the complex is then isolated from the cell and the isolated complex is assayed for activity using methods well known in the art, not limited to those described, supra.

This embodiment of the invention is well suited to screen chemical libraries for molecules which modulate, e.g., inhibit, antagonize, or agonize, the amount of, activity of, or protein component composition of the complex. The chemical libraries can be peptide libraries, peptidomimetic libraries, chemically synthesized libraries, recombinant,

e.g., phage display libraries, and in vitro translation-based libraries, other non-peptide synthetic organic libraries, etc.

Exemplary libraries are commercially available from several sources (ArQule, Tripos/PanLabs, ChemDesign, Pharmacopoeia). In some cases, these chemical libraries are generated using combinatorial strategies that encode the identity of each member of the library on a substrate to which the member compound is attached, thus allowing direct and immediate identification of a molecule that is an effective modulator. Thus, in many combinatorial approaches, the position on a plate of a compound specifies that compound's composition. Also, in one example, a single plate position may have from 1-20 chemicals that can be screened by administration to a well containing the interactions of interest. Thus, if modulation is detected, smaller and smaller pools of interacting pairs can be assayed for the modulation activity. By such methods, many candidate molecules can be screened.

Many diversity libraries suitable for use are known in the art and can be used to provide compounds to be tested according to the present invention. Alternatively, libraries can be constructed using standard methods. Chemical (synthetic) libraries, recombinant expression libraries, or polysome-based libraries are exemplary types of libraries that can be used.

The libraries can be constrained or semirigid (having some degree of structural rigidity), or linear or nonconstrained. The library can be a cDNA or genomic expression library, random peptide expression library or a chemically synthesized random peptide library, or non-peptide library. Expression libraries are introduced into the cells in which the assay occurs, where the nucleic acids of the library are expressed to produce their encoded proteins.

In one embodiment, peptide libraries that can be used in the present invention may be libraries that are chemically synthesized in vitro. Examples of such libraries are given in Houghten et al., 1991, *Nature* 354:84-86, which describes mixtures of free hexapeptides in which the first and second residues in each peptide were individually and specifically defined; Lam et al., 1991, *Nature* 354:82-84, which describes a "one bead, one peptide" approach in which a solid phase split synthesis scheme produced a library of peptides in which each bead in the collection had immobilized thereon a single, random sequence of amino acid residues; Medynski, 1994, *Bio/Technology* 12:709-710, which describes split synthesis and T-bag synthesis methods; and Gallop et al., 1994, *J. Med. Chem.* 37:1233-1251. Simply by way of other examples, a combinatorial library

may be prepared for use, according to the methods of Ohlmeyer et al., 1993, Proc. Natl. Acad. Sci. USA 90:10922-10926; Erb et al., 1994, Proc. Natl. Acad. Sci. USA 91:11422-11426; Houghten et al., 1992, Biotechniques 13:412; Jayawickreme et al., 1994, Proc. Natl. Acad. Sci. USA 91:1614-1618; or Salmon et al., 1993, Proc. Natl. Acad. Sci. USA 90:11708-11712. PCT Publication No. WO 93/20242 and Brenner and Lerner, 1992, Proc. Natl. Acad. Sci. USA 89:5381-5383 describe "encoded combinatorial chemical libraries," that contain oligonucleotide identifiers for each chemical polymer library member.

In a preferred embodiment, the library screened is a biological expression library that is a random peptide phage display library, where the random peptides are constrained (e.g., by virtue of having disulfide bonding).

Further, more general, structurally constrained, organic diversity (e.g., nonpeptide) libraries, can also be used. By way of example, a benzodiazepine library (see e.g., Bunin et al., 1994, Proc. Natl. Acad. Sci. USA 91:4708-4712) may be used.

Conformationally constrained libraries that can be used include but are not limited to those containing invariant cysteine residues which, in an oxidizing environment, cross-link by disulfide bonds to form cystines, modified peptides (e.g., incorporating fluorine, metals, isotopic labels, are phosphorylated, etc.), peptides containing one or more non-naturally occurring amino acids, non-peptide structures, and peptides containing a significant fraction of γ -carboxyglutamic acid.

Libraries of non-peptides, e.g., peptide derivatives (for example, that contain one or more non-naturally occurring amino acids) can also be used. One example of these are peptoid libraries (Simon et al., 1992, Proc. Natl. Acad. Sci. USA 89:9367-9371). Peptoids are polymers of non-natural amino acids that have naturally occurring side chains attached not to the α carbon but to the backbone amino nitrogen. Since peptoids are not easily degraded by human digestive enzymes, they are advantageously more easily adaptable to drug use. Another example of a library that can be used, in which the amide functionalities in peptides have been permethylated to generate a chemically transformed combinatorial library, is described by Ostresh et al., 1994, Proc. Natl. Acad. Sci. USA 91:11138-11142).

The members of the peptide libraries that can be screened according to the invention are not limited to containing the 20 naturally occurring amino acids. In particular, chemically synthesized libraries and polysome based libraries allow the use of amino acids in addition to the 20 naturally occurring amino acids (by their inclusion in the

precursor pool of amino acids used in library production). In specific embodiments, the library members contain one or more non-natural or non-classical amino acids or cyclic peptides. Non-classical amino acids include but are not limited to the D-isomers of the common amino acids, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid; γ -Abu, γ -Ahx, 6-amino hexanoic acid; Aib, 2-amino isobutyric acid; 3-amino propionic acid; ornithine; norleucine; norvaline, hydroxyproline, sarcosine, citrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, designer amino acids such as β -methyl amino acids, C-methyl amino acids, N-methyl amino acids, fluoro-amino acids and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

In a specific embodiment, fragments and/or analogs of complexes of the invention, or protein components thereof, especially peptidomimetics, are screened for activity as competitive or non-competitive inhibitors of complex activity or formation.

In another embodiment of the present invention, combinatorial chemistry can be used to identify modulators of a the complexes. Combinatorial chemistry is capable of creating libraries containing hundreds of thousands of compounds, many of which may be structurally similar. While high throughput screening programs are capable of screening these vast libraries for affinity for known targets, new approaches have been developed that achieve libraries of smaller dimension but which provide maximum chemical diversity. (See e.g., Matter, 1997, J. Med. Chem. 40:1219-1229).

One method of combinatorial chemistry, affinity fingerprinting, has previously been used to test a discrete library of small molecules for binding affinities for a defined panel of proteins. The fingerprints obtained by the screen are used to predict the affinity of the individual library members for other proteins or receptors of interest (in the instant invention, the protein complexes of the present invention and protein components thereof.) The fingerprints are compared with fingerprints obtained from other compounds known to react with the protein of interest to predict whether the library compound might similarly react. For example, rather than testing every ligand in a large library for interaction with a complex or protein component, only those ligands having a fingerprint similar to other compounds known to have that activity could be tested. (See, e.g., Kauvar et al., 1995, Chem. Biol. 2:107-118; Kauvar, 1995, Affinity fingerprinting, Pharmaceutical Manufacturing International. 8:25-28; and Kauvar, Toxic-Chemical Detection by Pattern Recognition in New Frontiers in Agrochemical Immunoassay, Kurtz, Stanker and Skerritt (eds), 1995, AOAC: Washington, D.C., 305-312).

Kay et al. (1993, Gene 128:59-65) disclosed a method of constructing peptide libraries that encode peptides of totally random sequence that are longer than those of any prior conventional libraries. The libraries disclosed in Kay et al. encode totally synthetic random peptides of greater than about 20 amino acids in length. Such libraries can be advantageously screened to identify complex modulators. (See also U.S. Patent No. 5,498,538 dated March 12, 1996; and PCT Publication No. WO 94/18318 dated August 18, 1994).

A comprehensive review of various types of peptide libraries can be found in Gallop et al., 1994, J. Med. Chem. 37:1233-1251.

4.7 PHARMACEUTICAL COMPOSITIONS AND THERAPEUTIC/PROPHYLACTIC ADMINISTRATION

The invention provides methods of treatment (and prophylaxis) by administration to a subject of an effective amount of a therapeutic of the invention. In a preferred aspect, the therapeutic is substantially purified. The subject is preferably an animal including, but not limited to animals such as cows, pigs, horses, chickens, cats, dogs, etc., and is preferably a mammal, and most preferably human. In a specific embodiment, a non-human mammal is the subject.

Various delivery systems are known and can be used to administer a therapeutic of the invention, e.g., encapsulation in liposomes, microparticles, and microcapsules; use of recombinant cells capable of expressing the therapeutic, use of receptor-mediated endocytosis (e.g., Wu and Wu, 1987, J. Biol. Chem. 262:4429-4432); construction of a therapeutic nucleic acid as part of a retroviral or other vector, etc. Methods of introduction include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The compounds may be administered by any convenient route, for example by infusion, by bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral, rectal and intestinal mucosa, etc.), and may be administered together with other biologically active agents. Administration can be systemic or local. In addition, it may be desirable to introduce the pharmaceutical compositions of the invention into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir,

such as an Ommaya reservoir. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compositions of the invention locally to the area in need of treatment. This may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. In one embodiment, administration can be by direct injection at the site (or former site) of a malignant tumor or neoplastic or pre-neoplastic tissue.

In another embodiment, the therapeutic can be delivered in a vesicle, in particular a liposome (Langer, 1990, *Science* 249:1527-1533; Treat et al., 1989, In: *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler, eds., Liss, New York, pp. 353-365; Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*)

In yet another embodiment, the therapeutic can be delivered via a controlled release system. In one embodiment, a pump may be used (Langer, *supra*; Sefton, 1987, *CRC Crit. Ref. Biomed. Eng.* 14:201-240; Buchwald et al., 1980, *Surgery* 88:507-516; Saudek et al., 1989, *N. Engl. J. Med.* 321:574-579). In another embodiment, polymeric materials can be used (*Medical Applications of Controlled Release*, Langer and Wise, eds., CRC Press, Boca Raton, Florida, 1974; *Controlled Drug Bioavailability, Drug Product Design and Performance*, Smolen and Ball, eds., Wiley, New York, 1984; Ranger and Peppas, 1983, *Macromol. Sci. Rev. Macromol. Chem.* 23:61; Levy et al., 1985, *Science* 228:190-192; During et al., 1989, *Ann. Neurol.* 25:351-356; Howard et al., 1989, *J. Neurosurg.* 71:858-863). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, i.e., the brain, thus requiring only a fraction of the systemic dose (e.g., Goodson, 1984, In: *Medical Applications of Controlled Release*, *supra*, Vol. 2, pp. 115-138). Other controlled release systems are discussed in the review by Langer (1990, *Science* 249:1527-1533).

In a specific embodiment where the therapeutic is a nucleic acid encoding a protein therapeutic, the nucleic acid can be administered in vivo to promote expression of its encoded protein, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by use of a retroviral vector (U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle

bombardment (e.g., a gene gun; Biolistic, Dupont), or by coating it with lipids, cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (e.g., Joliot et al., 1991, Proc. Natl. Acad. Sci. USA 88:1864-1868), etc. Alternatively, a nucleic acid therapeutic can be introduced intracellularly and incorporated by homologous recombination within host cell DNA for expression.

The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of a therapeutic, and a pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly, in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, including but not limited to peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered orally. Saline and aqueous dextrose are preferred carriers when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions are preferably employed as liquid carriers for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsions, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the therapeutic, preferably in purified form, together with a suitable amount of carrier so as to provide the form for

proper administration to the patient. The formulation should suit the mode of administration.

In a preferred embodiment, the composition is formulated, in accordance with routine procedures, as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lidocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water-free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water or saline for injection can be provided so that the ingredients may be mixed prior to administration.

The therapeutics of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free carboxyl groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., those formed with free amine groups such as those derived from isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc., and those derived from sodium, potassium, ammonium, calcium, and ferric hydroxides, etc.

The amount of the therapeutic of the invention which will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. However, suitable dosage ranges for intravenous administration are generally about 20-500 micrograms of active compound per kilogram body weight. Suitable dosage ranges for intranasal administration are generally about 0.01 pg/kg body weight to 1 mg/kg body weight. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

Suppositories generally contain active ingredient in the range of 0.5% to 10% by weight; oral formulations preferably contain 10% to 95% active ingredient.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. For example, the kit can comprise in one or more containers a first protein, or a functionally active fragment or functionally active derivative thereof, which first protein is selected from the group consisting of proteins listed in the fourth column of table 1; and a second protein, or a functionally active fragment or functionally active derivative thereof, which second protein is selected from the group consisting of proteins listed in the fifth column of table 1.

Alternatively, the kit can comprise in one or more containers, all proteins, functionally active fragments or functionally active derivatives thereof of from the group of proteins in the sixth column of table 1.

The kits of the present invention can also contain expression vectors encoding the essential components of the complex machinery, which components after being expressed can be reconstituted in order to form a biologically active complex. Such a kit preferably also contains the required buffers and reagents. Optionally associated with such container(s) can be instructions for use of the kit and/or a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

4.8 ANIMAL MODELS

The present invention also provides animal models. In one embodiment, animal models for diseases and disorders involving the protein complexes of the present invention are provided. These animal models are well known in the art. These animal models include,

but are not limited to those which are listed in the section 4.6 (supra) as exemplary animal models to study any of the complexes provided in the invention. Such animals can be initially produced by promoting homologous recombination or insertional mutagenesis between genes encoding the protein components of the complexes in the chromosome, and exogenous genes encoding the protein components of the complexes that have been rendered biologically inactive or deleted (preferably by insertion of a heterologous sequence, e.g., an antibiotic resistance gene). In a preferred aspect, homologous recombination is carried out by transforming embryo-derived stem (ES) cells with one or more vectors containing one or more insertionally inactivated genes, such that homologous recombination occurs, followed by injecting the transformed ES cells into a blastocyst, and implanting the blastocyst into a foster mother, followed by the birth of the chimeric animal ("knockout animal") in which a gene encoding a component protein from the fourth column of table 1, or a functionally active fragment or functionally active derivative thereof, and a gene encoding a component protein from the fifth column of table 1, or a functionally active fragment or functionally active derivative thereof, has been inactivated or deleted (Capecchi, 1989, Science 244:1288-1292).

In another preferred aspect, homologous recombination is carried out by transforming embryo-derived stem (ES) cells with one or more vectors containing one or more insertionally inactivated genes, such that homologous recombination occurs, followed by injecting the transformed ES cells into a blastocyst, and implanting the blastocyst into a foster mother, followed by the birth of the chimeric animal ("knockout animal") in which the genes of all component proteins from the group of proteins listed in the fourth column of table 1 or of all proteins from the group of proteins listed in the fifth column of table 1 have been inactivated or deleted.

The chimeric animal can be bred to produce additional knockout animals. Such animals can be mice, hamsters, sheep, pigs, cattle, etc., and are preferably non-human mammals. In a specific embodiment, a knockout mouse is produced.

Such knockout animals are expected to develop, or be predisposed to developing, diseases or disorders associated with mutations involving the protein complexes of the present invention, and thus, can have use as animal models of such diseases and disorders, e.g., to screen for or test molecules (e.g., potential therapeutics) for such diseases and disorders.

In a different embodiment of the invention, transgenic animals that have incorporated and express (or over-express or mis-express) a functional gene encoding a

protein component of the complex, e.g. by introducing the a gene encoding one or more of the components of the complex under the control of a heterologous promoter (i.e., a promoter that is not the native promoter of the gene) that either over-expresses the protein or proteins, or expresses them in tissues not normally expressing the complexes or proteins, can have use as animal models of diseases and disorders characterized by elevated levels of the protein complexes. Such animals can be used to screen or test molecules for the ability to treat or prevent the diseases and disorders cited supra.

In one embodiment, the present invention provides a recombinant non-human animal in which an endogenous gene encoding a first protein, or a functionally active fragment or functionally active derivative thereof, which first protein is selected from the group of proteins listed in the fourth column of table 1, and an endogenous gene encoding a second protein, or a functionally active fragment or functionally active derivative thereof, which second protein is selected from the group consisting of proteins listed in the fifth column of table 1 has been deleted or inactivated by homologous recombination or insertional mutagenesis of said animal or an ancestor thereof. In addition, the present invention provides a recombinant non-human animal in which the endogenous genes of all proteins, or functionally active fragments or functionally active derivatives thereof of one of the group of proteins listed in the sixth column have been deleted or inactivated by homologous recombination or insertional mutagenesis of said animal or an ancestor thereof:

In another embodiment, the present invention provides a recombinant non-human animal in which an endogenous gene encoding a first protein, or a functionally active fragment or functionally active derivative thereof, which first protein is selected from the group consisting of proteins of the fourth column of table 1, and an endogenous gene encoding a second protein, or a functionally active fragment or functionally active derivative thereof, which second protein is selected from the group consisting of proteins of the fifth column, of table 1 are recombinantly expressed in said animal or an ancestor thereof.

The following series of examples are presented by way of illustration and not by way of limitation on the scope of the invention.

EXAMPLES

An object of the present invention was to identify protein complexes of the APP processing pathway, component proteins of the said complexes, fragments and derivatives of the component proteins, and antibodies specific to the complexes. The present invention also relates to methods for use of the complexes of the APP processing pathway and their interacting proteins in, inter alia, screening, diagnosis, and therapy, as well as to methods of preparing the complexes.

By applying the process according to the invention said complexes were identified. The components are listed in table 1.

Those complexes are, as called herein, the following complexes:

Aph1a-complex, APP-695SW-complex, APP-C99-complex, Fe65-complex, Nicastrin-complex, Psen-2-complex, Pen2-complex, Tau-complex, X11 β -complex

Thus, the invention relates to the following embodiments:

The present invention relates to the Fe65-complex

1. A protein complex selected from complex (I) and comprising

(a) at least one first protein selected from the group consisting of:

- (i) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions,
- (ii) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,
- (iii) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iv) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,

- (v) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,
 - (vi) "RNB6" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RNB6" encoded by a nucleic acid that hybridizes to the "RNB6" nucleic acid or its complement under low stringency conditions, and
 - (vii) "Transcription factor CP2" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Transcription factor CP2" encoded by a nucleic acid that hybridizes to the "Transcription factor CP2" nucleic acid or its complement under low stringency conditions, and
- (b) at least one second protein, which second protein is selected from the group consisting of:
- (i) "14-3-3 protein epsilon" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein epsilon" encoded by a nucleic acid that hybridizes to the "14-3-3 protein epsilon" nucleic acid or its complement under low stringency conditions,
 - (ii) "14-3-3 protein beta/alpha" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein beta/alpha" encoded by a nucleic acid that hybridizes to the "14-3-3 protein beta/alpha" nucleic acid or its complement under low stringency conditions,
 - (iii) "14-3-3 protein eta" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein eta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein eta" nucleic acid or its complement under low stringency conditions,
 - (iv) "14-3-3 protein gamma" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein gamma" encoded by a nucleic acid that hybridizes to the "14-3-3 protein gamma" nucleic acid or its complement under low stringency conditions,
 - (v) "14-3-3 protein tau" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein tau" encoded by a nucleic acid that hybridizes to the "14-3-3 protein tau" nucleic acid or its complement under low stringency conditions,

- (vi) "14-3-3 protein zeta/delta" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein zeta/delta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein zeta/delta" nucleic acid or its complement under low stringency conditions,
- (vii) "ATP-binding cassette, sub-family B, member 7" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family B, member 7" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family B, member 7" nucleic acid or its complement under low stringency conditions,
- (viii) "ECP-51" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECP-51" encoded by a nucleic acid that hybridizes to the "ECP-51" nucleic acid or its complement under low stringency conditions,
- (ix) "GAP-associated tyrosine phosphoprotein p62" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GAP-associated tyrosine phosphoprotein p62" encoded by a nucleic acid that hybridizes to the "GAP-associated tyrosine phosphoprotein p62" nucleic acid or its complement under low stringency conditions,
- (x) "IPI00104084.1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IPI00104084.1" encoded by a nucleic acid that hybridizes to the "IPI00104084.1" nucleic acid or its complement under low stringency conditions,
- (xi) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,
- (xii) "Krab box protein ensp00000302970" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Krab box protein ensp00000302970" encoded by a nucleic acid that hybridizes to the "Krab box protein ensp00000302970" nucleic acid or its complement under low stringency conditions,
- (xiii) "PDZ domain protein MAGI-3" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"PDZ domain protein MAGI-3" encoded by a nucleic acid that hybridizes to the "PDZ domain protein MAGI-3" nucleic acid or its complement under low stringency conditions,

(xiv) "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" nucleic acid or its complement under low stringency conditions,

(xv) "Protein similar to probable mitotic centromere associated kinesin" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to probable mitotic centromere associated kinesin" encoded by a nucleic acid that hybridizes to the "Protein similar to probable mitotic centromere associated kinesin" nucleic acid or its complement under low stringency conditions,

(xvi) "SAP-62" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SAP-62" encoded by a nucleic acid that hybridizes to the "SAP-62" nucleic acid or its complement under low stringency conditions, and

(xvii) "Zinc finger protein 277" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 277" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 277" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein Fe65 (SEQ ID NO. 13), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'Fe65' encoded by a nucleic acid that hybridizes to the 'Fe65' under low stringency conditions.

3. The protein complex according to No. 1 selected from complex (I) and comprising the following proteins:

(i) "14-3-3 protein epsilon" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein epsilon" encoded by a nucleic acid that hybridizes to the "14-3-3 protein epsilon" nucleic acid or its complement under low stringency conditions,

(ii) "14-3-3 protein beta/alpha" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein beta/alpha" encoded by a nucleic acid that hybridizes to the "14-3-3 protein beta/alpha" nucleic acid or its complement under low stringency conditions,

(iii) "14-3-3 protein eta" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein eta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein eta" nucleic acid or its complement under low stringency conditions,

(iv) "14-3-3 protein gamma" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein gamma" encoded by a nucleic acid that hybridizes to the "14-3-3 protein gamma" nucleic acid or its complement under low stringency conditions,

(v) "14-3-3 protein tau" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein tau" encoded by a nucleic acid that hybridizes to the "14-3-3 protein tau" nucleic acid or its complement under low stringency conditions,

(vi) "14-3-3 protein zeta/delta" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein zeta/delta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein zeta/delta" nucleic acid or its complement under low stringency conditions,

(vii) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions,

(viii) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,

- (ix) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (x) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,
- (xi) "ATP-binding cassette, sub-family B, member 7" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family B, member 7" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family B, member 7" nucleic acid or its complement under low stringency conditions,
- (xii) "ECP-51" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECP-51" encoded by a nucleic acid that hybridizes to the "ECP-51" nucleic acid or its complement under low stringency conditions,
- (xiii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,
- (xiv) "GAP-associated tyrosine phosphoprotein p62" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GAP-associated tyrosine phosphoprotein p62" encoded by a nucleic acid that hybridizes to the "GAP-associated tyrosine phosphoprotein p62" nucleic acid or its complement under low stringency conditions,
- (xv) "IPI00104084.1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IPI00104084.1" encoded by a nucleic acid that hybridizes to the "IPI00104084.1" nucleic acid or its complement under low stringency conditions,
- (xvi) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that

hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,

(xvii) "Krab box protein ensp00000302970" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Krab box protein ensp00000302970" encoded by a nucleic acid that hybridizes to the "Krab box protein ensp00000302970" nucleic acid or its complement under low stringency conditions,

(xviii) "PDZ domain protein MAGI-3" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ domain protein MAGI-3" encoded by a nucleic acid that hybridizes to the "PDZ domain protein MAGI-3" nucleic acid or its complement under low stringency conditions,

(xix) "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" nucleic acid or its complement under low stringency conditions,

(xx) "Protein similar to probable mitotic centromere associated kinesin" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to probable mitotic centromere associated kinesin" encoded by a nucleic acid that hybridizes to the "Protein similar to probable mitotic centromere associated kinesin" nucleic acid or its complement under low stringency conditions,

(xxi) "RNB6" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RNB6" encoded by a nucleic acid that hybridizes to the "RNB6" nucleic acid or its complement under low stringency conditions,

(xxii) "SAP-62" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SAP-62" encoded by a nucleic acid that hybridizes to the "SAP-62" nucleic acid or its complement under low stringency conditions,

(xxiii) "Transcription factor CP2" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Transcription factor CP2" encoded by a nucleic acid that hybridizes to the "Transcription factor CP2" nucleic acid or its complement under low stringency conditions, and/or

- (xxiv) "Zinc finger protein 277" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 277" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 277" nucleic acid or its complement under low stringency conditions,
- and a protein complex selected from complex (II) and comprising the following proteins:
- (i) "14-3-3 protein epsilon" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein epsilon" encoded by a nucleic acid that hybridizes to the "14-3-3 protein epsilon" nucleic acid or its complement under low stringency conditions,
 - (ii) "14-3-3 protein beta/alpha" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein beta/alpha" encoded by a nucleic acid that hybridizes to the "14-3-3 protein beta/alpha" nucleic acid or its complement under low stringency conditions,
 - (iii) "14-3-3 protein eta" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein eta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein eta" nucleic acid or its complement under low stringency conditions,
 - (iv) "14-3-3 protein gamma" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein gamma" encoded by a nucleic acid that hybridizes to the "14-3-3 protein gamma" nucleic acid or its complement under low stringency conditions,
 - (v) "14-3-3 protein tau" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein tau" encoded by a nucleic acid that hybridizes to the "14-3-3 protein tau" nucleic acid or its complement under low stringency conditions,
 - (vi) "14-3-3 protein zeta/delta" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein zeta/delta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein zeta/delta" nucleic acid or its complement under low stringency conditions,
 - (vii) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions,

- (viii) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,
- (ix) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (x) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,
- (xi) "ATP-binding cassette, sub-family B, member 7" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family B, member 7" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family B, member 7" nucleic acid or its complement under low stringency conditions,
- (xii) "ECP-51" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECP-51" encoded by a nucleic acid that hybridizes to the "ECP-51" nucleic acid or its complement under low stringency conditions,
- (xiii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,
- (xiv) "GAP-associated tyrosine phosphoprotein p62" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GAP-associated tyrosine phosphoprotein p62" encoded by a nucleic acid that hybridizes to the "GAP-associated tyrosine phosphoprotein p62" nucleic acid or its complement under low stringency conditions,
- (xv) "IPI00104084.1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IPI00104084.1" encoded by a nucleic acid that hybridizes to the "IPI00104084.1" nucleic acid or its complement under low stringency conditions,

- (xvi) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,
- (xvii) "Krab box protein ensp00000302970" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Krab box protein ensp00000302970" encoded by a nucleic acid that hybridizes to the "Krab box protein ensp00000302970" nucleic acid or its complement under low stringency conditions,
- (xviii) "PDZ domain protein MAGI-3" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ domain protein MAGI-3" encoded by a nucleic acid that hybridizes to the "PDZ domain protein MAGI-3" nucleic acid or its complement under low stringency conditions,
- (xix) "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" nucleic acid or its complement under low stringency conditions,
- (xx) "Protein similar to probable mitotic centromere associated kinesin" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to probable mitotic centromere associated kinesin" encoded by a nucleic acid that hybridizes to the "Protein similar to probable mitotic centromere associated kinesin" nucleic acid or its complement under low stringency conditions,
- (xxi) "SAP-62" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SAP-62" encoded by a nucleic acid that hybridizes to the "SAP-62" nucleic acid or its complement under low stringency conditions, and/or
- (xxii) "Zinc finger protein 277" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 277" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 277" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 16 of the following proteins:

- (i) "14-3-3 protein epsilon" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein epsilon" encoded by a nucleic acid that hybridizes to the "14-3-3 protein epsilon" nucleic acid or its complement under low stringency conditions,
- (ii) "14-3-3 protein beta/alpha" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein beta/alpha" encoded by a nucleic acid that hybridizes to the "14-3-3 protein beta/alpha" nucleic acid or its complement under low stringency conditions,
- (iii) "14-3-3 protein eta" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein eta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein eta" nucleic acid or its complement under low stringency conditions,
- (iv) "14-3-3 protein gamma" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein gamma" encoded by a nucleic acid that hybridizes to the "14-3-3 protein gamma" nucleic acid or its complement under low stringency conditions,
- (v) "14-3-3 protein tau" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein tau" encoded by a nucleic acid that hybridizes to the "14-3-3 protein tau" nucleic acid or its complement under low stringency conditions,
- (vi) "14-3-3 protein zeta/delta" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein zeta/delta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein zeta/delta" nucleic acid or its complement under low stringency conditions,
- (vii) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions,
- (viii) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,

- (ix) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (x) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,
- (xi) "ATP-binding cassette, sub-family B, member 7" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family B, member 7" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family B, member 7" nucleic acid or its complement under low stringency conditions,
- (xii) "ECP-51" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECP-51" encoded by a nucleic acid that hybridizes to the "ECP-51" nucleic acid or its complement under low stringency conditions,
- (xiii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,
- (xiv) "GAP-associated tyrosine phosphoprotein p62" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GAP-associated tyrosine phosphoprotein p62" encoded by a nucleic acid that hybridizes to the "GAP-associated tyrosine phosphoprotein p62" nucleic acid or its complement under low stringency conditions,
- (xv) "IPI00104084.1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IPI00104084.1" encoded by a nucleic acid that hybridizes to the "IPI00104084.1" nucleic acid or its complement under low stringency conditions,
- (xvi) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that

hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,

(xvii) "Krab box protein ensp00000302970" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Krab box protein ensp00000302970" encoded by a nucleic acid that hybridizes to the "Krab box protein ensp00000302970" nucleic acid or its complement under low stringency conditions,

(xviii) "PDZ domain protein MAGI-3" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ domain protein MAGI-3" encoded by a nucleic acid that hybridizes to the "PDZ domain protein MAGI-3" nucleic acid or its complement under low stringency conditions,

(xix) "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" nucleic acid or its complement under low stringency conditions,

(xx) "Protein similar to probable mitotic centromere associated kinesin" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to probable mitotic centromere associated kinesin" encoded by a nucleic acid that hybridizes to the "Protein similar to probable mitotic centromere associated kinesin" nucleic acid or its complement under low stringency conditions,

(xxi) "RNB6" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RNB6" encoded by a nucleic acid that hybridizes to the "RNB6" nucleic acid or its complement under low stringency conditions,

(xxii) "SAP-62" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SAP-62" encoded by a nucleic acid that hybridizes to the "SAP-62" nucleic acid or its complement under low stringency conditions,

(xxiii) "Transcription factor CP2" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Transcription factor CP2" encoded by a nucleic acid that hybridizes to the "Transcription factor CP2" nucleic acid or its complement under low stringency conditions,

(xxiv) "Zinc finger protein 277" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 277" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 277" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.
6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.
7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of No. 1 - 7 that is involved in the transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).
9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex,

preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Fe65 complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the Fe65 complex selected from

- (i) "IPI00104084.1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IPI00104084.1" encoded by a nucleic acid that hybridizes to the "IPI00104084.1" nucleic acid or its complement under low stringency conditions,
- (ii) "Krab box protein ensp00000302970" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Krab box protein ensp00000302970" encoded by a nucleic acid that hybridizes to the "Krab box protein ensp00000302970" nucleic acid or its complement under low stringency conditions,
- (iii) "Protein similar to probable mitotic centromere associated kinesin" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to probable mitotic centromere associated kinesin" encoded by a nucleic acid that hybridizes to the "Protein similar to probable mitotic centromere associated kinesin" nucleic acid or its complement under low stringency conditions, and
- (iv) "Zinc finger protein 277" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 277" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 277" nucleic acid or its complement under low stringency conditions, wherein said low

stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease; inflammatory diseases such as chronic inflammatory disorders, rheumatoid arthritis and inflammatory bowel disease; cancer such as prostate cancer and breast cancer and skin cancer .

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

(i) "IPI00104084.1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IPI00104084.1" encoded by a nucleic acid that hybridizes to the "IPI00104084.1" nucleic acid or its complement under low stringency conditions,

(ii) "Krab box protein ensp00000302970" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Krab box protein ensp00000302970" encoded by a nucleic acid that hybridizes to the "Krab box protein ensp00000302970" nucleic acid or its complement under low stringency conditions,

(iii) "Protein similar to probable mitotic centromere associated kinesin" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a

homolog thereof, or a variant of "Protein similar to probable mitotic centromere associated kinesin" encoded by a nucleic acid that hybridizes to the "Protein similar to probable mitotic centromere associated kinesin" nucleic acid or its complement under low stringency conditions, and/or

(iv) "Zinc finger protein 277" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 277" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 277" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative disease such as Alzheimer's disease; inflammatory diseases such as chronic inflammatory disorders, rheumatoid arthritis and inflammatory bowel disease; cancer such as prostate cancer and breast cancer and skin cancer .

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

(i) "IPI00104084.1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IPI00104084.1" encoded by a nucleic acid that hybridizes to the "IPI00104084.1" nucleic acid or its complement under low stringency conditions,

(ii) "Krab box protein ensp00000302970" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Krab box protein ensp00000302970" encoded by a nucleic acid that hybridizes to the "Krab box protein ensp00000302970" nucleic acid or its complement under low stringency conditions,

(iii) "Protein similar to probable mitotic centromere associated kinesin" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to probable mitotic centromere associated kinesin" encoded by a nucleic acid that hybridizes to the "Protein similar to probable mitotic centromere associated kinesin" nucleic acid or its complement under low stringency conditions, and/or

(iv) "Zinc finger protein 277" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 277" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 277" nucleic acid or its complement under low stringency conditions, comprising the steps of
 (a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and
 (b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of (a) exposing said complex, or a cell or organism containing Fe65 complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether
(i) "14-3-3 protein epsilon" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein epsilon" encoded by a nucleic acid that hybridizes to the "14-3-3 protein epsilon" nucleic acid or its complement under low stringency conditions, and/or

(ii) "14-3-3 protein beta/alpha" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein beta/alpha" encoded by a nucleic acid that hybridizes to the "14-3-3 protein beta/alpha" nucleic acid or its complement under low stringency conditions, and/or

(iii) "14-3-3 protein eta" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein eta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein eta" nucleic acid or its complement under low stringency conditions, and/or

(iv) "14-3-3 protein gamma" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein gamma" encoded by a nucleic acid that hybridizes to the "14-3-3 protein gamma" nucleic acid or its complement under low stringency conditions, and/or

(v) "14-3-3 protein tau" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein tau" encoded by a nucleic acid that hybridizes to the "14-3-3 protein tau" nucleic acid or its complement under low stringency conditions, and/or

(vi) "14-3-3 protein zeta/delta" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein zeta/delta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein zeta/delta" nucleic acid or its complement under low stringency conditions, and/or

(vii) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions, and/or

- (viii) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or
- (x) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "ATP-binding cassette, sub-family B, member 7" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family B, member 7" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family B, member 7" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "ECP-51" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECP-51" encoded by a nucleic acid that hybridizes to the "ECP-51" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "GAP-associated tyrosine phosphoprotein p62" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GAP-associated tyrosine phosphoprotein p62" encoded by a nucleic acid that hybridizes to the "GAP-associated tyrosine phosphoprotein p62" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "IPI00104084.1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IPI00104084.1" encoded by a nucleic acid that hybridizes to the "IPI00104084.1" nucleic acid or its complement under low stringency conditions, and/or

- (xvi) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "Krab box protein ensp00000302970" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Krab box protein ensp00000302970" encoded by a nucleic acid that hybridizes to the "Krab box protein ensp00000302970" nucleic acid or its complement under low stringency conditions, and/or
- (xviii) "PDZ domain protein MAGI-3" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ domain protein MAGI-3" encoded by a nucleic acid that hybridizes to the "PDZ domain protein MAGI-3" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" nucleic acid or its complement under low stringency conditions, and/or
- (xx) "Protein similar to probable mitotic centromere associated kinesin" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to probable mitotic centromere associated kinesin" encoded by a nucleic acid that hybridizes to the "Protein similar to probable mitotic centromere associated kinesin" nucleic acid or its complement under low stringency conditions, and/or
- (xxi) "RNB6" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RNB6" encoded by a nucleic acid that hybridizes to the "RNB6" nucleic acid or its complement under low stringency conditions, and/or
- (xxii) "SAP-62" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SAP-62" encoded by a nucleic acid that hybridizes to the "SAP-62" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "Transcription factor CP2" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Transcription factor CP2" encoded by a nucleic acid that hybridizes to the "Transcription factor CP2" nucleic acid or its complement under low stringency conditions, and/or (xxiv) "Zinc finger protein 277" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 277" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 277" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease; inflammatory diseases such as chronic inflammatory disorders, rheumatoid arthritis and inflammatory bowel disease; cancer such as prostate cancer and breast cancer and skin cancer .

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease; inflammatory diseases such as chronic inflammatory disorders, rheumatoid arthritis and inflammatory bowel disease; cancer such as prostate cancer and breast cancer and skin cancer .

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the

complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether
(i) "14-3-3 protein epsilon" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein epsilon" encoded by a nucleic acid that hybridizes to the "14-3-3 protein epsilon" nucleic acid or its complement under low stringency conditions, and/or
(ii) "14-3-3 protein beta/alpha" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein beta/alpha" encoded by a nucleic acid that hybridizes to the "14-3-3 protein beta/alpha" nucleic acid or its complement under low stringency conditions, and/or
(iii) "14-3-3 protein eta" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein eta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein eta" nucleic acid or its complement under low stringency conditions, and/or

- (iv) "14-3-3 protein gamma" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein gamma" encoded by a nucleic acid that hybridizes to the "14-3-3 protein gamma" nucleic acid or its complement under low stringency conditions, and/or
- (v) "14-3-3 protein tau" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein tau" encoded by a nucleic acid that hybridizes to the "14-3-3 protein tau" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "14-3-3 protein zeta/delta" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein zeta/delta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein zeta/delta" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or
- (x) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "ATP-binding cassette, sub-family B, member 7" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family B, member 7" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family B, member 7" nucleic acid or its complement under low stringency conditions, and/or

- (xii) "ECP-51" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECP-51" encoded by a nucleic acid that hybridizes to the "ECP-51" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "GAP-associated tyrosine phosphoprotein p62" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GAP-associated tyrosine phosphoprotein p62" encoded by a nucleic acid that hybridizes to the "GAP-associated tyrosine phosphoprotein p62" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "IPI00104084.1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IPI00104084.1" encoded by a nucleic acid that hybridizes to the "IPI00104084.1" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "Krab box protein ensp00000302970" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Krab box protein ensp00000302970" encoded by a nucleic acid that hybridizes to the "Krab box protein ensp00000302970" nucleic acid or its complement under low stringency conditions, and/or
- (xviii) "PDZ domain protein MAGI-3" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ domain protein MAGI-3" encoded by a nucleic acid that hybridizes to the "PDZ domain protein MAGI-3" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a

homolog thereof, or a variant of "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" nucleic acid or its complement under low stringency conditions, and/or (xx) "Protein similar to probable mitotic centromere associated kinesin" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to probable mitotic centromere associated kinesin" encoded by a nucleic acid that hybridizes to the "Protein similar to probable mitotic centromere associated kinesin" nucleic acid or its complement under low stringency conditions, and/or (xxi) "RNB6" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RNB6" encoded by a nucleic acid that hybridizes to the "RNB6" nucleic acid or its complement under low stringency conditions, and/or (xxii) "SAP-62" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SAP-62" encoded by a nucleic acid that hybridizes to the "SAP-62" nucleic acid or its complement under low stringency conditions, and/or (xxiii) "Transcription factor CP2" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Transcription factor CP2" encoded by a nucleic acid that hybridizes to the "Transcription factor CP2" nucleic acid or its complement under low stringency conditions, and/or (xxiv) "Zinc finger protein 277" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 277" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 277" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative disease such as Alzheimer's disease; inflammatory diseases such as chronic inflammatory disorders, rheumatoid arthritis and inflammatory bowel disease; cancer such as prostate cancer and breast cancer and skin cancer .

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.
43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.
44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.
45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins
- (i) "14-3-3 protein epsilon" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein epsilon" encoded by a nucleic acid that hybridizes to the "14-3-3 protein epsilon" nucleic acid or its complement under low stringency conditions,
 - (ii) "14-3-3 protein beta/alpha" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein beta/alpha" encoded by a nucleic acid that hybridizes to the "14-3-3 protein beta/alpha" nucleic acid or its complement under low stringency conditions,
 - (iii) "14-3-3 protein eta" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein

eta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein eta" nucleic acid or its complement under low stringency conditions,

(iv) "14-3-3 protein gamma" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein gamma" encoded by a nucleic acid that hybridizes to the "14-3-3 protein gamma" nucleic acid or its complement under low stringency conditions,

(v) "14-3-3 protein tau" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein tau" encoded by a nucleic acid that hybridizes to the "14-3-3 protein tau" nucleic acid or its complement under low stringency conditions,

(vi) "14-3-3 protein zeta/delta" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein zeta/delta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein zeta/delta" nucleic acid or its complement under low stringency conditions,

(vii) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions,

(viii) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,

(ix) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(x) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,

(xi) "ATP-binding cassette, sub-family B, member 7" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family B, member 7" encoded by a nucleic

acid that hybridizes to the "ATP-binding cassette, sub-family B, member 7" nucleic acid or its complement under low stringency conditions,

(xii) "ECP-51" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECP-51" encoded by a nucleic acid that hybridizes to the "ECP-51" nucleic acid or its complement under low stringency conditions,

(xiii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,

(xiv) "GAP-associated tyrosine phosphoprotein p62" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GAP-associated tyrosine phosphoprotein p62" encoded by a nucleic acid that hybridizes to the "GAP-associated tyrosine phosphoprotein p62" nucleic acid or its complement under low stringency conditions,

(xv) "IPI00104084.1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IPI00104084.1" encoded by a nucleic acid that hybridizes to the "IPI00104084.1" nucleic acid or its complement under low stringency conditions,

(xvi) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,

(xvii) "Krab box protein ensp00000302970" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Krab box protein ensp00000302970" encoded by a nucleic acid that hybridizes to the "Krab box protein ensp00000302970" nucleic acid or its complement under low stringency conditions,

(xviii) "PDZ domain protein MAGI-3" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ domain protein MAGI-3" encoded by a nucleic acid that hybridizes to the "PDZ domain protein MAGI-3" nucleic acid or its complement under low stringency conditions,

(xix) "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)" nucleic acid or its complement under low stringency conditions,

(xx) "Protein similar to probable mitotic centromere associated kinesin" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to probable mitotic centromere associated kinesin" encoded by a nucleic acid that hybridizes to the "Protein similar to probable mitotic centromere associated kinesin" nucleic acid or its complement under low stringency conditions,

(xxi) "RNB6" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RNB6" encoded by a nucleic acid that hybridizes to the "RNB6" nucleic acid or its complement under low stringency conditions,

(xxii) "SAP-62" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SAP-62" encoded by a nucleic acid that hybridizes to the "SAP-62" nucleic acid or its complement under low stringency conditions,

(xxiii) "Transcription factor CP2" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Transcription factor CP2" encoded by a nucleic acid that hybridizes to the "Transcription factor CP2" nucleic acid or its complement under low stringency conditions, and/or (xxiv) "Zinc finger protein 277" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 277" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 277" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease; inflammatory diseases such as chronic inflammatory disorders, rheumatoid arthritis and inflammatory bowel disease; cancer such as prostate cancer and breast cancer and skin cancer .

The invention further relates to the following embodiments of the X11beta-complex:

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein selected from the group consisting of:
 - (i) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
 - (ii) "Hunc18a" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hunc18a" encoded by a nucleic acid that hybridizes to the "Hunc18a" nucleic acid or its complement under low stringency conditions,
 - (iii) "Neurexin-1" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurexin-1" encoded by a nucleic acid that hybridizes to the "Neurexin-1" nucleic acid or its complement under low stringency conditions,
 - (iv) "SNAP-25" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SNAP-25" encoded by a nucleic acid that hybridizes to the "SNAP-25" nucleic acid or its complement under low stringency conditions,
 - (v) "STX1A" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX1A" encoded by a nucleic acid that hybridizes to the "STX1A" nucleic acid or its complement under low stringency conditions, and
 - (vi) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions, and
 - (b) at least one second protein, which second protein is selected from the group consisting of:
 - (i) "ADAMTS-19" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ADAMTS-19" encoded by a nucleic acid that hybridizes to the "ADAMTS-19" nucleic acid or its complement under low stringency conditions,

- (ii) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions,
- (iii) "Axonemal dynein heavy chain 8" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Axonemal dynein heavy chain 8" encoded by a nucleic acid that hybridizes to the "Axonemal dynein heavy chain 8" nucleic acid or its complement under low stringency conditions,
- (iv) "BAT1" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAT1" encoded by a nucleic acid that hybridizes to the "BAT1" nucleic acid or its complement under low stringency conditions,
- (v) "C20orf11 (sim to a region of RANBPM)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "C20orf11 (sim to a region of RANBPM)" encoded by a nucleic acid that hybridizes to the "C20orf11 (sim to a region of RANBPM)" nucleic acid or its complement under low stringency conditions,
- (vi) "CGB0_HUMAN" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGB0_HUMAN" encoded by a nucleic acid that hybridizes to the "CGB0_HUMAN" nucleic acid or its complement under low stringency conditions,
- (vii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,
- (viii) "Calsyntenin-1" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-1" encoded by a nucleic acid that hybridizes to the "Calsyntenin-1" nucleic acid or its complement under low stringency conditions,
- (ix) "Calsyntenin-2" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-2"

encoded by a nucleic acid that hybridizes to the "Calsyntenin-2" nucleic acid or its complement under low stringency conditions,

(x) "Calsyntenin-3" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-3" encoded by a nucleic acid that hybridizes to the "Calsyntenin-3" nucleic acid or its complement under low stringency conditions,

(xi) "Chondroitin sulfate proteoglycan 6" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Chondroitin sulfate proteoglycan 6" encoded by a nucleic acid that hybridizes to the "Chondroitin sulfate proteoglycan 6" nucleic acid or its complement under low stringency conditions,

(xii) "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" encoded by a nucleic acid that hybridizes to the "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" nucleic acid or its complement under low stringency conditions,

(xiii) "DC6 protein" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DC6 protein" encoded by a nucleic acid that hybridizes to the "DC6 protein" nucleic acid or its complement under low stringency conditions,

(xiv) "Dkfzp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dkfzp586c1924" encoded by a nucleic acid that hybridizes to the "Dkfzp586c1924" nucleic acid or its complement under low stringency conditions,

(xv) "Dynein light chain 2A " (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain 2A " encoded by a nucleic acid that hybridizes to the "Dynein light chain 2A " nucleic acid or its complement under low stringency conditions,

(xvi) "Dynein light chain-A" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain-A" encoded by a nucleic acid that hybridizes to the "Dynein light chain-A" nucleic acid or its complement under low stringency conditions,

(xvii) "ELAVL3" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ELAVL3" encoded by a nucleic acid that hybridizes to the "ELAVL3" nucleic acid or its complement under low stringency conditions,

(xviii) "ENG00000168820 (hypothetical protein with p-loop)" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG00000168820 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ENG00000168820 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions,

(xix) "Eukaryotic translation initiation factor 4A, isoform" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Eukaryotic translation initiation factor 4A, isoform" encoded by a nucleic acid that hybridizes to the "Eukaryotic translation initiation factor 4A, isoform" nucleic acid or its complement under low stringency conditions,

(xx) "FLJ13910" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13910" encoded by a nucleic acid that hybridizes to the "FLJ13910" nucleic acid or its complement under low stringency conditions,

(xxi) "FRAP1" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FRAP1" encoded by a nucleic acid that hybridizes to the "FRAP1" nucleic acid or its complement under low stringency conditions,

(xxii) "Filamin, gamma" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Filamin, gamma" encoded by a nucleic acid that hybridizes to the "Filamin, gamma" nucleic acid or its complement under low stringency conditions,

(xxiii) "GTP-binding protein ERA" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTP-binding protein ERA" encoded by a nucleic acid that hybridizes to the "GTP-binding protein ERA" nucleic acid or its complement under low stringency conditions,

(xxiv) "HADH2/ERAB (mitochondrial enzyme)" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HADH2/ERAB (mitochondrial enzyme)" encoded by a nucleic acid that

hybridizes to the "HADH2/ERAB (mitochondrial enzyme)" nucleic acid or its complement under low stringency conditions,

(xxv) "HDAC2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HDAC2" encoded by a nucleic acid that hybridizes to the "HDAC2" nucleic acid or its complement under low stringency conditions,

(xxvi) "HERC2 protein" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HERC2 protein" encoded by a nucleic acid that hybridizes to the "HERC2 protein" nucleic acid or its complement under low stringency conditions,

(xxvii) "HSPC154" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC154" encoded by a nucleic acid that hybridizes to the "HSPC154" nucleic acid or its complement under low stringency conditions,

(xxviii) "HSPC245" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC245" encoded by a nucleic acid that hybridizes to the "HSPC245" nucleic acid or its complement under low stringency conditions,

(xxix) "HYPOTHETICAL PROTEIN FLJ10618" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ10618" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ10618" nucleic acid or its complement under low stringency conditions,

(xxx) "HYPOTHETICAL PROTEIN FLJ12599" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ12599" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ12599" nucleic acid or its complement under low stringency conditions,

(xxxi) "Hypothetical protein FLJ10795" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ10795" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ10795" nucleic acid or its complement under low stringency conditions,

(xxxii) "Hypothetical protein FLJ20397" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ20397" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ20397" nucleic acid or its complement under low stringency conditions,

(xxxiii) "IKAP" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IKAP" encoded by a nucleic acid that hybridizes to the "IKAP" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions,

(xxxv) "KIAA0056" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0056" encoded by a nucleic acid that hybridizes to the "KIAA0056" nucleic acid or its complement under low stringency conditions,

(xxxvi) "KIAA0166" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0166" encoded by a nucleic acid that hybridizes to the "KIAA0166" nucleic acid or its complement under low stringency conditions,

(xxxvii) "KIAA0325 (FRAGMENT)" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0325 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0325 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxxviii) "KIAA0564" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0564" encoded by a nucleic acid that hybridizes to the "KIAA0564" nucleic acid or its complement under low stringency conditions,

(xxxix) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,

- (xl) "LIB (leucine-rich repeat protein)" (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LIB (leucine-rich repeat protein)" encoded by a nucleic acid that hybridizes to the "LIB (leucine-rich repeat protein)" nucleic acid or its complement under low stringency conditions,
- (xli) "Laminin, gamma 1 " (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Laminin, gamma 1 " encoded by a nucleic acid that hybridizes to the "Laminin, gamma 1 " nucleic acid or its complement under low stringency conditions,
- (xlii) "MBIP" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MBIP" encoded by a nucleic acid that hybridizes to the "MBIP" nucleic acid or its complement under low stringency conditions,
- (xliii) "MEGF7 (FRAGMENT)" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEGF7 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "MEGF7 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xliv) "MT-ACT48" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MT-ACT48" encoded by a nucleic acid that hybridizes to the "MT-ACT48" nucleic acid or its complement under low stringency conditions,
- (xlv) "Myosin IXB" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Myosin IXB" encoded by a nucleic acid that hybridizes to the "Myosin IXB" nucleic acid or its complement under low stringency conditions,
- (xlvi) "NEU1" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NEU1" encoded by a nucleic acid that hybridizes to the "NEU1" nucleic acid or its complement under low stringency conditions,
- (xlvii) "NIPSNAP1" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP1" encoded by a nucleic acid that hybridizes to the "NIPSNAP1" nucleic acid or its complement under low stringency conditions,

- (xlviii) "NIPSNAP2" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP2" encoded by a nucleic acid that hybridizes to the "NIPSNAP2" nucleic acid or its complement under low stringency conditions,
- (xlix) "PDZ and LIM domain protein 1" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ and LIM domain protein 1" encoded by a nucleic acid that hybridizes to the "PDZ and LIM domain protein 1" nucleic acid or its complement under low stringency conditions,
- (i) "PILB" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILB" encoded by a nucleic acid that hybridizes to the "PILB" nucleic acid or its complement under low stringency conditions,
- (ii) "PILT" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILT" encoded by a nucleic acid that hybridizes to the "PILT" nucleic acid or its complement under low stringency conditions,
- (iii) "Paladin" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Paladin" encoded by a nucleic acid that hybridizes to the "Paladin" nucleic acid or its complement under low stringency conditions,
- (liii) "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" encoded by a nucleic acid that hybridizes to the "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" nucleic acid or its complement under low stringency conditions,
- (liv) "Procollagen C-endopeptidase enhancer" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Procollagen C-endopeptidase enhancer" encoded by a nucleic acid that hybridizes to the "Procollagen C-endopeptidase enhancer" nucleic acid or its complement under low stringency conditions,
- (lv) "Programmed cell death 10" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Programmed cell death 10" encoded by a nucleic acid that hybridizes to the

"Programmed cell death 10" nucleic acid or its complement under low stringency conditions,

(lvi) "Protein similar to AGCP6688" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to AGCP6688" encoded by a nucleic acid that hybridizes to the "Protein similar to AGCP6688" nucleic acid or its complement under low stringency conditions,

(lvii) "RAB7L1" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB7L1" encoded by a nucleic acid that hybridizes to the "RAB7L1" nucleic acid or its complement under low stringency conditions,

(lviii) "RANBP1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RANBP1" encoded by a nucleic acid that hybridizes to the "RANBP1" nucleic acid or its complement under low stringency conditions,

(lix) "RPGR-interacting protein 1" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RPGR-interacting protein 1" encoded by a nucleic acid that hybridizes to the "RPGR-interacting protein 1" nucleic acid or its complement under low stringency conditions,

(lx) "Reelin" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions,

(lxi) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions,

(lxii) "SUCLA2" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SUCLA2" encoded by a nucleic acid that hybridizes to the "SUCLA2" nucleic acid or its complement under low stringency conditions,

(lxiii) "Serine/threonine protein phosphatase 6" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 6" encoded by a nucleic acid that

hybridizes to the "Serine/threonine protein phosphatase 6" nucleic acid or its complement under low stringency conditions,

(lxiv) "Sortilin-related receptor " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor " encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor " nucleic acid or its complement under low stringency conditions,

(lxv) "Synaptogyrin 3" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Synaptogyrin 3" encoded by a nucleic acid that hybridizes to the "Synaptogyrin 3" nucleic acid or its complement under low stringency conditions,

(lxvi) "TYK2" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TYK2" encoded by a nucleic acid that hybridizes to the "TYK2" nucleic acid or its complement under low stringency conditions,

(lxvii) "Ubiquitin-protein ligase E3-alpha" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase E3-alpha" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase E3-alpha" nucleic acid or its complement under low stringency conditions,

(lxviii) "VGF nerve growth factor inducible protein" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VGF nerve growth factor inducible protein" encoded by a nucleic acid that hybridizes to the "VGF nerve growth factor inducible protein" nucleic acid or its complement under low stringency conditions,

(lxix) "Zinc finger protein 198" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 198" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 198" nucleic acid or its complement under low stringency conditions,

(lxx) "hypothetical protein MGC13186" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC13186" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC13186" nucleic acid or its complement under low stringency conditions, and

(lxxi) "similar to SD27354p [*Drosophila melanogaster*] " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "similar to SD27354p [*Drosophila melanogaster*] " encoded by a nucleic acid that hybridizes to the "similar to SD27354p [*Drosophila melanogaster*] " nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein X11beta (SEQ ID NO. 96), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'X11beta' encoded by a nucleic acid that hybridizes to the 'X11beta' under low stringency conditions.

3. The protein complex according to No. 1 selected from complex (I) and comprising the following proteins:

- (i) "ADAMTS-19" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ADAMTS-19" encoded by a nucleic acid that hybridizes to the "ADAMTS-19" nucleic acid or its complement under low stringency conditions,
- (ii) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions,
- (iii) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iv) "Axonemal dynein heavy chain 8" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"Axonemal dynein heavy chain 8" encoded by a nucleic acid that hybridizes to the "Axonemal dynein heavy chain 8" nucleic acid or its complement under low stringency conditions,

(v) "BAT1" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAT1" encoded by a nucleic acid that hybridizes to the "BAT1" nucleic acid or its complement under low stringency conditions,

(vi) "C20orf11 (sim to a region of RANBPM)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "C20orf11 (sim to a region of RANBPM)" encoded by a nucleic acid that hybridizes to the "C20orf11 (sim to a region of RANBPM)" nucleic acid or its complement under low stringency conditions,

(vii) "CGB0_HUMAN" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGB0_HUMAN" encoded by a nucleic acid that hybridizes to the "CGB0_HUMAN" nucleic acid or its complement under low stringency conditions,

(viii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,

(ix) "Calsyntenin-1" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-1" encoded by a nucleic acid that hybridizes to the "Calsyntenin-1" nucleic acid or its complement under low stringency conditions,

(x) "Calsyntenin-2" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-2" encoded by a nucleic acid that hybridizes to the "Calsyntenin-2" nucleic acid or its complement under low stringency conditions,

(xi) "Calsyntenin-3" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-3" encoded by a nucleic acid that hybridizes to the "Calsyntenin-3" nucleic acid or its complement under low stringency conditions,

- (xii) "Chondroitin sulfate proteoglycan 6" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Chondroitin sulfate proteoglycan 6" encoded by a nucleic acid that hybridizes to the "Chondroitin sulfate proteoglycan 6" nucleic acid or its complement under low stringency conditions,
- (xiii) "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" encoded by a nucleic acid that hybridizes to the "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" nucleic acid or its complement under low stringency conditions,
- (xiv) "DC6 protein" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DC6 protein" encoded by a nucleic acid that hybridizes to the "DC6 protein" nucleic acid or its complement under low stringency conditions,
- (xv) "Dkfzp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dkfzp586c1924" encoded by a nucleic acid that hybridizes to the "Dkfzp586c1924" nucleic acid or its complement under low stringency conditions,
- (xvi) "Dynein light chain 2A " (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain 2A " encoded by a nucleic acid that hybridizes to the "Dynein light chain 2A " nucleic acid or its complement under low stringency conditions,
- (xvii) "Dynein light chain-A" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain-A" encoded by a nucleic acid that hybridizes to the "Dynein light chain-A" nucleic acid or its complement under low stringency conditions,
- (xviii) "ELAVL3" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ELAVL3" encoded by a nucleic acid that hybridizes to the "ELAVL3" nucleic acid or its complement under low stringency conditions,
- (xix) "ENG00000168820 (hypothetical protein with p-loop)" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG00000168820 (hypothetical protein with p-loop)"

encoded by a nucleic acid that hybridizes to the "ENG00000168820 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions,

(xx) "Eukaryotic translation initiation factor 4A, isoform" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Eukaryotic translation initiation factor 4A, isoform" encoded by a nucleic acid that hybridizes to the "Eukaryotic translation initiation factor 4A, isoform" nucleic acid or its complement under low stringency conditions,

(xxi) "FLJ13910" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13910" encoded by a nucleic acid that hybridizes to the "FLJ13910" nucleic acid or its complement under low stringency conditions,

(xxii) "FRAP1" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FRAP1" encoded by a nucleic acid that hybridizes to the "FRAP1" nucleic acid or its complement under low stringency conditions,

(xxiii) "Filamin, gamma" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Filamin, gamma" encoded by a nucleic acid that hybridizes to the "Filamin, gamma" nucleic acid or its complement under low stringency conditions,

(xxiv) "GTP-binding protein ERA" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTP-binding protein ERA" encoded by a nucleic acid that hybridizes to the "GTP-binding protein ERA" nucleic acid or its complement under low stringency conditions,

(xxv) "HADH2/ERAB (mitochondrial enzyme)" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HADH2/ERAB (mitochondrial enzyme)" encoded by a nucleic acid that hybridizes to the "HADH2/ERAB (mitochondrial enzyme)" nucleic acid or its complement under low stringency conditions,

(xxvi) "HDAC2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HDAC2" encoded by a nucleic acid that hybridizes to the "HDAC2" nucleic acid or its complement under low stringency conditions,

(xxvii) "HERC2 protein" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HERC2

- protein" encoded by a nucleic acid that hybridizes to the "HERC2 protein" nucleic acid or its complement under low stringency conditions,
- (xxviii) "HSPC154" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC154" encoded by a nucleic acid that hybridizes to the "HSPC154" nucleic acid or its complement under low stringency conditions,
- (xxix) "HSPC245" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC245" encoded by a nucleic acid that hybridizes to the "HSPC245" nucleic acid or its complement under low stringency conditions,
- (xxx) "HYPOTHETICAL PROTEIN FLJ10618" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ10618" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ10618" nucleic acid or its complement under low stringency conditions,
- (xxxi) "HYPOTHETICAL PROTEIN FLJ12599" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ12599" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ12599" nucleic acid or its complement under low stringency conditions,
- (xxxii) "Hunc18a" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hunc18a" encoded by a nucleic acid that hybridizes to the "Hunc18a" nucleic acid or its complement under low stringency conditions,
- (xxxiii) "Hypothetical protein FLJ10795" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ10795" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ10795" nucleic acid or its complement under low stringency conditions,
- (xxxiv) "Hypothetical protein FLJ20397" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ20397" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ20397" nucleic acid or its complement under low stringency conditions,

(xxxv) "IKAP" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IKAP" encoded by a nucleic acid that hybridizes to the "IKAP" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions,

(xxxvii) "KIAA0056" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0056" encoded by a nucleic acid that hybridizes to the "KIAA0056" nucleic acid or its complement under low stringency conditions,

(xxxviii) "KIAA0166" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0166" encoded by a nucleic acid that hybridizes to the "KIAA0166" nucleic acid or its complement under low stringency conditions,

(xxxix) "KIAA0325 (FRAGMENT)" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0325 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0325 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xl) "KIAA0564" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0564" encoded by a nucleic acid that hybridizes to the "KIAA0564" nucleic acid or its complement under low stringency conditions,

(xli) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,

(xlii) "LIB (leucine-rich repeat protein)" (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LIB (leucine-rich repeat protein)" encoded by a nucleic acid that hybridizes to the "LIB (leucine-rich repeat protein)" nucleic acid or its complement under low stringency conditions,

- (xlili) "Laminin, gamma 1 " (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Laminin, gamma 1 " encoded by a nucleic acid that hybridizes to the "Laminin, gamma 1 " nucleic acid or its complement under low stringency conditions,
- (xliv) "MBIP" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MBIP" encoded by a nucleic acid that hybridizes to the "MBIP" nucleic acid or its complement under low stringency conditions,
- (xlv) "MEGF7 (FRAGMENT)" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEGF7 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "MEGF7 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xlvi) "MT-ACT48" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MT-ACT48" encoded by a nucleic acid that hybridizes to the "MT-ACT48" nucleic acid or its complement under low stringency conditions,
- (xlvii) "Myosin IXB" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Myosin IXB" encoded by a nucleic acid that hybridizes to the "Myosin IXB" nucleic acid or its complement under low stringency conditions,
- (xlviii) "NEU1" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NEU1" encoded by a nucleic acid that hybridizes to the "NEU1" nucleic acid or its complement under low stringency conditions,
- (xlix) "NIPSNAP1" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP1" encoded by a nucleic acid that hybridizes to the "NIPSNAP1" nucleic acid or its complement under low stringency conditions,
- (l) "NIPSNAP2" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP2" encoded by a nucleic acid that hybridizes to the "NIPSNAP2" nucleic acid or its complement under low stringency conditions,
- (li) "Neurexin-1" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurexin-1"

encoded by a nucleic acid that hybridizes to the "Neurexin-1" nucleic acid or its complement under low stringency conditions,

(lii) "PDZ and LIM domain protein 1" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ and LIM domain protein 1" encoded by a nucleic acid that hybridizes to the "PDZ and LIM domain protein 1" nucleic acid or its complement under low stringency conditions,

(liii) "PILB" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILB" encoded by a nucleic acid that hybridizes to the "PILB" nucleic acid or its complement under low stringency conditions,

(liv) "PILT" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILT" encoded by a nucleic acid that hybridizes to the "PILT" nucleic acid or its complement under low stringency conditions,

(lv) "Paladin" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Paladin" encoded by a nucleic acid that hybridizes to the "Paladin" nucleic acid or its complement under low stringency conditions,

(lvi) "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" encoded by a nucleic acid that hybridizes to the "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" nucleic acid or its complement under low stringency conditions,

(lvii) "Procollagen C-endopeptidase enhancer" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Procollagen C-endopeptidase enhancer" encoded by a nucleic acid that hybridizes to the "Procollagen C-endopeptidase enhancer" nucleic acid or its complement under low stringency conditions,

(lviii) "Programmed cell death 10" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Programmed cell death 10" encoded by a nucleic acid that hybridizes to the "Programmed cell death 10" nucleic acid or its complement under low stringency conditions,

- (lix) "Protein similar to AGCP6688" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to AGCP6688" encoded by a nucleic acid that hybridizes to the "Protein similar to AGCP6688" nucleic acid or its complement under low stringency conditions,
- (lx) "RAB7L1" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB7L1" encoded by a nucleic acid that hybridizes to the "RAB7L1" nucleic acid or its complement under low stringency conditions,
- (lxi) "RANBP1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RANBP1" encoded by a nucleic acid that hybridizes to the "RANBP1" nucleic acid or its complement under low stringency conditions,
- (lxii) "RPGR-interacting protein 1" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RPGR-interacting protein 1" encoded by a nucleic acid that hybridizes to the "RPGR-interacting protein 1" nucleic acid or its complement under low stringency conditions,
- (lxiii) "Reelin" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions,
- (lxiv) "SNAP-25" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SNAP-25" encoded by a nucleic acid that hybridizes to the "SNAP-25" nucleic acid or its complement under low stringency conditions,
- (lxv) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions,
- (lxvi) "STX1A" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX1A" encoded by a nucleic acid that hybridizes to the "STX1A" nucleic acid or its complement under low stringency conditions,
- (lxvii) "SUCLA2" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SUCLA2"

encoded by a nucleic acid that hybridizes to the "SUCLA2" nucleic acid or its complement under low stringency conditions,

(lxviii) "Serine/threonine protein phosphatase 6" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 6" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 6" nucleic acid or its complement under low stringency conditions,

(lix) "Sortilin-related receptor " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor " encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor " nucleic acid or its complement under low stringency conditions,

(lxx) "Synaptogyrin 3" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Synaptogyrin 3" encoded by a nucleic acid that hybridizes to the "Synaptogyrin 3" nucleic acid or its complement under low stringency conditions,

(lxxi) "TYK2" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TYK2" encoded by a nucleic acid that hybridizes to the "TYK2" nucleic acid or its complement under low stringency conditions,

(lxxii) "Ubiquitin-protein ligase E3-alpha" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase E3-alpha" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase E3-alpha" nucleic acid or its complement under low stringency conditions,

(lxxiii) "VGF nerve growth factor inducible protein" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VGF nerve growth factor inducible protein" encoded by a nucleic acid that hybridizes to the "VGF nerve growth factor inducible protein" nucleic acid or its complement under low stringency conditions,

(lxxiv) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions,

(lxxv) "Zinc finger protein 198" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 198" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 198" nucleic acid or its complement under low stringency conditions,

(lxxvi) "hypothetical protein MGC13186" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC13186" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC13186" nucleic acid or its complement under low stringency conditions, and/or

(lxxvii) "similar to SD27354p [Drosophila melanogaster] " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "similar to SD27354p [Drosophila melanogaster] " encoded by a nucleic acid that hybridizes to the "similar to SD27354p [Drosophila melanogaster] " nucleic acid or its complement under low stringency conditions, and a protein complex selected from complex (II) and comprising the following proteins:

(i) "ADAMTS-19" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ADAMTS-19" encoded by a nucleic acid that hybridizes to the "ADAMTS-19" nucleic acid or its complement under low stringency conditions,

(ii) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions,

(iii) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(iv) "Axonemal dynein heavy chain 8" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Axonemal dynein heavy chain 8" encoded by a nucleic acid that hybridizes to the "Axonemal dynein heavy chain 8" nucleic acid or its complement under low stringency conditions,

(v) "BAT1" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAT1" encoded by a

nucleic acid that hybridizes to the "BAT1" nucleic acid or its complement under low stringency conditions,

(vi) "C20orf11 (sim to a region of RANBPM)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "C20orf11 (sim to a region of RANBPM)" encoded by a nucleic acid that hybridizes to the "C20orf11 (sim to a region of RANBPM)" nucleic acid or its complement under low stringency conditions,

(vii) "CGB0_HUMAN" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGB0_HUMAN" encoded by a nucleic acid that hybridizes to the "CGB0_HUMAN" nucleic acid or its complement under low stringency conditions,

(viii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,

(ix) "Calsyntenin-1" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-1" encoded by a nucleic acid that hybridizes to the "Calsyntenin-1" nucleic acid or its complement under low stringency conditions,

(x) "Calsyntenin-2" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-2" encoded by a nucleic acid that hybridizes to the "Calsyntenin-2" nucleic acid or its complement under low stringency conditions,

(xi) "Calsyntenin-3" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-3" encoded by a nucleic acid that hybridizes to the "Calsyntenin-3" nucleic acid or its complement under low stringency conditions,

(xii) "Chondroitin sulfate proteoglycan 6" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Chondroitin sulfate proteoglycan 6" encoded by a nucleic acid that hybridizes to the "Chondroitin sulfate proteoglycan 6" nucleic acid or its complement under low stringency conditions,

- (xiii) "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" encoded by a nucleic acid that hybridizes to the "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" nucleic acid or its complement under low stringency conditions,
- (xiv) "DC6 protein" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DC6 protein" encoded by a nucleic acid that hybridizes to the "DC6 protein" nucleic acid or its complement under low stringency conditions,
- (xv) "Dkfpz586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dkfpz586c1924" encoded by a nucleic acid that hybridizes to the "Dkfpz586c1924" nucleic acid or its complement under low stringency conditions,
- (xvi) "Dynein light chain 2A " (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain 2A " encoded by a nucleic acid that hybridizes to the "Dynein light chain 2A " nucleic acid or its complement under low stringency conditions,
- (xvii) "Dynein light chain-A" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain-A" encoded by a nucleic acid that hybridizes to the "Dynein light chain-A" nucleic acid or its complement under low stringency conditions,
- (xviii) "ELAVL3" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ELAVL3" encoded by a nucleic acid that hybridizes to the "ELAVL3" nucleic acid or its complement under low stringency conditions,
- (xix) "ENG00000168820 (hypothetical protein with p-loop)" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG00000168820 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ENG00000168820 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions,
- (xx) "Eukaryotic translation initiation factor 4A, isoform" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Eukaryotic translation initiation factor 4A, isoform" encoded by a nucleic

acid that hybridizes to the "Eukaryotic translation initiation factor 4A, isoform" nucleic acid or its complement under low stringency conditions,

(xxi) "FLJ13910" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13910" encoded by a nucleic acid that hybridizes to the "FLJ13910" nucleic acid or its complement under low stringency conditions,

(xxii) "FRAP1" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FRAP1" encoded by a nucleic acid that hybridizes to the "FRAP1" nucleic acid or its complement under low stringency conditions,

(xxiii) "Filamin, gamma" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Filamin, gamma" encoded by a nucleic acid that hybridizes to the "Filamin, gamma" nucleic acid or its complement under low stringency conditions,

(xxiv) "GTP-binding protein ERA" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTP-binding protein ERA" encoded by a nucleic acid that hybridizes to the "GTP-binding protein ERA" nucleic acid or its complement under low stringency conditions,

(xxv) "HADH2/ERAB (mitochondrial enzyme)" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HADH2/ERAB (mitochondrial enzyme)" encoded by a nucleic acid that hybridizes to the "HADH2/ERAB (mitochondrial enzyme)" nucleic acid or its complement under low stringency conditions,

(xxvi) "HDAC2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HDAC2" encoded by a nucleic acid that hybridizes to the "HDAC2" nucleic acid or its complement under low stringency conditions,

(xxvii) "HERC2 protein" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HERC2 protein" encoded by a nucleic acid that hybridizes to the "HERC2 protein" nucleic acid or its complement under low stringency conditions,

(xxviii) "HSPC154" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC154"

encoded by a nucleic acid that hybridizes to the "HSPC154" nucleic acid or its complement under low stringency conditions,

(xxix) "HSPC245" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC245" encoded by a nucleic acid that hybridizes to the "HSPC245" nucleic acid or its complement under low stringency conditions,

(xxx) "HYPOTHETICAL PROTEIN FLJ10618" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ10618" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ10618" nucleic acid or its complement under low stringency conditions,

(xxxi) "HYPOTHETICAL PROTEIN FLJ12599" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ12599" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ12599" nucleic acid or its complement under low stringency conditions,

(xxxii) "Hypothetical protein FLJ10795" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ10795" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ10795" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Hypothetical protein FLJ20397" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ20397" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ20397" nucleic acid or its complement under low stringency conditions,

(xxxiv) "IKAP" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IKAP" encoded by a nucleic acid that hybridizes to the "IKAP" nucleic acid or its complement under low stringency conditions,

(xxxv) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that

hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions,

(xxxvi) "KIAA0056" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0056" encoded by a nucleic acid that hybridizes to the "KIAA0056" nucleic acid or its complement under low stringency conditions,

(xxxvii) "KIAA0166" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0166" encoded by a nucleic acid that hybridizes to the "KIAA0166" nucleic acid or its complement under low stringency conditions,

(xxxviii) "KIAA0325 (FRAGMENT)" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0325 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0325 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxxix) "KIAA0564" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0564" encoded by a nucleic acid that hybridizes to the "KIAA0564" nucleic acid or its complement under low stringency conditions,

(xl) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,

(xli) "LIB (leucine-rich repeat protein)" (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LIB (leucine-rich repeat protein)" encoded by a nucleic acid that hybridizes to the "LIB (leucine-rich repeat protein)" nucleic acid or its complement under low stringency conditions,

(xl ii) "Laminin, gamma 1 " (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Laminin, gamma 1 " encoded by a nucleic acid that hybridizes to the "Laminin, gamma 1 " nucleic acid or its complement under low stringency conditions,

(xl iii) "MBIP" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MBIP" encoded by a

nucleic acid that hybridizes to the "MBIP" nucleic acid or its complement under low stringency conditions,

(xiv) "MEGF7 (FRAGMENT)" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEGF7 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "MEGF7 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xlv) "MT-ACT48" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MT-ACT48" encoded by a nucleic acid that hybridizes to the "MT-ACT48" nucleic acid or its complement under low stringency conditions,

(xlvii) "Myosin IXB" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Myosin IXB" encoded by a nucleic acid that hybridizes to the "Myosin IXB" nucleic acid or its complement under low stringency conditions,

(xlviii) "NEU1" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NEU1" encoded by a nucleic acid that hybridizes to the "NEU1" nucleic acid or its complement under low stringency conditions,

(xlviii) "NIPSNAP1" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP1" encoded by a nucleic acid that hybridizes to the "NIPSNAP1" nucleic acid or its complement under low stringency conditions,

(xlix) "NIPSNAP2" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP2" encoded by a nucleic acid that hybridizes to the "NIPSNAP2" nucleic acid or its complement under low stringency conditions,

(l) "PDZ and LIM domain protein 1" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ and LIM domain protein 1" encoded by a nucleic acid that hybridizes to the "PDZ and LIM domain protein 1" nucleic acid or its complement under low stringency conditions,

(li) "PILB" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILB" encoded by a

nucleic acid that hybridizes to the "PILB" nucleic acid or its complement under low stringency conditions,

(lii) "PILT" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILT" encoded by a nucleic acid that hybridizes to the "PILT" nucleic acid or its complement under low stringency conditions,

(liii) "Paladin" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Paladin" encoded by a nucleic acid that hybridizes to the "Paladin" nucleic acid or its complement under low stringency conditions,

(liv) "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" encoded by a nucleic acid that hybridizes to the "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" nucleic acid or its complement under low stringency conditions,

(lv) "Procollagen C-endopeptidase enhancer" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Procollagen C-endopeptidase enhancer" encoded by a nucleic acid that hybridizes to the "Procollagen C-endopeptidase enhancer" nucleic acid or its complement under low stringency conditions,

(lvi) "Programmed cell death 10" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Programmed cell death 10" encoded by a nucleic acid that hybridizes to the "Programmed cell death 10" nucleic acid or its complement under low stringency conditions,

(lvii) "Protein similar to AGCP6688" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to AGCP6688" encoded by a nucleic acid that hybridizes to the "Protein similar to AGCP6688" nucleic acid or its complement under low stringency conditions,

(lviii) "RAB7L1" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB7L1" encoded by a nucleic acid that hybridizes to the "RAB7L1" nucleic acid or its complement under low stringency conditions,

- (lix) "RANBP1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RANBP1" encoded by a nucleic acid that hybridizes to the "RANBP1" nucleic acid or its complement under low stringency conditions,
- (lx) "RPGR-interacting protein 1" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RPGR-interacting protein 1" encoded by a nucleic acid that hybridizes to the "RPGR-interacting protein 1" nucleic acid or its complement under low stringency conditions,
- (lxi) "Reelin" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions,
- (lxii) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions,
- (lxiii) "SUCLA2" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SUCLA2" encoded by a nucleic acid that hybridizes to the "SUCLA2" nucleic acid or its complement under low stringency conditions,
- (lxiv) "Serine/threonine protein phosphatase 6" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 6" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 6" nucleic acid or its complement under low stringency conditions,
- (lxv) "Sortilin-related receptor " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor " encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor " nucleic acid or its complement under low stringency conditions,
- (lxvi) "Synaptogyrin 3" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Synaptogyrin 3" encoded by a nucleic acid that hybridizes to the "Synaptogyrin 3" nucleic acid or its complement under low stringency conditions,

(Ixxvii) "TYK2" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TYK2" encoded by a nucleic acid that hybridizes to the "TYK2" nucleic acid or its complement under low stringency conditions,

(Ixxviii) "Ubiquitin-protein ligase E3-alpha" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase E3-alpha" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase E3-alpha" nucleic acid or its complement under low stringency conditions,

(Ixxix) "VGF nerve growth factor inducible protein" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VGF nerve growth factor inducible protein" encoded by a nucleic acid that hybridizes to the "VGF nerve growth factor inducible protein" nucleic acid or its complement under low stringency conditions,

(Ixxx) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions,

(Ixxxi) "Zinc finger protein 198" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 198" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 198" nucleic acid or its complement under low stringency conditions,

(Ixxxii) "hypothetical protein MGC13186" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC13186" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC13186" nucleic acid or its complement under low stringency conditions, and/or

(Ixxxiii) "similar to SD27354p [Drosophila melanogaster] " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "similar to SD27354p [Drosophila melanogaster] " encoded by a nucleic acid that hybridizes to the "similar to SD27354p [Drosophila melanogaster] " nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 70 of the following proteins:

- (i) "ADAMTS-19" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ADAMTS-19" encoded by a nucleic acid that hybridizes to the "ADAMTS-19" nucleic acid or its complement under low stringency conditions,
- (ii) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions,
- (iii) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iv) "Axonemal dynein heavy chain 8" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Axonemal dynein heavy chain 8" encoded by a nucleic acid that hybridizes to the "Axonemal dynein heavy chain 8" nucleic acid or its complement under low stringency conditions,
- (v) "BAT1" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAT1" encoded by a nucleic acid that hybridizes to the "BAT1" nucleic acid or its complement under low stringency conditions,
- (vi) "C20orf11 (sim to a region of RANBPM)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "C20orf11 (sim to a region of RANBPM)" encoded by a nucleic acid that hybridizes to the "C20orf11 (sim to a region of RANBPM)" nucleic acid or its complement under low stringency conditions,
- (vii) "CGB0_HUMAN" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGB0_HUMAN" encoded by a nucleic acid that hybridizes to the "CGB0_HUMAN" nucleic acid or its complement under low stringency conditions,
- (viii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a

- homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,
- (ix) "Calsyntenin-1" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-1" encoded by a nucleic acid that hybridizes to the "Calsyntenin-1" nucleic acid or its complement under low stringency conditions,
- (x) "Calsyntenin-2" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-2" encoded by a nucleic acid that hybridizes to the "Calsyntenin-2" nucleic acid or its complement under low stringency conditions,
- (xi) "Calsyntenin-3" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-3" encoded by a nucleic acid that hybridizes to the "Calsyntenin-3" nucleic acid or its complement under low stringency conditions,
- (xii) "Chondroitin sulfate proteoglycan 6" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Chondroitin sulfate proteoglycan 6" encoded by a nucleic acid that hybridizes to the "Chondroitin sulfate proteoglycan 6" nucleic acid or its complement under low stringency conditions,
- (xiii) "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" encoded by a nucleic acid that hybridizes to the "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" nucleic acid or its complement under low stringency conditions,
- (xiv) "DC6 protein" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DC6 protein" encoded by a nucleic acid that hybridizes to the "DC6 protein" nucleic acid or its complement under low stringency conditions,
- (xv) "Dkfzp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dkfzp586c1924" encoded by a nucleic acid that hybridizes to the "Dkfzp586c1924" nucleic acid or its complement under low stringency conditions,

- (xvi) "Dynein light chain 2A " (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain 2A " encoded by a nucleic acid that hybridizes to the "Dynein light chain 2A " nucleic acid or its complement under low stringency conditions,
- (xvii) "Dynein light chain-A" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain-A" encoded by a nucleic acid that hybridizes to the "Dynein light chain-A" nucleic acid or its complement under low stringency conditions,
- (xviii) "ELAVL3" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ELAVL3" encoded by a nucleic acid that hybridizes to the "ELAVL3" nucleic acid or its complement under low stringency conditions,
- (xix) "ENG00000168820 (hypothetical protein with p-loop)" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG00000168820 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ENG00000168820 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions,
- (xx) "Eukaryotic translation initiation factor 4A, isoform" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Eukaryotic translation initiation factor 4A, isoform" encoded by a nucleic acid that hybridizes to the "Eukaryotic translation initiation factor 4A, isoform" nucleic acid or its complement under low stringency conditions,
- (xxi) "FLJ13910" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13910" encoded by a nucleic acid that hybridizes to the "FLJ13910" nucleic acid or its complement under low stringency conditions,
- (xxii) "FRAP1" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FRAP1" encoded by a nucleic acid that hybridizes to the "FRAP1" nucleic acid or its complement under low stringency conditions,
- (xxiii) "Filamin, gamma" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Filamin, gamma" encoded by a nucleic acid that hybridizes to the "Filamin, gamma" nucleic acid or its complement under low stringency conditions,

- (xxiv) "GTP-binding protein ERA" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTP-binding protein ERA" encoded by a nucleic acid that hybridizes to the "GTP-binding protein ERA" nucleic acid or its complement under low stringency conditions,
- (xxv) "HADH2/ERAB (mitochondrial enzyme)" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HADH2/ERAB (mitochondrial enzyme)" encoded by a nucleic acid that hybridizes to the "HADH2/ERAB (mitochondrial enzyme)" nucleic acid or its complement under low stringency conditions,
- (xxvi) "HDAC2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HDAC2" encoded by a nucleic acid that hybridizes to the "HDAC2" nucleic acid or its complement under low stringency conditions,
- (xxvii) "HERC2 protein" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HERC2 protein" encoded by a nucleic acid that hybridizes to the "HERC2 protein" nucleic acid or its complement under low stringency conditions,
- (xxviii) "HSPC154" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC154" encoded by a nucleic acid that hybridizes to the "HSPC154" nucleic acid or its complement under low stringency conditions,
- (xxix) "HSPC245" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC245" encoded by a nucleic acid that hybridizes to the "HSPC245" nucleic acid or its complement under low stringency conditions,
- (xxx) "HYPOTHETICAL PROTEIN FLJ10618" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ10618" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ10618" nucleic acid or its complement under low stringency conditions,
- (xxxi) "HYPOTHETICAL PROTEIN FLJ12599" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ12599" encoded by a nucleic acid that

hybridizes to the "HYPOTHETICAL PROTEIN FLJ12599" nucleic acid or its complement under low stringency conditions,

(xxxii) "Hunc18a" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hunc18a" encoded by a nucleic acid that hybridizes to the "Hunc18a" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Hypothetical protein FLJ10795" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ10795" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ10795" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Hypothetical protein FLJ20397" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ20397" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ20397" nucleic acid or its complement under low stringency conditions,

(xxxv) "IKAP" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IKAP" encoded by a nucleic acid that hybridizes to the "IKAP" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions,

(xxxvii) "KIAA0056" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0056" encoded by a nucleic acid that hybridizes to the "KIAA0056" nucleic acid or its complement under low stringency conditions,

(xxxviii) "KIAA0166" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0166" encoded by a nucleic acid that hybridizes to the "KIAA0166" nucleic acid or its complement under low stringency conditions,

(xxxix) "KIAA0325 (FRAGMENT)" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0325 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0325 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xli) "KIAA0564" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0564" encoded by a nucleic acid that hybridizes to the "KIAA0564" nucleic acid or its complement under low stringency conditions,

(xlii) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,

(xliii) "LIB (leucine-rich repeat protein)" (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LIB (leucine-rich repeat protein)" encoded by a nucleic acid that hybridizes to the "LIB (leucine-rich repeat protein)" nucleic acid or its complement under low stringency conditions,

(xliv) "Laminin, gamma 1 " (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Laminin, gamma 1 " encoded by a nucleic acid that hybridizes to the "Laminin, gamma 1 " nucleic acid or its complement under low stringency conditions,

(xlv) "MBIP" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MBIP" encoded by a nucleic acid that hybridizes to the "MBIP" nucleic acid or its complement under low stringency conditions,

(xlvi) "MEGF7 (FRAGMENT)" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEGF7 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "MEGF7 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xlvii) "MT-ACT48" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MT-ACT48" encoded by a nucleic acid that hybridizes to the "MT-ACT48" nucleic acid or its complement under low stringency conditions,

- (xlvii) "Myosin IXB" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Myosin IXB" encoded by a nucleic acid that hybridizes to the "Myosin IXB" nucleic acid or its complement under low stringency conditions,
- (xlviii) "NEU1" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NEU1" encoded by a nucleic acid that hybridizes to the "NEU1" nucleic acid or its complement under low stringency conditions,
- (xlix) "NIPSNAP1" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP1" encoded by a nucleic acid that hybridizes to the "NIPSNAP1" nucleic acid or its complement under low stringency conditions,
- (l) "NIPSNAP2" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP2" encoded by a nucleic acid that hybridizes to the "NIPSNAP2" nucleic acid or its complement under low stringency conditions,
- (li) "Neurexin-1" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurexin-1" encoded by a nucleic acid that hybridizes to the "Neurexin-1" nucleic acid or its complement under low stringency conditions,
- (lii) "PDZ and LIM domain protein 1" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ and LIM domain protein 1" encoded by a nucleic acid that hybridizes to the "PDZ and LIM domain protein 1" nucleic acid or its complement under low stringency conditions,
- (liii) "PILB" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILB" encoded by a nucleic acid that hybridizes to the "PILB" nucleic acid or its complement under low stringency conditions,
- (liv) "PILT" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILT" encoded by a nucleic acid that hybridizes to the "PILT" nucleic acid or its complement under low stringency conditions,

- (iv) "Paladin" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Paladin" encoded by a nucleic acid that hybridizes to the "Paladin" nucleic acid or its complement under low stringency conditions,
- (lvi) "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" encoded by a nucleic acid that hybridizes to the "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" nucleic acid or its complement under low stringency conditions,
- (lvii) "Procollagen C-endopeptidase enhancer" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Procollagen C-endopeptidase enhancer" encoded by a nucleic acid that hybridizes to the "Procollagen C-endopeptidase enhancer" nucleic acid or its complement under low stringency conditions,
- (lviii) "Programmed cell death 10" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Programmed cell death 10" encoded by a nucleic acid that hybridizes to the "Programmed cell death 10" nucleic acid or its complement under low stringency conditions,
- (lix) "Protein similar to AGCP6688" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to AGCP6688" encoded by a nucleic acid that hybridizes to the "Protein similar to AGCP6688" nucleic acid or its complement under low stringency conditions,
- (lx) "RAB7L1" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB7L1" encoded by a nucleic acid that hybridizes to the "RAB7L1" nucleic acid or its complement under low stringency conditions,
- (lxi) "RANBP1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RANBP1" encoded by a nucleic acid that hybridizes to the "RANBP1" nucleic acid or its complement under low stringency conditions,
- (lxii) "RPGR-interacting protein 1" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

- "RPGR-interacting protein 1" encoded by a nucleic acid that hybridizes to the "RPGR-interacting protein 1" nucleic acid or its complement under low stringency conditions,
- (lxiii) "Reelin" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions,
- (lxiv) "SNAP-25" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SNAP-25" encoded by a nucleic acid that hybridizes to the "SNAP-25" nucleic acid or its complement under low stringency conditions,
- (lxv) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions,
- (lxvi) "STX1A" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX1A" encoded by a nucleic acid that hybridizes to the "STX1A" nucleic acid or its complement under low stringency conditions,
- (lxvii) "SUCLA2" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SUCLA2" encoded by a nucleic acid that hybridizes to the "SUCLA2" nucleic acid or its complement under low stringency conditions,
- (lxviii) "Serine/threonine protein phosphatase 6" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 6" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 6" nucleic acid or its complement under low stringency conditions,
- (lxix) "Sortilin-related receptor " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor " encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor " nucleic acid or its complement under low stringency conditions,
- (lxx) "Synaptogyrin 3" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Synaptogyrin

3" encoded by a nucleic acid that hybridizes to the "Synaptogyrin 3" nucleic acid or its complement under low stringency conditions,

(lxxi) "TYK2" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TYK2" encoded by a nucleic acid that hybridizes to the "TYK2" nucleic acid or its complement under low stringency conditions,

(lxxii) "Ubiquitin-protein ligase E3-alpha" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase E3-alpha" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase E3-alpha" nucleic acid or its complement under low stringency conditions,

(lxxiii) "VGF nerve growth factor inducible protein" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VGF nerve growth factor inducible protein" encoded by a nucleic acid that hybridizes to the "VGF nerve growth factor inducible protein" nucleic acid or its complement under low stringency conditions,

(lxxiv) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions,

(lxxv) "Zinc finger protein 198" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 198" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 198" nucleic acid or its complement under low stringency conditions,

(lxxvi) "hypothetical protein MGC13186" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC13186" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC13186" nucleic acid or its complement under low stringency conditions,

(lxxvii) "similar to SD27354p [Drosophila melanogaster] " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "similar to SD27354p [Drosophila melanogaster] " encoded by a nucleic acid that hybridizes to the "similar to SD27354p [Drosophila melanogaster] " nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.
6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.
7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of No. 1 - 7 that is involved in the the transactivation of reporter genes by APP-Gal4/VP16 (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).
9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the X11beta complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the X11beta complex selected from

(i) "ADAMTS-19" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ADAMTS-19" encoded by a nucleic acid that hybridizes to the "ADAMTS-19" nucleic acid or its complement under low stringency conditions,

(ii) "BAT1" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAT1" encoded by a nucleic acid that hybridizes to the "BAT1" nucleic acid or its complement under low stringency conditions,

(iii) "C20orf11 (sim to a region of RANBPM)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "C20orf11 (sim to a region of RANBPM)" encoded by a nucleic acid that hybridizes to the "C20orf11 (sim to a region of RANBPM)" nucleic acid or its complement under low stringency conditions,

(iv) "CGB0_HUMAN" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGB0_HUMAN" encoded by a nucleic acid that hybridizes to the "CGB0_HUMAN" nucleic acid or its complement under low stringency conditions,

(v) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,

- (vi) "Calsyntenin-2" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-2" encoded by a nucleic acid that hybridizes to the "Calsyntenin-2" nucleic acid or its complement under low stringency conditions,
- (vii) "Calsyntenin-3" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-3" encoded by a nucleic acid that hybridizes to the "Calsyntenin-3" nucleic acid or its complement under low stringency conditions,
- (viii) "Dkfzp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dkfzp586c1924" encoded by a nucleic acid that hybridizes to the "Dkfzp586c1924" nucleic acid or its complement under low stringency conditions,
- (ix) "ENG00000168820 (hypothetical protein with p-loop)" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG00000168820 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ENG00000168820 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions,
- (x) "FLJ13910" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13910" encoded by a nucleic acid that hybridizes to the "FLJ13910" nucleic acid or its complement under low stringency conditions,
- (xi) "HERC2 protein" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HERC2 protein" encoded by a nucleic acid that hybridizes to the "HERC2 protein" nucleic acid or its complement under low stringency conditions,
- (xii) "HSPC154" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC154" encoded by a nucleic acid that hybridizes to the "HSPC154" nucleic acid or its complement under low stringency conditions,
- (xiii) "HSPC245" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC245" encoded by a nucleic acid that hybridizes to the "HSPC245" nucleic acid or its complement under low stringency conditions,

(xiv) "HYPOTHETICAL PROTEIN FLJ10618" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ10618" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ10618" nucleic acid or its complement under low stringency conditions,

(xv) "HYPOTHETICAL PROTEIN FLJ12599" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ12599" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ12599" nucleic acid or its complement under low stringency conditions,

(xvi) "Hypothetical protein FLJ20397" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ20397" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ20397" nucleic acid or its complement under low stringency conditions,

(xvii) "KIAA0056" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0056" encoded by a nucleic acid that hybridizes to the "KIAA0056" nucleic acid or its complement under low stringency conditions,

(xviii) "KIAA0166" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0166" encoded by a nucleic acid that hybridizes to the "KIAA0166" nucleic acid or its complement under low stringency conditions,

(xix) "KIAA0564" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0564" encoded by a nucleic acid that hybridizes to the "KIAA0564" nucleic acid or its complement under low stringency conditions,

(xx) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,

(xxi) "MEGF7 (FRAGMENT)" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEGF7

- (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "MEGF7 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xxii) "MT-ACT48" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MT-ACT48" encoded by a nucleic acid that hybridizes to the "MT-ACT48" nucleic acid or its complement under low stringency conditions,
- (xxiii) "NIPSNAP1" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP1" encoded by a nucleic acid that hybridizes to the "NIPSNAP1" nucleic acid or its complement under low stringency conditions,
- (xxiv) "PDZ and LIM domain protein 1" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ and LIM domain protein 1" encoded by a nucleic acid that hybridizes to the "PDZ and LIM domain protein 1" nucleic acid or its complement under low stringency conditions,
- (xxv) "PILB" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILB" encoded by a nucleic acid that hybridizes to the "PILB" nucleic acid or its complement under low stringency conditions,
- (xxvi) "PILT" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILT" encoded by a nucleic acid that hybridizes to the "PILT" nucleic acid or its complement under low stringency conditions,
- (xxvii) "Paladin" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Paladin" encoded by a nucleic acid that hybridizes to the "Paladin" nucleic acid or its complement under low stringency conditions,
- (xxviii) "Programmed cell death 10" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Programmed cell death 10" encoded by a nucleic acid that hybridizes to the "Programmed cell death 10" nucleic acid or its complement under low stringency conditions,
- (xxix) "Protein similar to AGCP6688" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"Protein similar to AGCP6688" encoded by a nucleic acid that hybridizes to the "Protein similar to AGCP6688" nucleic acid or its complement under low stringency conditions, (xxx) "RAB7L1" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB7L1" encoded by a nucleic acid that hybridizes to the "RAB7L1" nucleic acid or its complement under low stringency conditions,

(xxxi) "Ubiquitin-protein ligase E3-alpha" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase E3-alpha" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase E3-alpha" nucleic acid or its complement under low stringency conditions,

(xxxii) "hypothetical protein MGC13186" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC13186" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC13186" nucleic acid or its complement under low stringency conditions, and

(xxxiii) "similar to SD27354p [*Drosophila melanogaster*]" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "similar to SD27354p [*Drosophila melanogaster*]" encoded by a nucleic acid that hybridizes to the "similar to SD27354p [*Drosophila melanogaster*]" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease; inflammatory conditions such as ulcerative colitis, Crohn's disease and arteriosclerosis.

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

(i) "ADAMTS-19" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ADAMTS-19" encoded by a nucleic acid that hybridizes to the "ADAMTS-19" nucleic acid or its complement under low stringency conditions,

(ii) "BAT1" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAT1" encoded by a nucleic acid that hybridizes to the "BAT1" nucleic acid or its complement under low stringency conditions,

(iii) "C20orf11 (sim to a region of RANBPM)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "C20orf11 (sim to a region of RANBPM)" encoded by a nucleic acid that hybridizes to the "C20orf11 (sim to a region of RANBPM)" nucleic acid or its complement under low stringency conditions,

(iv) "CGB0_HUMAN" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGB0_HUMAN" encoded by a nucleic acid that hybridizes to the "CGB0_HUMAN" nucleic acid or its complement under low stringency conditions,

(v) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,

(vi) "Calsyntenin-2" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-2"

encoded by a nucleic acid that hybridizes to the "Calsyntenin-2" nucleic acid or its complement under low stringency conditions,

(vii) "Calsyntenin-3" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-3" encoded by a nucleic acid that hybridizes to the "Calsyntenin-3" nucleic acid or its complement under low stringency conditions,

(viii) "Dkfzp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dkfzp586c1924" encoded by a nucleic acid that hybridizes to the "Dkfzp586c1924" nucleic acid or its complement under low stringency conditions,

(ix) "ENG00000168820 (hypothetical protein with p-loop)" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG00000168820 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ENG00000168820 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions,

(x) "FLJ13910" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13910" encoded by a nucleic acid that hybridizes to the "FLJ13910" nucleic acid or its complement under low stringency conditions,

(xi) "HERC2 protein" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HERC2 protein" encoded by a nucleic acid that hybridizes to the "HERC2 protein" nucleic acid or its complement under low stringency conditions,

(xii) "HSPC154" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC154" encoded by a nucleic acid that hybridizes to the "HSPC154" nucleic acid or its complement under low stringency conditions,

(xiii) "HSPC245" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC245" encoded by a nucleic acid that hybridizes to the "HSPC245" nucleic acid or its complement under low stringency conditions,

(xiv) "HYPOTHETICAL PROTEIN FLJ10618" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ10618" encoded by a nucleic acid that

hybridizes to the "HYPOTHETICAL PROTEIN FLJ10618" nucleic acid or its complement under low stringency conditions,

(xv) "HYPOTHETICAL PROTEIN FLJ12599" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ12599" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ12599" nucleic acid or its complement under low stringency conditions,

(xvi) "Hypothetical protein FLJ20397" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ20397" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ20397" nucleic acid or its complement under low stringency conditions,

(xvii) "KIAA0056" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0056" encoded by a nucleic acid that hybridizes to the "KIAA0056" nucleic acid or its complement under low stringency conditions,

(xviii) "KIAA0166" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0166" encoded by a nucleic acid that hybridizes to the "KIAA0166" nucleic acid or its complement under low stringency conditions,

(xix) "KIAA0564" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0564" encoded by a nucleic acid that hybridizes to the "KIAA0564" nucleic acid or its complement under low stringency conditions,

(xx) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,

(xxi) "MEGF7 (FRAGMENT)" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEGF7 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "MEGF7 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxii) "MT-ACT48" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MT-ACT48"

encoded by a nucleic acid that hybridizes to the "MT-ACT48" nucleic acid or its complement under low stringency conditions,

(xxiii) "NIPSNAP1" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP1" encoded by a nucleic acid that hybridizes to the "NIPSNAP1" nucleic acid or its complement under low stringency conditions,

(xxiv) "PDZ and LIM domain protein 1" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ and LIM domain protein 1" encoded by a nucleic acid that hybridizes to the "PDZ and LIM domain protein 1" nucleic acid or its complement under low stringency conditions,

(xxv) "PILB" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILB" encoded by a nucleic acid that hybridizes to the "PILB" nucleic acid or its complement under low stringency conditions,

(xxvi) "PILT" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILT" encoded by a nucleic acid that hybridizes to the "PILT" nucleic acid or its complement under low stringency conditions,

(xxvii) "Paladin" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Paladin" encoded by a nucleic acid that hybridizes to the "Paladin" nucleic acid or its complement under low stringency conditions,

(xxviii) "Programmed cell death 10" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Programmed cell death 10" encoded by a nucleic acid that hybridizes to the "Programmed cell death 10" nucleic acid or its complement under low stringency conditions,

(xxix) "Protein similar to AGCP6688" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to AGCP6688" encoded by a nucleic acid that hybridizes to the "Protein similar to AGCP6688" nucleic acid or its complement under low stringency conditions,

(xxx) "RAB7L1" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB7L1"

encoded by a nucleic acid that hybridizes to the "RAB7L1" nucleic acid or its complement under low stringency conditions,

(xxxi) "Ubiquitin-protein ligase E3-alpha" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase E3-alpha" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase E3-alpha" nucleic acid or its complement under low stringency conditions,

(xxxii) "hypothetical protein MGC13186" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC13186" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC13186" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "similar to SD27354p [Drosophila melanogaster] " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "similar to SD27354p [Drosophila melanogaster] " encoded by a nucleic acid that hybridizes to the "similar to SD27354p [Drosophila melanogaster] " nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative disease such as Alzheimer's disease; inflammatory conditions such as ulcerative colitis, Crohn's disease and arteriosclerosis.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

(i) "ADAMTS-19" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ADAMTS-19" encoded by a nucleic acid that hybridizes to the "ADAMTS-19" nucleic acid or its complement under low stringency conditions,

(ii) "BAT1" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAT1" encoded by a

nucleic acid that hybridizes to the "BAT1" nucleic acid or its complement under low stringency conditions,

- (iii) "C20orf11 (sim to a region of RANBPM)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "C20orf11 (sim to a region of RANBPM)" encoded by a nucleic acid that hybridizes to the "C20orf11 (sim to a region of RANBPM)" nucleic acid or its complement under low stringency conditions,
- (iv) "CGB0_HUMAN" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGB0_HUMAN" encoded by a nucleic acid that hybridizes to the "CGB0_HUMAN" nucleic acid or its complement under low stringency conditions,
- (v) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,
- (vi) "Calsyntenin-2" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-2" encoded by a nucleic acid that hybridizes to the "Calsyntenin-2" nucleic acid or its complement under low stringency conditions,
- (vii) "Calsyntenin-3" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-3" encoded by a nucleic acid that hybridizes to the "Calsyntenin-3" nucleic acid or its complement under low stringency conditions,
- (viii) "Dkfzp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dkfzp586c1924" encoded by a nucleic acid that hybridizes to the "Dkfzp586c1924" nucleic acid or its complement under low stringency conditions,
- (ix) "ENG00000168820 (hypothetical protein with p-loop)" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG00000168820 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ENG00000168820 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions,

- (x) "FLJ13910" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13910" encoded by a nucleic acid that hybridizes to the "FLJ13910" nucleic acid or its complement under low stringency conditions,
- (xi) "HERC2 protein" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HERC2 protein" encoded by a nucleic acid that hybridizes to the "HERC2 protein" nucleic acid or its complement under low stringency conditions,
- (xii) "HSPC154" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC154" encoded by a nucleic acid that hybridizes to the "HSPC154" nucleic acid or its complement under low stringency conditions,
- (xiii) "HSPC245" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC245" encoded by a nucleic acid that hybridizes to the "HSPC245" nucleic acid or its complement under low stringency conditions,
- (xiv) "HYPOTHETICAL PROTEIN FLJ10618" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ10618" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ10618" nucleic acid or its complement under low stringency conditions,
- (xv) "HYPOTHETICAL PROTEIN FLJ12599" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ12599" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ12599" nucleic acid or its complement under low stringency conditions,
- (xvi) "Hypothetical protein FLJ20397" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ20397" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ20397" nucleic acid or its complement under low stringency conditions,
- (xvii) "KIAA0056" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0056"

encoded by a nucleic acid that hybridizes to the "KIAA0056" nucleic acid or its complement under low stringency conditions,

(xviii) "KIAA0166" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0166" encoded by a nucleic acid that hybridizes to the "KIAA0166" nucleic acid or its complement under low stringency conditions,

(xix) "KIAA0564" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0564" encoded by a nucleic acid that hybridizes to the "KIAA0564" nucleic acid or its complement under low stringency conditions,

(xx) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,

(xxi) "MEGF7 (FRAGMENT)" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEGF7 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "MEGF7 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxii) "MT-ACT48" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MT-ACT48" encoded by a nucleic acid that hybridizes to the "MT-ACT48" nucleic acid or its complement under low stringency conditions,

(xxiii) "NIPSNAP1" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP1" encoded by a nucleic acid that hybridizes to the "NIPSNAP1" nucleic acid or its complement under low stringency conditions,

(xxiv) "PDZ and LIM domain protein 1" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ and LIM domain protein 1" encoded by a nucleic acid that hybridizes to the "PDZ and LIM domain protein 1" nucleic acid or its complement under low stringency conditions,

(xxv) "PILB" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILB" encoded by a

nucleic acid that hybridizes to the "PILB" nucleic acid or its complement under low stringency conditions,

(xxvi) "PILT" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILT" encoded by a nucleic acid that hybridizes to the "PILT" nucleic acid or its complement under low stringency conditions,

(xxvii) "Paladin" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Paladin" encoded by a nucleic acid that hybridizes to the "Paladin" nucleic acid or its complement under low stringency conditions,

(xxviii) "Programmed cell death 10" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Programmed cell death 10" encoded by a nucleic acid that hybridizes to the "Programmed cell death 10" nucleic acid or its complement under low stringency conditions,

(xxix) "Protein similar to AGCP6688" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to AGCP6688" encoded by a nucleic acid that hybridizes to the "Protein similar to AGCP6688" nucleic acid or its complement under low stringency conditions,

(xxx) "RAB7L1" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB7L1" encoded by a nucleic acid that hybridizes to the "RAB7L1" nucleic acid or its complement under low stringency conditions,

(xxxi) "Ubiquitin-protein ligase E3-alpha" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase E3-alpha" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase E3-alpha" nucleic acid or its complement under low stringency conditions,

(xxxii) "hypothetical protein MGC13186" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC13186" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC13186" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "similar to SD27354p [*Drosophila melanogaster*] " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "similar to SD27354p [*Drosophila melanogaster*] " encoded by a nucleic acid that hybridizes to the "similar to SD27354p [*Drosophila melanogaster*] " nucleic acid or its complement under low stringency conditions, comprising the steps of

- (a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and
- (b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of (a) exposing said complex, or a cell or organism containing X11beta complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of

said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether
(i) "ADAMTS-19" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ADAMTS-19" encoded by a nucleic acid that hybridizes to the "ADAMTS-19" nucleic acid or its complement under low stringency conditions, and/or

(ii) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions, and/or

(iii) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or

(iv) "Axonemal dynein heavy chain 8" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Axonemal dynein heavy chain 8" encoded by a nucleic acid that hybridizes to the "Axonemal dynein heavy chain 8" nucleic acid or its complement under low stringency conditions, and/or

(v) "BAT1" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAT1" encoded by a nucleic acid that hybridizes to the "BAT1" nucleic acid or its complement under low stringency conditions, and/or

(vi) "C20orf11 (sim to a region of RANBPM)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "C20orf11 (sim to a region of RANBPM)" encoded by a nucleic acid that hybridizes to the "C20orf11 (sim to a region of RANBPM)" nucleic acid or its complement under low stringency conditions, and/or

- (vii) "CGB0_HUMAN" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGB0_HUMAN" encoded by a nucleic acid that hybridizes to the "CGB0_HUMAN" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "Calsyntenin-1" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-1" encoded by a nucleic acid that hybridizes to the "Calsyntenin-1" nucleic acid or its complement under low stringency conditions, and/or
- (x) "Calsyntenin-2" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-2" encoded by a nucleic acid that hybridizes to the "Calsyntenin-2" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "Calsyntenin-3" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-3" encoded by a nucleic acid that hybridizes to the "Calsyntenin-3" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "Chondroitin sulfate proteoglycan 6" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Chondroitin sulfate proteoglycan 6" encoded by a nucleic acid that hybridizes to the "Chondroitin sulfate proteoglycan 6" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" encoded by a nucleic acid that hybridizes to the "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "DC6 protein" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DC6 protein"

encoded by a nucleic acid that hybridizes to the "DC6 protein" nucleic acid or its complement under low stringency conditions, and/or

(xv) "Dkfzp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dkfzp586c1924" encoded by a nucleic acid that hybridizes to the "Dkfzp586c1924" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "Dynein light chain 2A " (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain 2A " encoded by a nucleic acid that hybridizes to the "Dynein light chain 2A " nucleic acid or its complement under low stringency conditions, and/or

(xvii) "Dynein light chain-A" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain-A" encoded by a nucleic acid that hybridizes to the "Dynein light chain-A" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "ELAVL3" (SEQ ID No:40) or a functionally active derivative thereof; or a functionally active fragment thereof, or a homolog thereof, or a variant of "ELAVL3" encoded by a nucleic acid that hybridizes to the "ELAVL3" nucleic acid or its complement under low stringency conditions, and/or

(xix) "ENG00000168820 (hypothetical protein with p-loop)" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG00000168820 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ENG00000168820 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions, and/or

(xx) "Eukaryotic translation initiation factor 4A, isoform" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Eukaryotic translation initiation factor 4A, isoform" encoded by a nucleic acid that hybridizes to the "Eukaryotic translation initiation factor 4A, isoform" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "FLJ13910" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13910" encoded by a nucleic acid that hybridizes to the "FLJ13910" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "FRAP1" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FRAP1" encoded by a

nucleic acid that hybridizes to the "FRAP1" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "Filamin, gamma" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Filamin, gamma" encoded by a nucleic acid that hybridizes to the "Filamin, gamma" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "GTP-binding protein ERA" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTP-binding protein ERA" encoded by a nucleic acid that hybridizes to the "GTP-binding protein ERA" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "HADH2/ERAB (mitochondrial enzyme)" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HADH2/ERAB (mitochondrial enzyme)" encoded by a nucleic acid that hybridizes to the "HADH2/ERAB (mitochondrial enzyme)" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "HDAC2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HDAC2" encoded by a nucleic acid that hybridizes to the "HDAC2" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "HERC2 protein" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HERC2 protein" encoded by a nucleic acid that hybridizes to the "HERC2 protein" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "HSPC154" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC154" encoded by a nucleic acid that hybridizes to the "HSPC154" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "HSPC245" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC245" encoded by a nucleic acid that hybridizes to the "HSPC245" nucleic acid or its complement under low stringency conditions, and/or

(xxx) "HYPOTHETICAL PROTEIN FLJ10618" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "HYPOTHETICAL PROTEIN FLJ10618" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ10618" nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "HYPOTHETICAL PROTEIN FLJ12599" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ12599" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ12599" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "Hunc18a" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hunc18a" encoded by a nucleic acid that hybridizes to the "Hunc18a" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "Hypothetical protein FLJ10795" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ10795" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ10795" nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "Hypothetical protein FLJ20397" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ20397" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ20397" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "IKAP" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IKAP" encoded by a nucleic acid that hybridizes to the "IKAP" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "KIAA0056" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0056"

- encoded by a nucleic acid that hybridizes to the "KIAA0056" nucleic acid or its complement under low stringency conditions, and/or
- (xxxviii) "KIAA0166" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0166" encoded by a nucleic acid that hybridizes to the "KIAA0166" nucleic acid or its complement under low stringency conditions, and/or
- (xxxix) "KIAA0325 (FRAGMENT)" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0325 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0325 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or
- (xl) "KIAA0564" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0564" encoded by a nucleic acid that hybridizes to the "KIAA0564" nucleic acid or its complement under low stringency conditions, and/or
- (xli) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions, and/or
- (xlii) "LIB (leucine-rich repeat protein)" (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LIB (leucine-rich repeat protein)" encoded by a nucleic acid that hybridizes to the "LIB (leucine-rich repeat protein)" nucleic acid or its complement under low stringency conditions, and/or
- (xliii) "Laminin, gamma 1 " (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Laminin, gamma 1 " encoded by a nucleic acid that hybridizes to the "Laminin, gamma 1 " nucleic acid or its complement under low stringency conditions, and/or
- (xliv) "MBIP" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MBIP" encoded by a nucleic acid that hybridizes to the "MBIP" nucleic acid or its complement under low stringency conditions, and/or
- (xlv) "MEGF7 (FRAGMENT)" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEGF7

(FRAGMENT)" encoded by a nucleic acid that hybridizes to the "MEGF7 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xlv) "MT-ACT48" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MT-ACT48" encoded by a nucleic acid that hybridizes to the "MT-ACT48" nucleic acid or its complement under low stringency conditions, and/or

(xlvii) "Myosin IXB" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Myosin IXB" encoded by a nucleic acid that hybridizes to the "Myosin IXB" nucleic acid or its complement under low stringency conditions, and/or

(xlviii) "NEU1" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NEU1" encoded by a nucleic acid that hybridizes to the "NEU1" nucleic acid or its complement under low stringency conditions, and/or

(xlix) "NIPSNAP1" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP1" encoded by a nucleic acid that hybridizes to the "NIPSNAP1" nucleic acid or its complement under low stringency conditions, and/or

(l) "NIPSNAP2" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP2" encoded by a nucleic acid that hybridizes to the "NIPSNAP2" nucleic acid or its complement under low stringency conditions, and/or

(li) "Neurexin-1" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurexin-1" encoded by a nucleic acid that hybridizes to the "Neurexin-1" nucleic acid or its complement under low stringency conditions, and/or

(lii) "PDZ and LIM domain protein 1" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ and LIM domain protein 1" encoded by a nucleic acid that hybridizes to the "PDZ and LIM domain protein 1" nucleic acid or its complement under low stringency conditions, and/or

(liii) "PILB" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILB" encoded by a

nucleic acid that hybridizes to the "PILB" nucleic acid or its complement under low stringency conditions, and/or

(liv) "PILT" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILT" encoded by a nucleic acid that hybridizes to the "PILT" nucleic acid or its complement under low stringency conditions, and/or

(lv) "Paladin" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Paladin" encoded by a nucleic acid that hybridizes to the "Paladin" nucleic acid or its complement under low stringency conditions, and/or

(lvi) "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" encoded by a nucleic acid that hybridizes to the "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" nucleic acid or its complement under low stringency conditions, and/or

(lvii) "Procollagen C-endopeptidase enhancer" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Procollagen C-endopeptidase enhancer" encoded by a nucleic acid that hybridizes to the "Procollagen C-endopeptidase enhancer" nucleic acid or its complement under low stringency conditions, and/or

(lviii) "Programmed cell death 10" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Programmed cell death 10" encoded by a nucleic acid that hybridizes to the "Programmed cell death 10" nucleic acid or its complement under low stringency conditions, and/or

(lix) "Protein similar to AGCP6688" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to AGCP6688" encoded by a nucleic acid that hybridizes to the "Protein similar to AGCP6688" nucleic acid or its complement under low stringency conditions, and/or

(lx) "RAB7L1" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB7L1" encoded by a nucleic acid that hybridizes to the "RAB7L1" nucleic acid or its complement under low stringency conditions, and/or

- (lxi) "RANBP1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RANBP1" encoded by a nucleic acid that hybridizes to the "RANBP1" nucleic acid or its complement under low stringency conditions, and/or
- (lxii) "RPGR-interacting protein 1" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RPGR-interacting protein 1" encoded by a nucleic acid that hybridizes to the "RPGR-interacting protein 1" nucleic acid or its complement under low stringency conditions, and/or
- (lxiii) "Reelin" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions, and/or
- (lxiv) "SNAP-25" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SNAP-25" encoded by a nucleic acid that hybridizes to the "SNAP-25" nucleic acid or its complement under low stringency conditions, and/or
- (lxv) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions, and/or
- (lxvi) "STX1A" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX1A" encoded by a nucleic acid that hybridizes to the "STX1A" nucleic acid or its complement under low stringency conditions, and/or
- (lxvii) "SUCLA2" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SUCLA2" encoded by a nucleic acid that hybridizes to the "SUCLA2" nucleic acid or its complement under low stringency conditions, and/or
- (lxviii) "Serine/threonine protein phosphatase 6" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 6" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 6" nucleic acid or its complement under low stringency conditions, and/or

- (Ixxix) "Sortilin-related receptor " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor " encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor " nucleic acid or its complement under low stringency conditions, and/or
- (Ixxx) "Synaptogyrin 3" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Synaptogyrin 3" encoded by a nucleic acid that hybridizes to the "Synaptogyrin 3" nucleic acid or its complement under low stringency conditions, and/or
- (Ixxxi) "TYK2" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TYK2" encoded by a nucleic acid that hybridizes to the "TYK2" nucleic acid or its complement under low stringency conditions, and/or
- (Ixxxii) "Ubiquitin-protein ligase E3-alpha" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase E3-alpha" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase E3-alpha" nucleic acid or its complement under low stringency conditions, and/or
- (Ixxxiii) "VGF nerve growth factor inducible protein" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VGF nerve growth factor inducible protein" encoded by a nucleic acid that hybridizes to the "VGF nerve growth factor inducible protein" nucleic acid or its complement under low stringency conditions, and/or
- (Ixxxiv) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions, and/or
- (Ixxxv) "Zinc finger protein 198" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 198" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 198" nucleic acid or its complement under low stringency conditions, and/or
- (Ixxxvi) "hypothetical protein MGC13186" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC13186" encoded by a nucleic acid that hybridizes to

the "hypothetical protein MGC13186" nucleic acid or its complement under low stringency conditions, and/or (lxxvii) "similar to SD27354p [Drosophila melanogaster] " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "similar to SD27354p [Drosophila melanogaster] " encoded by a nucleic acid that hybridizes to the "similar to SD27354p [Drosophila melanogaster] " nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease; inflammatory conditions such as ulcerative colitis, Crohn's disease and arteriosclerosis.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease; inflammatory conditions such as ulcerative colitis, Crohn's disease and arteriosclerosis.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity,

or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether

- (i) "ADAMTS-19" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ADAMTS-19" encoded by a nucleic acid that hybridizes to the "ADAMTS-19" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "Axonemal dynein heavy chain 8" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Axonemal dynein heavy chain 8" encoded by a nucleic acid that hybridizes to the

"Axonemal dynein heavy chain 8" nucleic acid or its complement under low stringency conditions, and/or

(v) "BAT1" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAT1" encoded by a nucleic acid that hybridizes to the "BAT1" nucleic acid or its complement under low stringency conditions, and/or

(vi) "C20orf11 (sim to a region of RANBPM)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "C20orf11 (sim to a region of RANBPM)" encoded by a nucleic acid that hybridizes to the "C20orf11 (sim to a region of RANBPM)" nucleic acid or its complement under low stringency conditions, and/or

(vii) "CGB0_HUMAN" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGB0_HUMAN" encoded by a nucleic acid that hybridizes to the "CGB0_HUMAN" nucleic acid or its complement under low stringency conditions, and/or

(viii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions, and/or

(ix) "Calsyntenin-1" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-1" encoded by a nucleic acid that hybridizes to the "Calsyntenin-1" nucleic acid or its complement under low stringency conditions, and/or

(x) "Calsyntenin-2" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-2" encoded by a nucleic acid that hybridizes to the "Calsyntenin-2" nucleic acid or its complement under low stringency conditions, and/or

(xi) "Calsyntenin-3" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-3" encoded by a nucleic acid that hybridizes to the "Calsyntenin-3" nucleic acid or its complement under low stringency conditions, and/or

(xii) "Chondroitin sulfate proteoglycan 6" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "Chondroitin sulfate proteoglycan 6" encoded by a nucleic acid that hybridizes to the "Chondroitin sulfate proteoglycan 6" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" encoded by a nucleic acid that hybridizes to the "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "DC6 protein" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DC6 protein" encoded by a nucleic acid that hybridizes to the "DC6 protein" nucleic acid or its complement under low stringency conditions, and/or

(xv) "Dkfzp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dkfzp586c1924" encoded by a nucleic acid that hybridizes to the "Dkfzp586c1924" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "Dynein light chain 2A " (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain 2A " encoded by a nucleic acid that hybridizes to the "Dynein light chain 2A " nucleic acid or its complement under low stringency conditions, and/or

(xvii) "Dynein light chain-A" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain-A" encoded by a nucleic acid that hybridizes to the "Dynein light chain-A" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "ELAVL3" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ELAVL3" encoded by a nucleic acid that hybridizes to the "ELAVL3" nucleic acid or its complement under low stringency conditions, and/or

(xix) "ENG00000168820 (hypothetical protein with p-loop)" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG00000168820 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ENG00000168820 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions, and/or

(xx) "Eukaryotic translation initiation factor 4A, isoform" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Eukaryotic translation initiation factor 4A, isoform" encoded by a nucleic acid that hybridizes to the "Eukaryotic translation initiation factor 4A, isoform" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "FLJ13910" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13910" encoded by a nucleic acid that hybridizes to the "FLJ13910" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "FRAP1" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FRAP1" encoded by a nucleic acid that hybridizes to the "FRAP1" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "Filamin, gamma" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Filamin, gamma" encoded by a nucleic acid that hybridizes to the "Filamin, gamma" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "GTP-binding protein ERA" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTP-binding protein ERA" encoded by a nucleic acid that hybridizes to the "GTP-binding protein ERA" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "HADH2/ERAB (mitochondrial enzyme)" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HADH2/ERAB (mitochondrial enzyme)" encoded by a nucleic acid that hybridizes to the "HADH2/ERAB (mitochondrial enzyme)" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "HDAC2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HDAC2" encoded by a nucleic acid that hybridizes to the "HDAC2" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "HERC2 protein" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HERC2

protein" encoded by a nucleic acid that hybridizes to the "HERC2 protein" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "HSPC154" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC154" encoded by a nucleic acid that hybridizes to the "HSPC154" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "HSPC245" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC245" encoded by a nucleic acid that hybridizes to the "HSPC245" nucleic acid or its complement under low stringency conditions, and/or

(xxx) "HYPOTHETICAL PROTEIN FLJ10618" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ10618" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ10618" nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "HYPOTHETICAL PROTEIN FLJ12599" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ12599" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ12599" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "Hunc18a" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hunc18a" encoded by a nucleic acid that hybridizes to the "Hunc18a" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "Hypothetical protein FLJ10795" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ10795" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ10795" nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "Hypothetical protein FLJ20397" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ20397" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ20397" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "IKAP" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IKAP" encoded by a nucleic acid that hybridizes to the "IKAP" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "KIAA0056" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0056" encoded by a nucleic acid that hybridizes to the "KIAA0056" nucleic acid or its complement under low stringency conditions, and/or

(xxxviii) "KIAA0166" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0166" encoded by a nucleic acid that hybridizes to the "KIAA0166" nucleic acid or its complement under low stringency conditions, and/or

(xxxix) "KIAA0325 (FRAGMENT)" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0325 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0325 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xl) "KIAA0564" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0564" encoded by a nucleic acid that hybridizes to the "KIAA0564" nucleic acid or its complement under low stringency conditions, and/or

(xli) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions, and/or

(xlii) "LIB (leucine-rich repeat protein)" (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LIB (leucine-rich repeat protein)" encoded by a nucleic acid that hybridizes to the "LIB (leucine-rich repeat protein)" nucleic acid or its complement under low stringency conditions, and/or

- (xlili) "Laminin, gamma 1 " (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Laminin, gamma 1 " encoded by a nucleic acid that hybridizes to the "Laminin, gamma 1 " nucleic acid or its complement under low stringency conditions, and/or
- (xliv) "MBIP" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MBIP" encoded by a nucleic acid that hybridizes to the "MBIP" nucleic acid or its complement under low stringency conditions, and/or
- (xlv) "MEGF7 (FRAGMENT)" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEGF7 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "MEGF7 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or
- (xlvi) "MT-ACT48" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MT-ACT48" encoded by a nucleic acid that hybridizes to the "MT-ACT48" nucleic acid or its complement under low stringency conditions, and/or
- (xlvii) "Myosin IXB" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Myosin IXB" encoded by a nucleic acid that hybridizes to the "Myosin IXB" nucleic acid or its complement under low stringency conditions, and/or
- (xlviii) "NEU1" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NEU1" encoded by a nucleic acid that hybridizes to the "NEU1" nucleic acid or its complement under low stringency conditions, and/or
- (xlix) "NIPSNAP1" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP1" encoded by a nucleic acid that hybridizes to the "NIPSNAP1" nucleic acid or its complement under low stringency conditions, and/or
- (l) "NIPSNAP2" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP2" encoded by a nucleic acid that hybridizes to the "NIPSNAP2" nucleic acid or its complement under low stringency conditions, and/or
- (li) "Neurexin-1" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurexin-1"

encoded by a nucleic acid that hybridizes to the "Neurexin-1" nucleic acid or its complement under low stringency conditions, and/or

(iii) "PDZ and LIM domain protein 1" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDZ and LIM domain protein 1" encoded by a nucleic acid that hybridizes to the "PDZ and LIM domain protein 1" nucleic acid or its complement under low stringency conditions, and/or

(liii) "PILB" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILB" encoded by a nucleic acid that hybridizes to the "PILB" nucleic acid or its complement under low stringency conditions, and/or

(liv) "PILT" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILT" encoded by a nucleic acid that hybridizes to the "PILT" nucleic acid or its complement under low stringency conditions, and/or

(lv) "Paladin" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Paladin" encoded by a nucleic acid that hybridizes to the "Paladin" nucleic acid or its complement under low stringency conditions, and/or

(lvi) "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" encoded by a nucleic acid that hybridizes to the "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" nucleic acid or its complement under low stringency conditions, and/or

(lvii) "Procollagen C-endopeptidase enhancer" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Procollagen C-endopeptidase enhancer" encoded by a nucleic acid that hybridizes to the "Procollagen C-endopeptidase enhancer" nucleic acid or its complement under low stringency conditions, and/or

(lviii) "Programmed cell death 10" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Programmed cell death 10" encoded by a nucleic acid that hybridizes to the "Programmed cell death 10" nucleic acid or its complement under low stringency conditions, and/or

- (lix) "Protein similar to AGCP6688" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to AGCP6688" encoded by a nucleic acid that hybridizes to the "Protein similar to AGCP6688" nucleic acid or its complement under low stringency conditions, and/or
- (lx) "RAB7L1" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB7L1" encoded by a nucleic acid that hybridizes to the "RAB7L1" nucleic acid or its complement under low stringency conditions, and/or
- (lxi) "RANBP1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RANBP1" encoded by a nucleic acid that hybridizes to the "RANBP1" nucleic acid or its complement under low stringency conditions, and/or
- (lxii) "RPGR-interacting protein 1" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RPGR-interacting protein 1" encoded by a nucleic acid that hybridizes to the "RPGR-interacting protein 1" nucleic acid or its complement under low stringency conditions, and/or
- (lxiii) "Reelin" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions, and/or
- (lxiv) "SNAP-25" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SNAP-25" encoded by a nucleic acid that hybridizes to the "SNAP-25" nucleic acid or its complement under low stringency conditions, and/or
- (lxv) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions, and/or
- (lxvi) "STX1A" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX1A" encoded by a nucleic acid that hybridizes to the "STX1A" nucleic acid or its complement under low stringency conditions, and/or

(lxvii) "SUCLA2" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SUCLA2" encoded by a nucleic acid that hybridizes to the "SUCLA2" nucleic acid or its complement under low stringency conditions, and/or

(lxviii) "Serine/threonine protein phosphatase 6" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 6" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 6" nucleic acid or its complement under low stringency conditions, and/or

(lix) "Sortilin-related receptor " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor " encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor " nucleic acid or its complement under low stringency conditions, and/or

(lxx) "Synaptogyrin 3" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Synaptogyrin 3" encoded by a nucleic acid that hybridizes to the "Synaptogyrin 3" nucleic acid or its complement under low stringency conditions, and/or

(lxxi) "TYK2" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TYK2" encoded by a nucleic acid that hybridizes to the "TYK2" nucleic acid or its complement under low stringency conditions, and/or

(lxxii) "Ubiquitin-protein ligase E3-alpha" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase E3-alpha" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase E3-alpha" nucleic acid or its complement under low stringency conditions, and/or

(lxxiii) "VGF nerve growth factor inducible protein" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VGF nerve growth factor inducible protein" encoded by a nucleic acid that hybridizes to the "VGF nerve growth factor inducible protein" nucleic acid or its complement under low stringency conditions, and/or

(lxxiv) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta"

encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions, and/or

(lxxv) "Zinc finger protein 198" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 198" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 198" nucleic acid or its complement under low stringency conditions, and/or

(lxxvi) "hypothetical protein MGC13186" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC13186" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC13186" nucleic acid or its complement under low stringency conditions, and/or

(lxxvii) "similar to SD27354p [Drosophila melanogaster] " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "similar to SD27354p [Drosophila melanogaster] " encoded by a nucleic acid that hybridizes to the "similar to SD27354p [Drosophila melanogaster] " nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative disease such as Alzheimer's disease; inflammatory conditions such as ulcerative colitis, Crohn's disease and atherosclerosis.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, the transactivation of reporter genes by APP-Gal4/VP16 (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or

transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins

- (i) "ADAMTS-19" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ADAMTS-19" encoded by a nucleic acid that hybridizes to the "ADAMTS-19" nucleic acid or its complement under low stringency conditions,
- (ii) "APLP1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP1" encoded by a nucleic acid that hybridizes to the "APLP1" nucleic acid or its complement under low stringency conditions,
- (iii) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iv) "Axonemal dynein heavy chain 8" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Axonemal dynein heavy chain 8" encoded by a nucleic acid that hybridizes to the "Axonemal dynein heavy chain 8" nucleic acid or its complement under low stringency conditions,
- (v) "BAT1" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BAT1" encoded by a

nucleic acid that hybridizes to the "BAT1" nucleic acid or its complement under low stringency conditions,

(vi) "C20orf11 (sim to a region of RANBPM)" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "C20orf11 (sim to a region of RANBPM)" encoded by a nucleic acid that hybridizes to the "C20orf11 (sim to a region of RANBPM)" nucleic acid or its complement under low stringency conditions,

(vii) "CGB0_HUMAN" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGB0_HUMAN" encoded by a nucleic acid that hybridizes to the "CGB0_HUMAN" nucleic acid or its complement under low stringency conditions,

(viii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,

(ix) "Calsyntenin-1" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-1" encoded by a nucleic acid that hybridizes to the "Calsyntenin-1" nucleic acid or its complement under low stringency conditions,

(x) "Calsyntenin-2" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-2" encoded by a nucleic acid that hybridizes to the "Calsyntenin-2" nucleic acid or its complement under low stringency conditions,

(xi) "Calsyntenin-3" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin-3" encoded by a nucleic acid that hybridizes to the "Calsyntenin-3" nucleic acid or its complement under low stringency conditions,

(xii) "Chondroitin sulfate proteoglycan 6" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Chondroitin sulfate proteoglycan 6" encoded by a nucleic acid that hybridizes to the "Chondroitin sulfate proteoglycan 6" nucleic acid or its complement under low stringency conditions,

- (xiii) "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" encoded by a nucleic acid that hybridizes to the "Chromatin-specific transcription elongation factor FACT 140 kDa subunit" nucleic acid or its complement under low stringency conditions,
- (xiv) "DC6 protein" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DC6 protein" encoded by a nucleic acid that hybridizes to the "DC6 protein" nucleic acid or its complement under low stringency conditions,
- (xv) "Dkfzp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dkfzp586c1924" encoded by a nucleic acid that hybridizes to the "Dkfzp586c1924" nucleic acid or its complement under low stringency conditions,
- (xvi) "Dynein light chain 2A " (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain 2A " encoded by a nucleic acid that hybridizes to the "Dynein light chain 2A " nucleic acid or its complement under low stringency conditions,
- (xvii) "Dynein light chain-A" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynein light chain-A" encoded by a nucleic acid that hybridizes to the "Dynein light chain-A" nucleic acid or its complement under low stringency conditions,
- (xviii) "ELAVL3" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ELAVL3" encoded by a nucleic acid that hybridizes to the "ELAVL3" nucleic acid or its complement under low stringency conditions,
- (xix) "ENG00000168820 (hypothetical protein with p-loop)" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG00000168820 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ENG00000168820 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions,
- (xx) "Eukaryotic translation initiation factor 4A, isoform" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Eukaryotic translation initiation factor 4A, isoform" encoded by a nucleic

acid that hybridizes to the "Eukaryotic translation initiation factor 4A, isoform" nucleic acid or its complement under low stringency conditions,

(xxi) "FLJ13910" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13910" encoded by a nucleic acid that hybridizes to the "FLJ13910" nucleic acid or its complement under low stringency conditions,

(xxii) "FRAP1" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FRAP1" encoded by a nucleic acid that hybridizes to the "FRAP1" nucleic acid or its complement under low stringency conditions,

(xxiii) "Filamin, gamma" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Filamin, gamma" encoded by a nucleic acid that hybridizes to the "Filamin, gamma" nucleic acid or its complement under low stringency conditions,

(xxiv) "GTP-binding protein ERA" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTP-binding protein ERA" encoded by a nucleic acid that hybridizes to the "GTP-binding protein ERA" nucleic acid or its complement under low stringency conditions,

(xxv) "HADH2/ERAB (mitochondrial enzyme)" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HADH2/ERAB (mitochondrial enzyme)" encoded by a nucleic acid that hybridizes to the "HADH2/ERAB (mitochondrial enzyme)" nucleic acid or its complement under low stringency conditions,

(xxvi) "HDAC2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HDAC2" encoded by a nucleic acid that hybridizes to the "HDAC2" nucleic acid or its complement under low stringency conditions,

(xxvii) "HERC2 protein" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HERC2 protein" encoded by a nucleic acid that hybridizes to the "HERC2 protein" nucleic acid or its complement under low stringency conditions,

(xxviii) "HSPC154" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC154"

encoded by a nucleic acid that hybridizes to the "HSPC154" nucleic acid or its complement under low stringency conditions,

(xxix) "HSPC245" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HSPC245" encoded by a nucleic acid that hybridizes to the "HSPC245" nucleic acid or its complement under low stringency conditions,

(xxx) "HYPOTHETICAL PROTEIN FLJ10618" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ10618" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ10618" nucleic acid or its complement under low stringency conditions,

(xxxi) "HYPOTHETICAL PROTEIN FLJ12599" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN FLJ12599" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN FLJ12599" nucleic acid or its complement under low stringency conditions,

(xxxii) "Hunc18a" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hunc18a" encoded by a nucleic acid that hybridizes to the "Hunc18a" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Hypothetical protein FLJ10795" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ10795" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ10795" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Hypothetical protein FLJ20397" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ20397" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ20397" nucleic acid or its complement under low stringency conditions,

(xxxv) "IKAP" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IKAP" encoded by a nucleic acid that hybridizes to the "IKAP" nucleic acid or its complement under low stringency conditions,

- (xxxvi) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions,
- (xxxvii) "KIAA0056" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0056" encoded by a nucleic acid that hybridizes to the "KIAA0056" nucleic acid or its complement under low stringency conditions,
- (xxxviii) "KIAA0166" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0166" encoded by a nucleic acid that hybridizes to the "KIAA0166" nucleic acid or its complement under low stringency conditions,
- (xxxix) "KIAA0325 (FRAGMENT)" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0325 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0325 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xl) "KIAA0564" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0564" encoded by a nucleic acid that hybridizes to the "KIAA0564" nucleic acid or its complement under low stringency conditions,
- (xli) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,
- (xlii) "LIB (leucine-rich repeat protein)" (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LIB (leucine-rich repeat protein)" encoded by a nucleic acid that hybridizes to the "LIB (leucine-rich repeat protein)" nucleic acid or its complement under low stringency conditions,
- (xliii) "Laminin, gamma 1 " (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Laminin, gamma 1 " encoded by a nucleic acid that hybridizes to the "Laminin, gamma 1 " nucleic acid or its complement under low stringency conditions,

(xliv) "MBIP" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MBIP" encoded by a nucleic acid that hybridizes to the "MBIP" nucleic acid or its complement under low stringency conditions,

(xlv) "MEGF7 (FRAGMENT)" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEGF7 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "MEGF7 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xlvii) "MT-ACT48" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MT-ACT48" encoded by a nucleic acid that hybridizes to the "MT-ACT48" nucleic acid or its complement under low stringency conditions,

(xlviii) "Myosin IXB" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Myosin IXB" encoded by a nucleic acid that hybridizes to the "Myosin IXB" nucleic acid or its complement under low stringency conditions,

(xlix) "NEU1" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NEU1" encoded by a nucleic acid that hybridizes to the "NEU1" nucleic acid or its complement under low stringency conditions,

(l) "NIPSNAP1" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP1" encoded by a nucleic acid that hybridizes to the "NIPSNAP1" nucleic acid or its complement under low stringency conditions,

(li) "NIPSNAP2" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NIPSNAP2" encoded by a nucleic acid that hybridizes to the "NIPSNAP2" nucleic acid or its complement under low stringency conditions,

(lii) "Neurexin-1" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurexin-1" encoded by a nucleic acid that hybridizes to the "Neurexin-1" nucleic acid or its complement under low stringency conditions,

(liii) "PDZ and LIM domain protein 1" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"PDZ and LIM domain protein 1" encoded by a nucleic acid that hybridizes to the "PDZ and LIM domain protein 1" nucleic acid or its complement under low stringency conditions,

(liii) "PILB" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILB" encoded by a nucleic acid that hybridizes to the "PILB" nucleic acid or its complement under low stringency conditions,

(liv) "PILT" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PILT" encoded by a nucleic acid that hybridizes to the "PILT" nucleic acid or its complement under low stringency conditions,

(lv) "Paladin" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Paladin" encoded by a nucleic acid that hybridizes to the "Paladin" nucleic acid or its complement under low stringency conditions,

(lvi) "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" encoded by a nucleic acid that hybridizes to the "Phosphoenolpyruvate carboxykinase 2 (mitochondrial)" nucleic acid or its complement under low stringency conditions,

(lvii) "Procollagen C-endopeptidase enhancer" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Procollagen C-endopeptidase enhancer" encoded by a nucleic acid that hybridizes to the "Procollagen C-endopeptidase enhancer" nucleic acid or its complement under low stringency conditions,

(lviii) "Programmed cell death 10" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Programmed cell death 10" encoded by a nucleic acid that hybridizes to the "Programmed cell death 10" nucleic acid or its complement under low stringency conditions,

(lix) "Protein similar to AGCP6688" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to AGCP6688" encoded by a nucleic acid that hybridizes to the "Protein similar to AGCP6688" nucleic acid or its complement under low stringency conditions,

- (Ix) "RAB7L1" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB7L1" encoded by a nucleic acid that hybridizes to the "RAB7L1" nucleic acid or its complement under low stringency conditions,
- (Ixi) "RANBP1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RANBP1" encoded by a nucleic acid that hybridizes to the "RANBP1" nucleic acid or its complement under low stringency conditions,
- (Ixi) "RPGR-interacting protein 1" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RPGR-interacting protein 1" encoded by a nucleic acid that hybridizes to the "RPGR-interacting protein 1" nucleic acid or its complement under low stringency conditions,
- (Ixi) "Reelin" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions,
- (Ixiv) "SNAP-25" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SNAP-25" encoded by a nucleic acid that hybridizes to the "SNAP-25" nucleic acid or its complement under low stringency conditions,
- (Ixv) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions,
- (Ixvi) "STX1A" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX1A" encoded by a nucleic acid that hybridizes to the "STX1A" nucleic acid or its complement under low stringency conditions,
- (Ixvii) "SUCLA2" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SUCLA2" encoded by a nucleic acid that hybridizes to the "SUCLA2" nucleic acid or its complement under low stringency conditions,
- (Ixviii) "Serine/threonine protein phosphatase 6" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "Serine/threonine protein phosphatase 6" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 6" nucleic acid or its complement under low stringency conditions,

(Ixxix) "Sortilin-related receptor " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor " encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor " nucleic acid or its complement under low stringency conditions,

(Ixx) "Synaptogyrin 3" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Synaptogyrin 3" encoded by a nucleic acid that hybridizes to the "Synaptogyrin 3" nucleic acid or its complement under low stringency conditions,

(Ixxi) "TYK2" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TYK2" encoded by a nucleic acid that hybridizes to the "TYK2" nucleic acid or its complement under low stringency conditions,

(Ixxii) "Ubiquitin-protein ligase E3-alpha" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase E3-alpha" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase E3-alpha" nucleic acid or its complement under low stringency conditions,

(Ixxiii) "VGF nerve growth factor inducible protein" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VGF nerve growth factor inducible protein" encoded by a nucleic acid that hybridizes to the "VGF nerve growth factor inducible protein" nucleic acid or its complement under low stringency conditions,

(Ixxiv) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions,

(Ixxv) "Zinc finger protein 198" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Zinc finger protein 198" encoded by a nucleic acid that hybridizes to the "Zinc finger protein 198" nucleic acid or its complement under low stringency conditions,

(lxxvi) "hypothetical protein MGC13186" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC13186" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC13186" nucleic acid or its complement under low stringency conditions, and/or (lxxvii) "similar to SD27354p [Drosophila melanogaster] " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "similar to SD27354p [Drosophila melanogaster] " encoded by a nucleic acid that hybridizes to the "similar to SD27354p [Drosophila melanogaster] " nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease; inflammatory conditions such as ulcerative colitis, Crohn's disease and atherosclerosis.

The present invention further relates to the following embodiments of the Presenilin-2 complex

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein selected from the group consisting of:
 - (i) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
 - (ii) "DOCK3" (SEQ ID No:123) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DOCK3" encoded by a nucleic acid that hybridizes to the "DOCK3" nucleic acid or its complement under low stringency conditions,
 - (iii) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and
 - (iv) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2"

encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions, and

(b) at least one second protein, which second protein is selected from the group consisting of:

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
- (ii) "200 kDa proteasome activator" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "200 kDa proteasome activator" encoded by a nucleic acid that hybridizes to the "200 kDa proteasome activator" nucleic acid or its complement under low stringency conditions,
- (iii) "ABCB11" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCB11" encoded by a nucleic acid that hybridizes to the "ABCB11" nucleic acid or its complement under low stringency conditions,
- (iv) "ATM" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATM" encoded by a nucleic acid that hybridizes to the "ATM" nucleic acid or its complement under low stringency conditions,
- (v) "ATP-binding cassette protein, sub-family B, member 1" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette protein, sub-family B, member 1" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette protein, sub-family B, member 1" nucleic acid or its complement under low stringency conditions,
- (vi) "ATP-dependent metalloprotease FtsH1 homolog" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-dependent metalloprotease FtsH1 homolog" encoded by a nucleic acid that hybridizes to the "ATP-dependent metalloprotease FtsH1 homolog" nucleic acid or its complement under low stringency conditions,
- (vii) "ATP7A" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP7A" encoded by a

nucleic acid that hybridizes to the "ATP7A" nucleic acid or its complement under low stringency conditions,

(viii) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions,

(ix) "Adrenoleukodystrophy protein" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Adrenoleukodystrophy protein" encoded by a nucleic acid that hybridizes to the "Adrenoleukodystrophy protein" nucleic acid or its complement under low stringency conditions,

(x) "BIG1" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BIG1" encoded by a nucleic acid that hybridizes to the "BIG1" nucleic acid or its complement under low stringency conditions,

(xi) "BTAF1" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BTAF1" encoded by a nucleic acid that hybridizes to the "BTAF1" nucleic acid or its complement under low stringency conditions,

(xii) "CD97" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CD97" encoded by a nucleic acid that hybridizes to the "CD97" nucleic acid or its complement under low stringency conditions,

(xiii) "CDM_HUMAN" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDM_HUMAN" encoded by a nucleic acid that hybridizes to the "CDM_HUMAN" nucleic acid or its complement under low stringency conditions,

(xiv) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(xv) "CGI-51" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-51" encoded by a

nucleic acid that hybridizes to the "CGI-51" nucleic acid or its complement under low stringency conditions,

(xvi) "CHRNA3" (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CHRNA3" encoded by a nucleic acid that hybridizes to the "CHRNA3" nucleic acid or its complement under low stringency conditions,

(xvii) "Calcium-binding protein P22" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calcium-binding protein P22" encoded by a nucleic acid that hybridizes to the "Calcium-binding protein P22" nucleic acid or its complement under low stringency conditions,

(xviii) "Cation-chloride cotransporter-interacting protein" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cation-chloride cotransporter-interacting protein" encoded by a nucleic acid that hybridizes to the "Cation-chloride cotransporter-interacting protein" nucleic acid or its complement under low stringency conditions,

(xix) "Centromere/kinetochore protein ZW10 homolog" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Centromere/kinetochore protein ZW10 homolog" encoded by a nucleic acid that hybridizes to the "Centromere/kinetochore protein ZW10 homolog" nucleic acid or its complement under low stringency conditions,

(xx) "Cerebral protein 10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein 10" encoded by a nucleic acid that hybridizes to the "Cerebral protein 10" nucleic acid or its complement under low stringency conditions,

(xxi) "DAAM1" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DAAM1" encoded by a nucleic acid that hybridizes to the "DAAM1" nucleic acid or its complement under low stringency conditions,

(xxii) "DAPK1" (SEQ ID No:122) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DAPK1" encoded by a nucleic acid that hybridizes to the "DAPK1" nucleic acid or its complement under low stringency conditions,

(xxiii) "DKFZp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"DKFZp586c1924" encoded by a nucleic acid that hybridizes to the "DKFZp586c1924" nucleic acid or its complement under low stringency conditions,

(xxiv) "Down syndrome critical region protein 2" (SEQ ID No:124) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Down syndrome critical region protein 2" encoded by a nucleic acid that hybridizes to the "Down syndrome critical region protein 2" nucleic acid or its complement under low stringency conditions,

(xxv) "ECSIT" (SEQ ID No:125) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,

(xxvi) "FACL1" (SEQ ID No:126) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL1" encoded by a nucleic acid that hybridizes to the "FACL1" nucleic acid or its complement under low stringency conditions,

(xxvii) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xxviii) "FLJ20420" (SEQ ID No:128) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20420" encoded by a nucleic acid that hybridizes to the "FLJ20420" nucleic acid or its complement under low stringency conditions,

(xxix) "FLJ22555" (SEQ ID No:129) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22555" encoded by a nucleic acid that hybridizes to the "FLJ22555" nucleic acid or its complement under low stringency conditions,

(xxx) "FLJ22678" (SEQ ID No:130) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22678" encoded by a nucleic acid that hybridizes to the "FLJ22678" nucleic acid or its complement under low stringency conditions,

(xxxi) "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" (SEQ ID No:131) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Galactosylgalactosylxylosylprotein 3-beta-

- glucuronosyltransferase 3" encoded by a nucleic acid that hybridizes to the "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" nucleic acid or its complement under low stringency conditions,
- (xxxii) "HTRA2" (SEQ ID No:132) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HTRA2" encoded by a nucleic acid that hybridizes to the "HTRA2" nucleic acid or its complement under low stringency conditions,
- (xxxiii) "HU-K4 " (SEQ ID No:133) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HU-K4 " encoded by a nucleic acid that hybridizes to the "HU-K4 " nucleic acid or its complement under low stringency conditions,
- (xxxiv) "HYPOTHETICAL PROTEIN XP_174405" (SEQ ID No:134) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN XP_174405" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN XP_174405" nucleic acid or its complement under low stringency conditions,
- (xxxv) "Hypothetical protein FLJ23356" (SEQ ID No:135) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23356" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23356" nucleic acid or its complement under low stringency conditions,
- (xxxvi) "Hypothetical protein KIAA0455" (SEQ ID No:136) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0455" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0455" nucleic acid or its complement under low stringency conditions,
- (xxxvii) "Hypothetical protein KIAA0971-I" (SEQ ID No:137) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0971-I" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0971-I" nucleic acid or its complement under low stringency conditions,
- (xxxviii) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
 (xxxix) "KIAA0090" (SEQ ID No:139) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,

(xi) "KIAA0103" (SEQ ID No:140) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0103" encoded by a nucleic acid that hybridizes to the "KIAA0103" nucleic acid or its complement under low stringency conditions,

(xli) "MGC4248" (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248" encoded by a nucleic acid that hybridizes to the "MGC4248" nucleic acid or its complement under low stringency conditions,

(xlii) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions,

(xliii) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xliv) "NPC1" (SEQ ID No:144) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPC1" encoded by a nucleic acid that hybridizes to the "NPC1" nucleic acid or its complement under low stringency conditions,

(xlv) "NPD002" (SEQ ID No:145) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPD002" encoded by a nucleic acid that hybridizes to the "NPD002" nucleic acid or its complement under low stringency conditions,

(xlii) "NPL4, a component of the nuclear pore complex" (SEQ ID No:146) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPL4, a component of the nuclear pore complex"

encoded by a nucleic acid that hybridizes to the "NPL4, a component of the nuclear pore complex" nucleic acid or its complement under low stringency conditions,

(xlvii) "P63 protein" (SEQ ID No:148) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "P63 protein" encoded by a nucleic acid that hybridizes to the "P63 protein" nucleic acid or its complement under low stringency conditions,

(xlviii) "PSMA1" (SEQ ID No:149) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA1" encoded by a nucleic acid that hybridizes to the "PSMA1" nucleic acid or its complement under low stringency conditions,

(xlix) "PSMA3" (SEQ ID No:150) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA3" encoded by a nucleic acid that hybridizes to the "PSMA3" nucleic acid or its complement under low stringency conditions,

(l) "PSMA4" (SEQ ID No:151) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA4" encoded by a nucleic acid that hybridizes to the "PSMA4" nucleic acid or its complement under low stringency conditions,

(li) "PSMA6" (SEQ ID No:152) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA6" encoded by a nucleic acid that hybridizes to the "PSMA6" nucleic acid or its complement under low stringency conditions,

(lii) "PSMB1" (SEQ ID No:153) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB1" encoded by a nucleic acid that hybridizes to the "PSMB1" nucleic acid or its complement under low stringency conditions,

(liii) "PSMB2" (SEQ ID No:154) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB2" encoded by a nucleic acid that hybridizes to the "PSMB2" nucleic acid or its complement under low stringency conditions,

(liv) "PSMB3" (SEQ ID No:155) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB3" encoded by a nucleic acid that hybridizes to the "PSMB3" nucleic acid or its complement under low stringency conditions,

- (iv) "PSMB4" (SEQ ID No:156) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB4" encoded by a nucleic acid that hybridizes to the "PSMB4" nucleic acid or its complement under low stringency conditions,
- (lvi) "PSMB5" (SEQ ID No:157) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB5" encoded by a nucleic acid that hybridizes to the "PSMB5" nucleic acid or its complement under low stringency conditions,
- (lvii) "PSMB6" (SEQ ID No:158) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB6" encoded by a nucleic acid that hybridizes to the "PSMB6" nucleic acid or its complement under low stringency conditions,
- (lviii) "PSMC1" (SEQ ID No:159) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC1" encoded by a nucleic acid that hybridizes to the "PSMC1" nucleic acid or its complement under low stringency conditions,
- (lix) "PSMC2" (SEQ ID No:160) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC2" encoded by a nucleic acid that hybridizes to the "PSMC2" nucleic acid or its complement under low stringency conditions,
- (lx) "PSMC3" (SEQ ID No:161) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC3" encoded by a nucleic acid that hybridizes to the "PSMC3" nucleic acid or its complement under low stringency conditions,
- (lxi) "PSMC4" (SEQ ID No:162) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC4" encoded by a nucleic acid that hybridizes to the "PSMC4" nucleic acid or its complement under low stringency conditions,
- (lxii) "PSMC5" (SEQ ID No:163) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC5" encoded by a nucleic acid that hybridizes to the "PSMC5" nucleic acid or its complement under low stringency conditions,
- (lxiii) "PSMC6" (SEQ ID No:164) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC6"

encoded by a nucleic acid that hybridizes to the "PSMC6" nucleic acid or its complement under low stringency conditions,

(lxiv) "PSMD1" (SEQ ID No:165) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD1" encoded by a nucleic acid that hybridizes to the "PSMD1" nucleic acid or its complement under low stringency conditions,

(lxv) "PSMD11" (SEQ ID No:166) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD11" encoded by a nucleic acid that hybridizes to the "PSMD11" nucleic acid or its complement under low stringency conditions,

(lxvi) "PSMD12" (SEQ ID No:167) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD12" encoded by a nucleic acid that hybridizes to the "PSMD12" nucleic acid or its complement under low stringency conditions,

(lxvii) "PSMD13" (SEQ ID No:168) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD13" encoded by a nucleic acid that hybridizes to the "PSMD13" nucleic acid or its complement under low stringency conditions,

(lxviii) "PSMD2" (SEQ ID No:169) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD2" encoded by a nucleic acid that hybridizes to the "PSMD2" nucleic acid or its complement under low stringency conditions,

(lxix) "PSMD3" (SEQ ID No:170) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD3" encoded by a nucleic acid that hybridizes to the "PSMD3" nucleic acid or its complement under low stringency conditions,

(lxx) "PSMD4" (SEQ ID No:171) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD4" encoded by a nucleic acid that hybridizes to the "PSMD4" nucleic acid or its complement under low stringency conditions,

(lxxi) "Prohibitin" (SEQ ID No:173) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Prohibitin" encoded by a nucleic acid that hybridizes to the "Prohibitin" nucleic acid or its complement under low stringency conditions,

(lxxii) "RPS6KA3" (SEQ ID No:174) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RPS6KA3" encoded by a nucleic acid that hybridizes to the "RPS6KA3" nucleic acid or its complement under low stringency conditions,

(lxxiii) "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" (SEQ ID No:175) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" encoded by a nucleic acid that hybridizes to the "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" nucleic acid or its complement under low stringency conditions,

(lxxiv) "STRA6 isoform 1" (SEQ ID No:176) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STRA6 isoform 1" encoded by a nucleic acid that hybridizes to the "STRA6 isoform 1" nucleic acid or its complement under low stringency conditions,

(lxxv) "Serine/threonine protein phosphatase 6" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 6" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 6" nucleic acid or its complement under low stringency conditions,

(lxxvi) "Sortilin 1" (SEQ ID No:177) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin 1" encoded by a nucleic acid that hybridizes to the "Sortilin 1" nucleic acid or its complement under low stringency conditions,

(lxxvii) "Stearoyl-CoA desaturase" (SEQ ID No:178) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "Stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(lxxviii) "Tparl" (SEQ ID No:179) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tparl" encoded by a nucleic acid that hybridizes to the "Tparl" nucleic acid or its complement under low stringency conditions,

(lxxix) "Ubiquitin-protein ligase EDD" (SEQ ID No:180) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"Ubiquitin-protein ligase EDD" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase EDD" nucleic acid or its complement under low stringency conditions, (lxxx) "Voltage-dependent anion channel 2" (SEQ ID No:181) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Voltage-dependent anion channel 2" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 2" nucleic acid or its complement under low stringency conditions,

(lxxxi) "Wolframin" (SEQ ID No:182) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(lxxxii) "cholinergic receptor, nicotinic, alpha polypeptide 3" (SEQ ID No:183) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "cholinergic receptor, nicotinic, alpha polypeptide 3" encoded by a nucleic acid that hybridizes to the "cholinergic receptor, nicotinic, alpha polypeptide 3" nucleic acid or its complement under low stringency conditions, and (lxxxiii) "ensp00000297280 (hypothetical protein with p-loop)" (SEQ ID No:184) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ensp00000297280 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ensp00000297280 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein "Presenilin-2" (SEQ ID NO. 172), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'Presenilin-2'

encoded by a nucleic acid that hybridizes to the 'Presenilin-2' under low stringency conditions.

3. The protein complex according to No. 1 selected from complex (I) and comprising the following proteins:

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
- (ii) "200 kDa proteasome activator" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "200 kDa proteasome activator" encoded by a nucleic acid that hybridizes to the "200 kDa proteasome activator" nucleic acid or its complement under low stringency conditions,
- (iii) "ABCB11" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCB11" encoded by a nucleic acid that hybridizes to the "ABCB11" nucleic acid or its complement under low stringency conditions,
- (iv) "ATM" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATM" encoded by a nucleic acid that hybridizes to the "ATM" nucleic acid or its complement under low stringency conditions,
- (v) "ATP-binding cassette protein, sub-family B, member 1" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette protein, sub-family B, member 1" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette protein, sub-family B, member 1" nucleic acid or its complement under low stringency conditions,
- (vi) "ATP-dependent metalloprotease FtsH1 homolog" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-dependent metalloprotease FtsH1 homolog" encoded by a nucleic acid that hybridizes to the "ATP-dependent metalloprotease FtsH1 homolog" nucleic acid or its complement under low stringency conditions,

- (vii) "ATP7A" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP7A" encoded by a nucleic acid that hybridizes to the "ATP7A" nucleic acid or its complement under low stringency conditions,
- (viii) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions,
- (ix) "Adrenoleukodystrophy protein" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Adrenoleukodystrophy protein" encoded by a nucleic acid that hybridizes to the "Adrenoleukodystrophy protein" nucleic acid or its complement under low stringency conditions,
- (x) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
- (xi) "BIG1" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BIG1" encoded by a nucleic acid that hybridizes to the "BIG1" nucleic acid or its complement under low stringency conditions,
- (xii) "BTAF1" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BTAF1" encoded by a nucleic acid that hybridizes to the "BTAF1" nucleic acid or its complement under low stringency conditions,
- (xiii) "CD97" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CD97" encoded by a nucleic acid that hybridizes to the "CD97" nucleic acid or its complement under low stringency conditions,
- (xiv) "CDM_HUMAN" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDM_HUMAN" encoded by a nucleic acid that hybridizes to the "CDM_HUMAN" nucleic acid or its complement under low stringency conditions,

- (xv) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (xvi) "CGI-51" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-51" encoded by a nucleic acid that hybridizes to the "CGI-51" nucleic acid or its complement under low stringency conditions,
- (xvii) "CHRNA3" (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CHRNA3" encoded by a nucleic acid that hybridizes to the "CHRNA3" nucleic acid or its complement under low stringency conditions,
- (xviii) "Calcium-binding protein P22" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calcium-binding protein P22" encoded by a nucleic acid that hybridizes to the "Calcium-binding protein P22" nucleic acid or its complement under low stringency conditions,
- (xix) "Cation-chloride cotransporter-interacting protein" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cation-chloride cotransporter-interacting protein" encoded by a nucleic acid that hybridizes to the "Cation-chloride cotransporter-interacting protein" nucleic acid or its complement under low stringency conditions,
- (xx) "Centromere/kinetochore protein ZW10 homolog" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Centromere/kinetochore protein ZW10 homolog" encoded by a nucleic acid that hybridizes to the "Centromere/kinetochore protein ZW10 homolog" nucleic acid or its complement under low stringency conditions,
- (xxi) "Cerebral protein 10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein 10" encoded by a nucleic acid that hybridizes to the "Cerebral protein 10" nucleic acid or its complement under low stringency conditions,
- (xxii) "DAAM1" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DAAM1" encoded by a nucleic acid that hybridizes to the "DAAM1" nucleic acid or its complement under low stringency conditions,

- (xxiii) "DAPK1" (SEQ ID No:122) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DAPK1" encoded by a nucleic acid that hybridizes to the "DAPK1" nucleic acid or its complement under low stringency conditions,
- (xxiv) "DKFZp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DKFZp586c1924" encoded by a nucleic acid that hybridizes to the "DKFZp586c1924" nucleic acid or its complement under low stringency conditions,
- (xxv) "DOCK3" (SEQ ID No:123) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DOCK3" encoded by a nucleic acid that hybridizes to the "DOCK3" nucleic acid or its complement under low stringency conditions,
- (xxvi) "Down syndrome critical region protein 2" (SEQ ID No:124) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Down syndrome critical region protein 2" encoded by a nucleic acid that hybridizes to the "Down syndrome critical region protein 2" nucleic acid or its complement under low stringency conditions,
- (xxvii) "ECSIT" (SEQ ID No:125) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,
- (xxviii) "FACL1" (SEQ ID No:126) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL1" encoded by a nucleic acid that hybridizes to the "FACL1" nucleic acid or its complement under low stringency conditions,
- (xxix) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (xxx) "FLJ20420" (SEQ ID No:128) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20420" encoded by a nucleic acid that hybridizes to the "FLJ20420" nucleic acid or its complement under low stringency conditions,

(xxxi) "FLJ22555" (SEQ ID No:129) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22555" encoded by a nucleic acid that hybridizes to the "FLJ22555" nucleic acid or its complement under low stringency conditions,

(xxxii) "FLJ22678" (SEQ ID No:130) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22678" encoded by a nucleic acid that hybridizes to the "FLJ22678" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" (SEQ ID No:131) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" encoded by a nucleic acid that hybridizes to the "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" nucleic acid or its complement under low stringency conditions,

(xxxiv) "HTRA2" (SEQ ID No:132) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HTRA2" encoded by a nucleic acid that hybridizes to the "HTRA2" nucleic acid or its complement under low stringency conditions,

(xxxv) "HU-K4 " (SEQ ID No:133) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HU-K4 " encoded by a nucleic acid that hybridizes to the "HU-K4 " nucleic acid or its complement under low stringency conditions,

(xxxvi) "HYPOTHETICAL PROTEIN XP_174405" (SEQ ID No:134) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN XP_174405" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN XP_174405" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Hypothetical protein FLJ23356" (SEQ ID No:135) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23356" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23356" nucleic acid or its complement under low stringency conditions,

(xxxviii) "Hypothetical protein KIAA0455" (SEQ ID No:136) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "Hypothetical protein KIAA0455" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0455" nucleic acid or its complement under low stringency conditions,

(xxxix) "Hypothetical protein KIAA0971-I" (SEQ ID No:137) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0971-I" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0971-I" nucleic acid or its complement under low stringency conditions,

(xli) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xlii) "KIAA0090" (SEQ ID No:139) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,

(xliii) "KIAA0103" (SEQ ID No:140) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0103" encoded by a nucleic acid that hybridizes to the "KIAA0103" nucleic acid or its complement under low stringency conditions,

(xliv) "MGC4248" (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248" encoded by a nucleic acid that hybridizes to the "MGC4248" nucleic acid or its complement under low stringency conditions,

(xlv) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions,

(xli) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xlii) "NPC1" (SEQ ID No:144) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPC1" encoded by a

nucleic acid that hybridizes to the "NPC1" nucleic acid or its complement under low stringency conditions,

(xlvii) "NPD002" (SEQ ID No:145) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPD002" encoded by a nucleic acid that hybridizes to the "NPD002" nucleic acid or its complement under low stringency conditions,

(xlviii) "NPL4, a component of the nuclear pore complex" (SEQ ID No:146) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPL4, a component of the nuclear pore complex" encoded by a nucleic acid that hybridizes to the "NPL4, a component of the nuclear pore complex" nucleic acid or its complement under low stringency conditions,

(xlix) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(l) "P63 protein" (SEQ ID No:148) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "P63 protein" encoded by a nucleic acid that hybridizes to the "P63 protein" nucleic acid or its complement under low stringency conditions,

(li) "PSMA1" (SEQ ID No:149) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA1" encoded by a nucleic acid that hybridizes to the "PSMA1" nucleic acid or its complement under low stringency conditions,

(lii) "PSMA3" (SEQ ID No:150) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA3" encoded by a nucleic acid that hybridizes to the "PSMA3" nucleic acid or its complement under low stringency conditions,

(liii) "PSMA4" (SEQ ID No:151) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA4" encoded by a nucleic acid that hybridizes to the "PSMA4" nucleic acid or its complement under low stringency conditions,

(liv) "PSMA6" (SEQ ID No:152) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA6"

encoded by a nucleic acid that hybridizes to the "PSMA6" nucleic acid or its complement under low stringency conditions,

(lv) "PSMB1" (SEQ ID No:153) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB1" encoded by a nucleic acid that hybridizes to the "PSMB1" nucleic acid or its complement under low stringency conditions,

(lvi) "PSMB2" (SEQ ID No:154) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB2" encoded by a nucleic acid that hybridizes to the "PSMB2" nucleic acid or its complement under low stringency conditions,

(lvii) "PSMB3" (SEQ ID No:155) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB3" encoded by a nucleic acid that hybridizes to the "PSMB3" nucleic acid or its complement under low stringency conditions,

(lviii) "PSMB4" (SEQ ID No:156) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB4" encoded by a nucleic acid that hybridizes to the "PSMB4" nucleic acid or its complement under low stringency conditions,

(lix) "PSMB5" (SEQ ID No:157) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB5" encoded by a nucleic acid that hybridizes to the "PSMB5" nucleic acid or its complement under low stringency conditions,

(lx) "PSMB6" (SEQ ID No:158) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB6" encoded by a nucleic acid that hybridizes to the "PSMB6" nucleic acid or its complement under low stringency conditions,

(lxi) "PSMC1" (SEQ ID No:159) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC1" encoded by a nucleic acid that hybridizes to the "PSMC1" nucleic acid or its complement under low stringency conditions,

(lxii) "PSMC2" (SEQ ID No:160) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC2" encoded by a nucleic acid that hybridizes to the "PSMC2" nucleic acid or its complement under low stringency conditions,

(Ixm) "PSMC3" (SEQ ID No:161) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC3" encoded by a nucleic acid that hybridizes to the "PSMC3" nucleic acid or its complement under low stringency conditions,

(Ixiv) "PSMC4" (SEQ ID No:162) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC4" encoded by a nucleic acid that hybridizes to the "PSMC4" nucleic acid or its complement under low stringency conditions,

(Ixv) "PSMC5" (SEQ ID No:163) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC5" encoded by a nucleic acid that hybridizes to the "PSMC5" nucleic acid or its complement under low stringency conditions,

(Ixvi) "PSMC6" (SEQ ID No:164) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC6" encoded by a nucleic acid that hybridizes to the "PSMC6" nucleic acid or its complement under low stringency conditions,

(Ixvii) "PSMD1" (SEQ ID No:165) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD1" encoded by a nucleic acid that hybridizes to the "PSMD1" nucleic acid or its complement under low stringency conditions,

(Ixviii) "PSMD11" (SEQ ID No:166) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD11" encoded by a nucleic acid that hybridizes to the "PSMD11" nucleic acid or its complement under low stringency conditions,

(Ixix) "PSMD12" (SEQ ID No:167) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD12" encoded by a nucleic acid that hybridizes to the "PSMD12" nucleic acid or its complement under low stringency conditions,

(Ixx) "PSMD13" (SEQ ID No:168) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD13" encoded by a nucleic acid that hybridizes to the "PSMD13" nucleic acid or its complement under low stringency conditions,

(Ixxi) "PSMD2" (SEQ ID No:169) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD2"

encoded by a nucleic acid that hybridizes to the "PSMD2" nucleic acid or its complement under low stringency conditions,

(lxxii) "PSMD3" (SEQ ID No:170) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD3" encoded by a nucleic acid that hybridizes to the "PSMD3" nucleic acid or its complement under low stringency conditions,

(lxxiii) "PSMD4" (SEQ ID No:171) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD4" encoded by a nucleic acid that hybridizes to the "PSMD4" nucleic acid or its complement under low stringency conditions,

(lxxiv) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions,

(lxxv) "Prohibitin" (SEQ ID No:173) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Prohibitin" encoded by a nucleic acid that hybridizes to the "Prohibitin" nucleic acid or its complement under low stringency conditions,

(lxxvi) "RPS6KA3" (SEQ ID No:174) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RPS6KA3" encoded by a nucleic acid that hybridizes to the "RPS6KA3" nucleic acid or its complement under low stringency conditions,

(lxxvii) "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" (SEQ ID No:175) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" encoded by a nucleic acid that hybridizes to the "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" nucleic acid or its complement under low stringency conditions,

(lxxviii) "STRA6 isoform 1" (SEQ ID No:176) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STRA6 isoform 1" encoded by a nucleic acid that hybridizes to the "STRA6 isoform 1" nucleic acid or its complement under low stringency conditions,

(lxxix) "Serine/threonine protein phosphatase 6" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "Serine/threonine protein phosphatase 6" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 6" nucleic acid or its complement under low stringency conditions,

(lxxx) "Sortilin 1" (SEQ ID No:177) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin 1" encoded by a nucleic acid that hybridizes to the "Sortilin 1" nucleic acid or its complement under low stringency conditions,

(lxxxi) "Stearoyl-CoA desaturase" (SEQ ID No:178) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "Stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(lxxxii) "Tpar1" (SEQ ID No:179) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tpar1" encoded by a nucleic acid that hybridizes to the "Tpar1" nucleic acid or its complement under low stringency conditions,

(lxxxiii) "Ubiquitin-protein ligase EDD" (SEQ ID No:180) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase EDD" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase EDD" nucleic acid or its complement under low stringency conditions,

(lxxxiv) "Voltage-dependent anion channel 2" (SEQ ID No:181) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Voltage-dependent anion channel 2" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 2" nucleic acid or its complement under low stringency conditions,

(lxxxv) "Wolframin" (SEQ ID No:182) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(lxxxvi) "cholinergic receptor, nicotinic, alpha polypeptide 3" (SEQ ID No:183) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "cholinergic receptor, nicotinic, alpha polypeptide 3" encoded by a nucleic acid that hybridizes to the "cholinergic receptor, nicotinic, alpha polypeptide 3" nucleic acid or its complement under low stringency conditions, and/or

(lxxxvii) "ensp00000297280 (hypothetical protein with p-loop)" (SEQ ID No:184) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ensp00000297280 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ensp00000297280 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 82 of the following proteins:

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
- (ii) "200 kDa proteasome activator" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "200 kDa proteasome activator" encoded by a nucleic acid that hybridizes to the "200 kDa proteasome activator" nucleic acid or its complement under low stringency conditions,
- (iii) "ABCB11" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCB11" encoded by a nucleic acid that hybridizes to the "ABCB11" nucleic acid or its complement under low stringency conditions,
- (iv) "ATM" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATM" encoded by a nucleic acid that hybridizes to the "ATM" nucleic acid or its complement under low stringency conditions,
- (v) "ATP-binding cassette protein, sub-family B, member 1" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette protein, sub-family B, member 1" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette protein, sub-family B, member 1" nucleic acid or its complement under low stringency conditions,
- (vi) "ATP-dependent metalloprotease FtsH1 homolog" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-dependent metalloprotease FtsH1 homolog" encoded by a nucleic

acid that hybridizes to the "ATP-dependent metalloprotease FtsH1 homolog" nucleic acid or its complement under low stringency conditions,

(vii) "ATP7A" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP7A" encoded by a nucleic acid that hybridizes to the "ATP7A" nucleic acid or its complement under low stringency conditions,

(viii) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions,

(ix) "Adrenoleukodystrophy protein" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Adrenoleukodystrophy protein" encoded by a nucleic acid that hybridizes to the "Adrenoleukodystrophy protein" nucleic acid or its complement under low stringency conditions,

(x) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(xi) "BIG1" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BIG1" encoded by a nucleic acid that hybridizes to the "BIG1" nucleic acid or its complement under low stringency conditions,

(xii) "BTAF1" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BTAF1" encoded by a nucleic acid that hybridizes to the "BTAF1" nucleic acid or its complement under low stringency conditions,

(xiii) "CD97" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CD97" encoded by a nucleic acid that hybridizes to the "CD97" nucleic acid or its complement under low stringency conditions,

(xiv) "CDM_HUMAN" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

- "CDM_HUMAN" encoded by a nucleic acid that hybridizes to the "CDM_HUMAN" nucleic acid or its complement under low stringency conditions,
- (xv) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (xvi) "CGI-51" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-51" encoded by a nucleic acid that hybridizes to the "CGI-51" nucleic acid or its complement under low stringency conditions,
- (xvii) "CHRNA3" (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CHRNA3" encoded by a nucleic acid that hybridizes to the "CHRNA3" nucleic acid or its complement under low stringency conditions,
- (xviii) "Calcium-binding protein P22" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calcium-binding protein P22" encoded by a nucleic acid that hybridizes to the "Calcium-binding protein P22" nucleic acid or its complement under low stringency conditions,
- (xix) "Cation-chloride cotransporter-interacting protein" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cation-chloride cotransporter-interacting protein" encoded by a nucleic acid that hybridizes to the "Cation-chloride cotransporter-interacting protein" nucleic acid or its complement under low stringency conditions,
- (xx) "Centromere/kinetochore protein ZW10 homolog" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Centromere/kinetochore protein ZW10 homolog" encoded by a nucleic acid that hybridizes to the "Centromere/kinetochore protein ZW10 homolog" nucleic acid or its complement under low stringency conditions,
- (xxi) "Cerebral protein 10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein 10" encoded by a nucleic acid that hybridizes to the "Cerebral protein 10" nucleic acid or its complement under low stringency conditions,
- (xxii) "DAAM1" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DAAM1"

encoded by a nucleic acid that hybridizes to the "DAAM1" nucleic acid or its complement under low stringency conditions,

(xxiii) "DAPK1" (SEQ ID No:122) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DAPK1" encoded by a nucleic acid that hybridizes to the "DAPK1" nucleic acid or its complement under low stringency conditions,

(xxiv) "DKFZp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DKFZp586c1924" encoded by a nucleic acid that hybridizes to the "DKFZp586c1924" nucleic acid or its complement under low stringency conditions,

(xxv) "DOCK3" (SEQ ID No:123) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DOCK3" encoded by a nucleic acid that hybridizes to the "DOCK3" nucleic acid or its complement under low stringency conditions,

(xxvi) "Down syndrome critical region protein 2" (SEQ ID No:124) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Down syndrome critical region protein 2" encoded by a nucleic acid that hybridizes to the "Down syndrome critical region protein 2" nucleic acid or its complement under low stringency conditions,

(xxvii) "ECSIT" (SEQ ID No:125) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,

(xxviii) "FACL1" (SEQ ID No:126) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL1" encoded by a nucleic acid that hybridizes to the "FACL1" nucleic acid or its complement under low stringency conditions,

(xxix) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xxx) "FLJ20420" (SEQ ID No:128) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20420"

encoded by a nucleic acid that hybridizes to the "FLJ20420" nucleic acid or its complement under low stringency conditions,

(xxxi) "FLJ22555" (SEQ ID No:129) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22555" encoded by a nucleic acid that hybridizes to the "FLJ22555" nucleic acid or its complement under low stringency conditions,

(xxxii) "FLJ22678" (SEQ ID No:130) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22678" encoded by a nucleic acid that hybridizes to the "FLJ22678" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" (SEQ ID No:131) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" encoded by a nucleic acid that hybridizes to the "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" nucleic acid or its complement under low stringency conditions,

(xxxiv) "HTRA2" (SEQ ID No:132) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HTRA2" encoded by a nucleic acid that hybridizes to the "HTRA2" nucleic acid or its complement under low stringency conditions,

(xxxv) "HU-K4 " (SEQ ID No:133) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HU-K4 " encoded by a nucleic acid that hybridizes to the "HU-K4 " nucleic acid or its complement under low stringency conditions,

(xxxvi) "HYPOTHETICAL PROTEIN XP_174405" (SEQ ID No:134) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN XP_174405" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN XP_174405" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Hypothetical protein FLJ23356" (SEQ ID No:135) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23356" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23356" nucleic acid or its complement under low stringency conditions,

(xxxviii) "Hypothetical protein KIAA0455" (SEQ ID No:136) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0455" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0455" nucleic acid or its complement under low stringency conditions,

(xxxix) "Hypothetical protein KIAA0971-I" (SEQ ID No:137) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0971-I" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0971-I" nucleic acid or its complement under low stringency conditions,

(xl) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xli) "KIAA0090" (SEQ ID No:139) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,

(xlii) "KIAA0103" (SEQ ID No:140) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0103" encoded by a nucleic acid that hybridizes to the "KIAA0103" nucleic acid or its complement under low stringency conditions,

(xliii) "MGC4248" (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248" encoded by a nucleic acid that hybridizes to the "MGC4248" nucleic acid or its complement under low stringency conditions,

(xliv) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions,

(xlv) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

- (xlvii) "NPC1" (SEQ ID No:144) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPC1" encoded by a nucleic acid that hybridizes to the "NPC1" nucleic acid or its complement under low stringency conditions,
- (xlviii) "NPD002" (SEQ ID No:145) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPD002" encoded by a nucleic acid that hybridizes to the "NPD002" nucleic acid or its complement under low stringency conditions,
- (xlix) "NPL4, a component of the nuclear pore complex" (SEQ ID No:146) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPL4, a component of the nuclear pore complex" encoded by a nucleic acid that hybridizes to the "NPL4, a component of the nuclear pore complex" nucleic acid or its complement under low stringency conditions,
- (l) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (ii) "P63 protein" (SEQ ID No:148) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "P63 protein" encoded by a nucleic acid that hybridizes to the "P63 protein" nucleic acid or its complement under low stringency conditions,
- (iii) "PSMA1" (SEQ ID No:149) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA1" encoded by a nucleic acid that hybridizes to the "PSMA1" nucleic acid or its complement under low stringency conditions,
- (iv) "PSMA3" (SEQ ID No:150) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA3" encoded by a nucleic acid that hybridizes to the "PSMA3" nucleic acid or its complement under low stringency conditions,
- (v) "PSMA4" (SEQ ID No:151) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA4" encoded by a nucleic acid that hybridizes to the "PSMA4" nucleic acid or its complement under low stringency conditions,

- (liv) "PSMA6" (SEQ ID No:152) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA6" encoded by a nucleic acid that hybridizes to the "PSMA6" nucleic acid or its complement under low stringency conditions,
- (lv) "PSMB1" (SEQ ID No:153) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB1" encoded by a nucleic acid that hybridizes to the "PSMB1" nucleic acid or its complement under low stringency conditions,
- (lvi) "PSMB2" (SEQ ID No:154) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB2" encoded by a nucleic acid that hybridizes to the "PSMB2" nucleic acid or its complement under low stringency conditions,
- (lvii) "PSMB3" (SEQ ID No:155) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB3" encoded by a nucleic acid that hybridizes to the "PSMB3" nucleic acid or its complement under low stringency conditions,
- (lviii) "PSMB4" (SEQ ID No:156) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB4" encoded by a nucleic acid that hybridizes to the "PSMB4" nucleic acid or its complement under low stringency conditions,
- (lix) "PSMB5" (SEQ ID No:157) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB5" encoded by a nucleic acid that hybridizes to the "PSMB5" nucleic acid or its complement under low stringency conditions,
- (lx) "PSMB6" (SEQ ID No:158) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB6" encoded by a nucleic acid that hybridizes to the "PSMB6" nucleic acid or its complement under low stringency conditions,
- (lxi) "PSMC1" (SEQ ID No:159) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC1" encoded by a nucleic acid that hybridizes to the "PSMC1" nucleic acid or its complement under low stringency conditions,
- (lxii) "PSMC2" (SEQ ID No:160) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC2"

encoded by a nucleic acid that hybridizes to the "PSMC2" nucleic acid or its complement under low stringency conditions,

(Ixm) "PSMC3" (SEQ ID No:161) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC3" encoded by a nucleic acid that hybridizes to the "PSMC3" nucleic acid or its complement under low stringency conditions,

(Ixiv) "PSMC4" (SEQ ID No:162) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC4" encoded by a nucleic acid that hybridizes to the "PSMC4" nucleic acid or its complement under low stringency conditions,

(Ixv) "PSMC5" (SEQ ID No:163) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC5" encoded by a nucleic acid that hybridizes to the "PSMC5" nucleic acid or its complement under low stringency conditions,

(Ixvi) "PSMC6" (SEQ ID No:164) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC6" encoded by a nucleic acid that hybridizes to the "PSMC6" nucleic acid or its complement under low stringency conditions,

(Ixvii) "PSMD1" (SEQ ID No:165) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD1" encoded by a nucleic acid that hybridizes to the "PSMD1" nucleic acid or its complement under low stringency conditions,

(Ixviii) "PSMD11" (SEQ ID No:166) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD11" encoded by a nucleic acid that hybridizes to the "PSMD11" nucleic acid or its complement under low stringency conditions,

(Ixix) "PSMD12" (SEQ ID No:167) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD12" encoded by a nucleic acid that hybridizes to the "PSMD12" nucleic acid or its complement under low stringency conditions,

(Ixx) "PSMD13" (SEQ ID No:168) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD13" encoded by a nucleic acid that hybridizes to the "PSMD13" nucleic acid or its complement under low stringency conditions,

(lxxi) "PSMD2" (SEQ ID No:169) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD2" encoded by a nucleic acid that hybridizes to the "PSMD2" nucleic acid or its complement under low stringency conditions,

(lxxii) "PSMD3" (SEQ ID No:170) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD3" encoded by a nucleic acid that hybridizes to the "PSMD3" nucleic acid or its complement under low stringency conditions,

(lxxiii) "PSMD4" (SEQ ID No:171) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD4" encoded by a nucleic acid that hybridizes to the "PSMD4" nucleic acid or its complement under low stringency conditions,

(lxxiv) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions,

(lxxv) "Prohibitin" (SEQ ID No:173) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Prohibitin" encoded by a nucleic acid that hybridizes to the "Prohibitin" nucleic acid or its complement under low stringency conditions,

(lxxvi) "RPS6KA3" (SEQ ID No:174) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RPS6KA3" encoded by a nucleic acid that hybridizes to the "RPS6KA3" nucleic acid or its complement under low stringency conditions,

(lxxvii) "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" (SEQ ID No:175) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" encoded by a nucleic acid that hybridizes to the "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" nucleic acid or its complement under low stringency conditions,

(lxxviii) "STRA6 isoform 1" (SEQ ID No:176) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STRA6 isoform 1" encoded by a nucleic acid that hybridizes to the "STRA6 isoform 1" nucleic acid or its complement under low stringency conditions,

(lxxix) "Serine/threonine protein phosphatase 6" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 6" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 6" nucleic acid or its complement under low stringency conditions,

(lxxx) "Sortilin 1" (SEQ ID No:177) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin 1" encoded by a nucleic acid that hybridizes to the "Sortilin 1" nucleic acid or its complement under low stringency conditions,

(lxxxi) "Stearoyl-CoA desaturase" (SEQ ID No:178) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "Stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(lxxxii) "Tparl" (SEQ ID No:179) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tparl" encoded by a nucleic acid that hybridizes to the "Tparl" nucleic acid or its complement under low stringency conditions,

(lxxxiii) "Ubiquitin-protein ligase EDD" (SEQ ID No:180) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase EDD" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase EDD" nucleic acid or its complement under low stringency conditions,

(lxxxiv) "Voltage-dependent anion channel 2" (SEQ ID No:181) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Voltage-dependent anion channel 2" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 2" nucleic acid or its complement under low stringency conditions,

(lxxxv) "Wolframin" (SEQ ID No:182) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(lxxxvi) "cholinergic receptor, nicotinic, alpha polypeptide 3" (SEQ ID No:183) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "cholinergic receptor, nicotinic, alpha polypeptide 3"

encoded by a nucleic acid that hybridizes to the "cholinergic receptor, nicotinic, alpha polypeptide 3" nucleic acid or its complement under low stringency conditions, (lxxxvii) "ensp00000297280 (hypothetical protein with p-loop)" (SEQ ID No:184) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ensp00000297280 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ensp00000297280 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.
10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.
12. Component of the Presenilin 2 complex obtainable by a process according to any of No. 9 - 11.
13. Protein of the Presenilin 2 complex selected from
- (i) "CDM_HUMAN" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDM_HUMAN" encoded by a nucleic acid that hybridizes to the "CDM_HUMAN" nucleic acid or its complement under low stringency conditions,
 - (ii) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
 - (iii) "CGI-51" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-51" encoded by a nucleic acid that hybridizes to the "CGI-51" nucleic acid or its complement under low stringency conditions,
 - (iv) "Cerebral protein 10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein 10" encoded by a nucleic acid that hybridizes to the "Cerebral protein 10" nucleic acid or its complement under low stringency conditions,

- (v) "DKFZp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DKFZp586c1924" encoded by a nucleic acid that hybridizes to the "DKFZp586c1924" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (vii) "FLJ20420" (SEQ ID No:128) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20420" encoded by a nucleic acid that hybridizes to the "FLJ20420" nucleic acid or its complement under low stringency conditions,
- (viii) "FLJ22555" (SEQ ID No:129) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22555" encoded by a nucleic acid that hybridizes to the "FLJ22555" nucleic acid or its complement under low stringency conditions,
- (ix) "FLJ22678" (SEQ ID No:130) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22678" encoded by a nucleic acid that hybridizes to the "FLJ22678" nucleic acid or its complement under low stringency conditions,
- (x) "HYPOTHETICAL PROTEIN XP_174405" (SEQ ID No:134) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN XP_174405" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN XP_174405" nucleic acid or its complement under low stringency conditions,
- (xi) "Hypothetical protein FLJ23356" (SEQ ID No:135) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23356" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23356" nucleic acid or its complement under low stringency conditions,
- (xii) "Hypothetical protein KIAA0455" (SEQ ID No:136) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0455" encoded by a nucleic acid that hybridizes to the

"Hypothetical protein KIAA0455" nucleic acid or its complement under low stringency conditions,

(xiii) "Hypothetical protein KIAA0971-I" (SEQ ID No:137) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0971-I" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0971-I" nucleic acid or its complement under low stringency conditions,

(xiv) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xv) "KIAA0090" (SEQ ID No:139) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,

(xvi) "KIAA0103" (SEQ ID No:140) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0103" encoded by a nucleic acid that hybridizes to the "KIAA0103" nucleic acid or its complement under low stringency conditions,

(xvii) "MGC4248" (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248" encoded by a nucleic acid that hybridizes to the "MGC4248" nucleic acid or its complement under low stringency conditions,

(xviii) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions,

(xix) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xx) "NPL4, a component of the nuclear pore complex" (SEQ ID No:146) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPL4, a component of the nuclear pore complex" encoded by a nucleic

acid that hybridizes to the "NPL4, a component of the nuclear pore complex" nucleic acid or its complement under low stringency conditions,

(xxi) "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" (SEQ ID No:175) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" encoded by a nucleic acid that hybridizes to the "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" nucleic acid or its complement under low stringency conditions,

(xxii) "STRA6 isoform 1" (SEQ ID No:176) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STRA6 isoform 1" encoded by a nucleic acid that hybridizes to the "STRA6 isoform 1" nucleic acid or its complement under low stringency conditions,

(xxiii) "Tparl" (SEQ ID No:179) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tparl" encoded by a nucleic acid that hybridizes to the "Tparl" nucleic acid or its complement under low stringency conditions, and

(xxiv) "ensp00000297280 (hypothetical protein with p-loop)" (SEQ ID No:184) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ensp00000297280 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ensp00000297280 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

- (i) "CDM_HUMAN" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDM_HUMAN" encoded by a nucleic acid that hybridizes to the "CDM_HUMAN" nucleic acid or its complement under low stringency conditions,
- (ii) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (iii) "CGI-51" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-51" encoded by a nucleic acid that hybridizes to the "CGI-51" nucleic acid or its complement under low stringency conditions,
- (iv) "Cerebral protein 10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein 10" encoded by a nucleic acid that hybridizes to the "Cerebral protein 10" nucleic acid or its complement under low stringency conditions,
- (v) "DKFZp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DKFZp586c1924" encoded by a nucleic acid that hybridizes to the "DKFZp586c1924" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342"

- encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (vii) "FLJ20420" (SEQ ID No:128) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20420" encoded by a nucleic acid that hybridizes to the "FLJ20420" nucleic acid or its complement under low stringency conditions,
- (viii) "FLJ22555" (SEQ ID No:129) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22555" encoded by a nucleic acid that hybridizes to the "FLJ22555" nucleic acid or its complement under low stringency conditions,
- (ix) "FLJ22678" (SEQ ID No:130) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22678" encoded by a nucleic acid that hybridizes to the "FLJ22678" nucleic acid or its complement under low stringency conditions,
- (x) "HYPOTHETICAL PROTEIN XP_174405" (SEQ ID No:134) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN XP_174405" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN XP_174405" nucleic acid or its complement under low stringency conditions,
- (xi) "Hypothetical protein FLJ23356" (SEQ ID No:135) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23356" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23356" nucleic acid or its complement under low stringency conditions,
- (xii) "Hypothetical protein KIAA0455" (SEQ ID No:136) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0455" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0455" nucleic acid or its complement under low stringency conditions,
- (xiii) "Hypothetical protein KIAA0971-I" (SEQ ID No:137) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0971-I" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0971-I" nucleic acid or its complement under low stringency conditions,

- (xiv) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xv) "KIAA0090" (SEQ ID No:139) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,
- (xvi) "KIAA0103" (SEQ ID No:140) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0103" encoded by a nucleic acid that hybridizes to the "KIAA0103" nucleic acid or its complement under low stringency conditions,
- (xvii) "MGC4248" (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248" encoded by a nucleic acid that hybridizes to the "MGC4248" nucleic acid or its complement under low stringency conditions,
- (xviii) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions,
- (xix) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,
- (xx) "NPL4, a component of the nuclear pore complex" (SEQ ID No:146) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPL4, a component of the nuclear pore complex" encoded by a nucleic acid that hybridizes to the "NPL4, a component of the nuclear pore complex" nucleic acid or its complement under low stringency conditions,
- (xxi) "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" (SEQ ID No:175) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" encoded by a nucleic acid that hybridizes to the "SIMILAR TO GAMMA

INTERFERON INDUCIBLE GENE IP10" nucleic acid or its complement under low stringency conditions,

(xxii) "STRA6 isoform 1" (SEQ ID No:176) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STRA6 isoform 1" encoded by a nucleic acid that hybridizes to the "STRA6 isoform 1" nucleic acid or its complement under low stringency conditions,

(xxiii) "Tparl" (SEQ ID No:179) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tparl" encoded by a nucleic acid that hybridizes to the "Tparl" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "ensp00000297280 (hypothetical protein with p-loop)" (SEQ ID No:184) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ensp00000297280 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ensp00000297280 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

(i) "CDM_HUMAN" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDM_HUMAN" encoded by a nucleic acid that hybridizes to the "CDM_HUMAN" nucleic acid or its complement under low stringency conditions,

(ii) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

- (iii) "CGI-51" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-51" encoded by a nucleic acid that hybridizes to the "CGI-51" nucleic acid or its complement under low stringency conditions,
- (iv) "Cerebral protein 10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein 10" encoded by a nucleic acid that hybridizes to the "Cerebral protein 10" nucleic acid or its complement under low stringency conditions,
- (v) "DKFZp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DKFZp586c1924" encoded by a nucleic acid that hybridizes to the "DKFZp586c1924" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (vii) "FLJ20420" (SEQ ID No:128) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20420" encoded by a nucleic acid that hybridizes to the "FLJ20420" nucleic acid or its complement under low stringency conditions,
- (viii) "FLJ22555" (SEQ ID No:129) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22555" encoded by a nucleic acid that hybridizes to the "FLJ22555" nucleic acid or its complement under low stringency conditions,
- (ix) "FLJ22678" (SEQ ID No:130) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22678" encoded by a nucleic acid that hybridizes to the "FLJ22678" nucleic acid or its complement under low stringency conditions,
- (x) "HYPOTHETICAL PROTEIN XP_174405" (SEQ ID No:134) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN XP_174405" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN XP_174405" nucleic acid or its complement under low stringency conditions,

- (xi) "Hypothetical protein FLJ23356" (SEQ ID No:135) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23356" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23356" nucleic acid or its complement under low stringency conditions,
- (xii) "Hypothetical protein KIAA0455" (SEQ ID No:136) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0455" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0455" nucleic acid or its complement under low stringency conditions,
- (xiii) "Hypothetical protein KIAA0971-I" (SEQ ID No:137) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0971-I" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0971-I" nucleic acid or its complement under low stringency conditions,
- (xiv) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xv) "KIAA0090" (SEQ ID No:139) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,
- (xvi) "KIAA0103" (SEQ ID No:140) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0103" encoded by a nucleic acid that hybridizes to the "KIAA0103" nucleic acid or its complement under low stringency conditions,
- (xvii) "MGC4248" (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248" encoded by a nucleic acid that hybridizes to the "MGC4248" nucleic acid or its complement under low stringency conditions,
- (xviii) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442"

encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions,

(xix) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xx) "NPL4, a component of the nuclear pore complex" (SEQ ID No:146) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPL4, a component of the nuclear pore complex" encoded by a nucleic acid that hybridizes to the "NPL4, a component of the nuclear pore complex" nucleic acid or its complement under low stringency conditions,

(xxi) "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" (SEQ ID No:175) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" encoded by a nucleic acid that hybridizes to the "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" nucleic acid or its complement under low stringency conditions,

(xxii) "STRA6 isoform 1" (SEQ ID No:176) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STRA6 isoform 1" encoded by a nucleic acid that hybridizes to the "STRA6 isoform 1" nucleic acid or its complement under low stringency conditions,

(xxiii) "Tparl" (SEQ ID No:179) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tparl" encoded by a nucleic acid that hybridizes to the "Tparl" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "ensp00000297280 (hypothetical protein with p-loop)" (SEQ ID No:184) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ensp00000297280 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ensp00000297280 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions, comprising the steps of

(a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and

(b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of (a) exposing said complex, or a cell or organism containing Presenilin 2 complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof,

or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or

(ii) "200 kDa proteasome activator" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "200 kDa proteasome activator" encoded by a nucleic acid that hybridizes to the "200 kDa proteasome activator" nucleic acid or its complement under low stringency conditions, and/or

(iii) "ABCB11" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCB11" encoded by a nucleic acid that hybridizes to the "ABCB11" nucleic acid or its complement under low stringency conditions, and/or

(iv) "ATM" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATM" encoded by a nucleic acid that hybridizes to the "ATM" nucleic acid or its complement under low stringency conditions, and/or

(v) "ATP-binding cassette protein, sub-family B, member 1" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette protein, sub-family B, member 1" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette protein, sub-family B, member 1" nucleic acid or its complement under low stringency conditions, and/or

(vi) "ATP-dependent metalloprotease FtsH1 homolog" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-dependent metalloprotease FtsH1 homolog" encoded by a nucleic acid that hybridizes to the "ATP-dependent metalloprotease FtsH1 homolog" nucleic acid or its complement under low stringency conditions, and/or

(vii) "ATP7A" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP7A" encoded by a nucleic acid that hybridizes to the "ATP7A" nucleic acid or its complement under low stringency conditions, and/or

(viii) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the

- "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "Adrenoleukodystrophy protein" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Adrenoleukodystrophy protein" encoded by a nucleic acid that hybridizes to the "Adrenoleukodystrophy protein" nucleic acid or its complement under low stringency conditions, and/or
- (x) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "BIG1" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BIG1" encoded by a nucleic acid that hybridizes to the "BIG1" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "BTAF1" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BTAF1" encoded by a nucleic acid that hybridizes to the "BTAF1" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "CD97" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CD97" encoded by a nucleic acid that hybridizes to the "CD97" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "CDM_HUMAN" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDM_HUMAN" encoded by a nucleic acid that hybridizes to the "CDM_HUMAN" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "CGI-51" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-51"

encoded by a nucleic acid that hybridizes to the "CGI-51" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "CHRNA3" (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CHRNA3" encoded by a nucleic acid that hybridizes to the "CHRNA3" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "Calcium-binding protein P22" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calcium-binding protein P22" encoded by a nucleic acid that hybridizes to the "Calcium-binding protein P22" nucleic acid or its complement under low stringency conditions, and/or

(xix) "Cation-chloride cotransporter-interacting protein" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cation-chloride cotransporter-interacting protein" encoded by a nucleic acid that hybridizes to the "Cation-chloride cotransporter-interacting protein" nucleic acid or its complement under low stringency conditions, and/or

(xx) "Centromere/kinetochore protein ZW10 homolog" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Centromere/kinetochore protein ZW10 homolog" encoded by a nucleic acid that hybridizes to the "Centromere/kinetochore protein ZW10 homolog" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "Cerebral protein 10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein 10" encoded by a nucleic acid that hybridizes to the "Cerebral protein 10" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "DAAM1" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DAAM1" encoded by a nucleic acid that hybridizes to the "DAAM1" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "DAPK1" (SEQ ID No:122) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DAPK1" encoded by a nucleic acid that hybridizes to the "DAPK1" nucleic acid or its complement under low stringency conditions, and/or

- (xxiv) "DKFZp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DKFZp586c1924" encoded by a nucleic acid that hybridizes to the "DKFZp586c1924" nucleic acid or its complement under low stringency conditions, and/or
- (xxv) "DOCK3" (SEQ ID No:123) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DOCK3" encoded by a nucleic acid that hybridizes to the "DOCK3" nucleic acid or its complement under low stringency conditions, and/or
- (xxvi) "Down syndrome critical region protein 2" (SEQ ID No:124) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Down syndrome critical region protein 2" encoded by a nucleic acid that hybridizes to the "Down syndrome critical region protein 2" nucleic acid or its complement under low stringency conditions, and/or
- (xxvii) "ECSIT" (SEQ ID No:125) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions, and/or
- (xxviii) "FACL1" (SEQ ID No:126) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL1" encoded by a nucleic acid that hybridizes to the "FACL1" nucleic acid or its complement under low stringency conditions, and/or
- (xxix) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions, and/or
- (xxx) "FLJ20420" (SEQ ID No:128) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20420" encoded by a nucleic acid that hybridizes to the "FLJ20420" nucleic acid or its complement under low stringency conditions, and/or
- (xxxi) "FLJ22555" (SEQ ID No:129) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22555" encoded by a nucleic acid that hybridizes to the "FLJ22555" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "FLJ22678" (SEQ ID No:130) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22678" encoded by a nucleic acid that hybridizes to the "FLJ22678" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" (SEQ ID No:131) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" encoded by a nucleic acid that hybridizes to the "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "HTRA2" (SEQ ID No:132) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HTRA2" encoded by a nucleic acid that hybridizes to the "HTRA2" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "HU-K4 " (SEQ ID No:133) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HU-K4 " encoded by a nucleic acid that hybridizes to the "HU-K4 " nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "HYPOTHETICAL PROTEIN XP_174405" (SEQ ID No:134) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN XP_174405" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN XP_174405" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "Hypothetical protein FLJ23356" (SEQ ID No:135) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23356" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23356" nucleic acid or its complement under low stringency conditions, and/or

(xxxviii) "Hypothetical protein KIAA0455" (SEQ ID No:136) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0455" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0455" nucleic acid or its complement under low stringency conditions, and/or

- (xxxix) "Hypothetical protein KIAA0971-I" (SEQ ID No:137) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0971-I" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0971-I" nucleic acid or its complement under low stringency conditions, and/or
- (xli) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or
- (xlii) "KIAA0090" (SEQ ID No:139) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions, and/or
- (xlii) "KIAA0103" (SEQ ID No:140) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0103" encoded by a nucleic acid that hybridizes to the "KIAA0103" nucleic acid or its complement under low stringency conditions, and/or
- (xliii) "MGC4248" (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248" encoded by a nucleic acid that hybridizes to the "MGC4248" nucleic acid or its complement under low stringency conditions, and/or
- (xliv) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions, and/or
- (xlv) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions, and/or
- (xlvi) "NPC1" (SEQ ID No:144) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPC1" encoded by a nucleic acid that hybridizes to the "NPC1" nucleic acid or its complement under low stringency conditions, and/or

(xlvii) "NPD002" (SEQ ID No:145) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPD002" encoded by a nucleic acid that hybridizes to the "NPD002" nucleic acid or its complement under low stringency conditions, and/or

(xlviii) "NPL4, a component of the nuclear pore complex" (SEQ ID No:146) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPL4, a component of the nuclear pore complex" encoded by a nucleic acid that hybridizes to the "NPL4, a component of the nuclear pore complex" nucleic acid or its complement under low stringency conditions, and/or

(xlix) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(l) "P63 protein" (SEQ ID No:148) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "P63 protein" encoded by a nucleic acid that hybridizes to the "P63 protein" nucleic acid or its complement under low stringency conditions, and/or

(li) "PSMA1" (SEQ ID No:149) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA1" encoded by a nucleic acid that hybridizes to the "PSMA1" nucleic acid or its complement under low stringency conditions, and/or

(lii) "PSMA3" (SEQ ID No:150) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA3" encoded by a nucleic acid that hybridizes to the "PSMA3" nucleic acid or its complement under low stringency conditions, and/or

(liii) "PSMA4" (SEQ ID No:151) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA4" encoded by a nucleic acid that hybridizes to the "PSMA4" nucleic acid or its complement under low stringency conditions, and/or

(liv) "PSMA6" (SEQ ID No:152) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA6" encoded by a nucleic acid that hybridizes to the "PSMA6" nucleic acid or its complement under low stringency conditions, and/or

- (iv) "PSMB1" (SEQ ID No:153) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB1" encoded by a nucleic acid that hybridizes to the "PSMB1" nucleic acid or its complement under low stringency conditions, and/or
- (lvi) "PSMB2" (SEQ ID No:154) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB2" encoded by a nucleic acid that hybridizes to the "PSMB2" nucleic acid or its complement under low stringency conditions, and/or
- (lvii) "PSMB3" (SEQ ID No:155) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB3" encoded by a nucleic acid that hybridizes to the "PSMB3" nucleic acid or its complement under low stringency conditions, and/or
- (lviii) "PSMB4" (SEQ ID No:156) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB4" encoded by a nucleic acid that hybridizes to the "PSMB4" nucleic acid or its complement under low stringency conditions, and/or
- (lix) "PSMB5" (SEQ ID No:157) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB5" encoded by a nucleic acid that hybridizes to the "PSMB5" nucleic acid or its complement under low stringency conditions, and/or
- (lx) "PSMB6" (SEQ ID No:158) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB6" encoded by a nucleic acid that hybridizes to the "PSMB6" nucleic acid or its complement under low stringency conditions, and/or
- (lxi) "PSMC1" (SEQ ID No:159) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC1" encoded by a nucleic acid that hybridizes to the "PSMC1" nucleic acid or its complement under low stringency conditions, and/or
- (lxii) "PSMC2" (SEQ ID No:160) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC2" encoded by a nucleic acid that hybridizes to the "PSMC2" nucleic acid or its complement under low stringency conditions, and/or
- (lxiii) "PSMC3" (SEQ ID No:161) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC3"

encoded by a nucleic acid that hybridizes to the "PSMC3" nucleic acid or its complement under low stringency conditions, and/or

(lxiv) "PSMC4" (SEQ ID No:162) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC4" encoded by a nucleic acid that hybridizes to the "PSMC4" nucleic acid or its complement under low stringency conditions, and/or

(lxv) "PSMC5" (SEQ ID No:163) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC5" encoded by a nucleic acid that hybridizes to the "PSMC5" nucleic acid or its complement under low stringency conditions, and/or

(lxvi) "PSMC6" (SEQ ID No:164) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC6" encoded by a nucleic acid that hybridizes to the "PSMC6" nucleic acid or its complement under low stringency conditions, and/or

(lxvii) "PSMD1" (SEQ ID No:165) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD1" encoded by a nucleic acid that hybridizes to the "PSMD1" nucleic acid or its complement under low stringency conditions, and/or

(lxviii) "PSMD11" (SEQ ID No:166) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD11" encoded by a nucleic acid that hybridizes to the "PSMD11" nucleic acid or its complement under low stringency conditions, and/or

(lxix) "PSMD12" (SEQ ID No:167) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD12" encoded by a nucleic acid that hybridizes to the "PSMD12" nucleic acid or its complement under low stringency conditions, and/or

(lxx) "PSMD13" (SEQ ID No:168) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD13" encoded by a nucleic acid that hybridizes to the "PSMD13" nucleic acid or its complement under low stringency conditions, and/or

(lxxi) "PSMD2" (SEQ ID No:169) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD2" encoded by a nucleic acid that hybridizes to the "PSMD2" nucleic acid or its complement under low stringency conditions, and/or

- (lxxii) "PSMD3" (SEQ ID No:170) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD3" encoded by a nucleic acid that hybridizes to the "PSMD3" nucleic acid or its complement under low stringency conditions, and/or
- (lxxiii) "PSMD4" (SEQ ID No:171) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD4" encoded by a nucleic acid that hybridizes to the "PSMD4" nucleic acid or its complement under low stringency conditions, and/or
- (lxxiv) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions, and/or
- (lxxv) "Prohibitin" (SEQ ID No:173) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Prohibitin" encoded by a nucleic acid that hybridizes to the "Prohibitin" nucleic acid or its complement under low stringency conditions, and/or
- (lxxvi) "RPS6KA3" (SEQ ID No:174) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RPS6KA3" encoded by a nucleic acid that hybridizes to the "RPS6KA3" nucleic acid or its complement under low stringency conditions, and/or
- (lxxvii) "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" (SEQ ID No:175) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" encoded by a nucleic acid that hybridizes to the "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" nucleic acid or its complement under low stringency conditions, and/or
- (lxxviii) "STRA6 isoform 1" (SEQ ID No:176) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STRA6 isoform 1" encoded by a nucleic acid that hybridizes to the "STRA6 isoform 1" nucleic acid or its complement under low stringency conditions, and/or
- (lxxix) "Serine/threonine protein phosphatase 6" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 6" encoded by a nucleic acid that

hybridizes to the "Serine/threonine protein phosphatase 6" nucleic acid or its complement under low stringency conditions, and/or

(lxxx) "Sortilin 1" (SEQ ID No:177) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin 1" encoded by a nucleic acid that hybridizes to the "Sortilin 1" nucleic acid or its complement under low stringency conditions, and/or

(lxxxi) "Stearoyl-CoA desaturase" (SEQ ID No:178) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "Stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or

(lxxxii) "Tparl" (SEQ ID No:179) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tparl" encoded by a nucleic acid that hybridizes to the "Tparl" nucleic acid or its complement under low stringency conditions, and/or

(lxxxiii) "Ubiquitin-protein ligase EDD" (SEQ ID No:180) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase EDD" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase EDD" nucleic acid or its complement under low stringency conditions, and/or

(lxxxiv) "Voltage-dependent anion channel 2" (SEQ ID No:181) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Voltage-dependent anion channel 2" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 2" nucleic acid or its complement under low stringency conditions, and/or

(lxxxv) "Wolframin" (SEQ ID No:182) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions, and/or

(lxxxvi) "cholinergic receptor, nicotinic, alpha polypeptide 3" (SEQ ID No:183) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "cholinergic receptor, nicotinic, alpha polypeptide 3" encoded by a nucleic acid that hybridizes to the "cholinergic receptor, nicotinic, alpha polypeptide 3" nucleic acid or its complement under low stringency conditions, and/or

(lxxxvii) "ensp00000297280 (hypothetical protein with p-loop)" (SEQ ID No:184) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ensp00000297280 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ensp00000297280 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or

(ii) "200 kDa proteasome activator" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "200 kDa proteasome activator" encoded by a nucleic acid that hybridizes to the "200 kDa proteasome activator" nucleic acid or its complement under low stringency conditions, and/or

(iii) "ABCB11" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCB11" encoded by a nucleic acid that hybridizes to the "ABCB11" nucleic acid or its complement under low stringency conditions, and/or

(iv) "ATM" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATM" encoded by a nucleic acid that hybridizes to the "ATM" nucleic acid or its complement under low stringency conditions, and/or

- (v) "ATP-binding cassette protein, sub-family B, member 1" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette protein, sub-family B, member 1" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette protein, sub-family B, member 1" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "ATP-dependent metalloprotease FtsH1 homolog" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-dependent metalloprotease FtsH1 homolog" encoded by a nucleic acid that hybridizes to the "ATP-dependent metalloprotease FtsH1 homolog" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "ATP7A" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP7A" encoded by a nucleic acid that hybridizes to the "ATP7A" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "Adrenoleukodystrophy protein" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Adrenoleukodystrophy protein" encoded by a nucleic acid that hybridizes to the "Adrenoleukodystrophy protein" nucleic acid or its complement under low stringency conditions, and/or
- (x) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "BIG1" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BIG1" encoded by a nucleic acid that hybridizes to the "BIG1" nucleic acid or its complement under low stringency conditions, and/or

- (xii) "BTAF1" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BTAF1" encoded by a nucleic acid that hybridizes to the "BTAF1" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "CD97" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CD97" encoded by a nucleic acid that hybridizes to the "CD97" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "CDM_HUMAN" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDM_HUMAN" encoded by a nucleic acid that hybridizes to the "CDM_HUMAN" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "CGI-51" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-51" encoded by a nucleic acid that hybridizes to the "CGI-51" nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "CHRNA3" (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CHRNA3" encoded by a nucleic acid that hybridizes to the "CHRNA3" nucleic acid or its complement under low stringency conditions, and/or
- (xviii) "Calcium-binding protein P22" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calcium-binding protein P22" encoded by a nucleic acid that hybridizes to the "Calcium-binding protein P22" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "Cation-chloride cotransporter-interacting protein" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cation-chloride cotransporter-interacting protein" encoded by a nucleic acid that hybridizes to the "Cation-chloride cotransporter-interacting protein" nucleic acid or its complement under low stringency conditions, and/or

- (xx) "Centromere/kinetochore protein ZW10 homolog" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Centromere/kinetochore protein ZW10 homolog" encoded by a nucleic acid that hybridizes to the "Centromere/kinetochore protein ZW10 homolog" nucleic acid or its complement under low stringency conditions, and/or
- (xxi) "Cerebral protein 10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein 10" encoded by a nucleic acid that hybridizes to the "Cerebral protein 10" nucleic acid or its complement under low stringency conditions, and/or
- (xxii) "DAAM1" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DAAM1" encoded by a nucleic acid that hybridizes to the "DAAM1" nucleic acid or its complement under low stringency conditions, and/or
- (xxiii) "DAPK1" (SEQ ID No:122) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DAPK1" encoded by a nucleic acid that hybridizes to the "DAPK1" nucleic acid or its complement under low stringency conditions, and/or
- (xxiv) "DKFZp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DKFZp586c1924" encoded by a nucleic acid that hybridizes to the "DKFZp586c1924" nucleic acid or its complement under low stringency conditions, and/or
- (xxv) "DOCK3" (SEQ ID No:123) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DOCK3" encoded by a nucleic acid that hybridizes to the "DOCK3" nucleic acid or its complement under low stringency conditions, and/or
- (xxvi) "Down syndrome critical region protein 2" (SEQ ID No:124) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Down syndrome critical region protein 2" encoded by a nucleic acid that hybridizes to the "Down syndrome critical region protein 2" nucleic acid or its complement under low stringency conditions, and/or
- (xxvii) "ECSIT" (SEQ ID No:125) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "FACL1" (SEQ ID No:126) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL1" encoded by a nucleic acid that hybridizes to the "FACL1" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions, and/or

(xxx) "FLJ20420" (SEQ ID No:128) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20420" encoded by a nucleic acid that hybridizes to the "FLJ20420" nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "FLJ22555" (SEQ ID No:129) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22555" encoded by a nucleic acid that hybridizes to the "FLJ22555" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "FLJ22678" (SEQ ID No:130) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22678" encoded by a nucleic acid that hybridizes to the "FLJ22678" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" (SEQ ID No:131) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" encoded by a nucleic acid that hybridizes to the "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "HTRA2" (SEQ ID No:132) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HTRA2" encoded by a nucleic acid that hybridizes to the "HTRA2" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "HU-K4 " (SEQ ID No:133) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HU-K4 " encoded by a nucleic acid that hybridizes to the "HU-K4 " nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "HYPOTHETICAL PROTEIN XP_174405" (SEQ ID No:134) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN XP_174405" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN XP_174405" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "Hypothetical protein FLJ23356" (SEQ ID No:135) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23356" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23356" nucleic acid or its complement under low stringency conditions, and/or

(xxxviii) "Hypothetical protein KIAA0455" (SEQ ID No:136) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0455" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0455" nucleic acid or its complement under low stringency conditions, and/or

(xxxix) "Hypothetical protein KIAA0971-I" (SEQ ID No:137) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0971-I" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0971-I" nucleic acid or its complement under low stringency conditions, and/or

(xl) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xli) "KIAA0090" (SEQ ID No:139) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions, and/or

(xlii) "KIAA0103" (SEQ ID No:140) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0103" encoded by a nucleic acid that hybridizes to the "KIAA0103" nucleic acid or its complement under low stringency conditions, and/or

(xliii) "MGC4248" (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248"

encoded by a nucleic acid that hybridizes to the "MGC4248" nucleic acid or its complement under low stringency conditions, and/or

(xlv) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions, and/or

(xlvi) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions, and/or

(xlvii) "NPC1" (SEQ ID No:144) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPC1" encoded by a nucleic acid that hybridizes to the "NPC1" nucleic acid or its complement under low stringency conditions, and/or

(xlviii) "NPD002" (SEQ ID No:145) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPD002" encoded by a nucleic acid that hybridizes to the "NPD002" nucleic acid or its complement under low stringency conditions, and/or

(xlix) "NPL4, a component of the nuclear pore complex" (SEQ ID No:146) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPL4, a component of the nuclear pore complex" encoded by a nucleic acid that hybridizes to the "NPL4, a component of the nuclear pore complex" nucleic acid or its complement under low stringency conditions, and/or

(l) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(li) "P63 protein" (SEQ ID No:148) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "P63 protein" encoded by a nucleic acid that hybridizes to the "P63 protein" nucleic acid or its complement under low stringency conditions, and/or

(lii) "PSMA1" (SEQ ID No:149) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA1" encoded by a

nucleic acid that hybridizes to the "PSMA1" nucleic acid or its complement under low stringency conditions, and/or

(iii) "PSMA3" (SEQ ID No:150) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA3" encoded by a nucleic acid that hybridizes to the "PSMA3" nucleic acid or its complement under low stringency conditions, and/or

(liii) "PSMA4" (SEQ ID No:151) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA4" encoded by a nucleic acid that hybridizes to the "PSMA4" nucleic acid or its complement under low stringency conditions, and/or

(liv) "PSMA6" (SEQ ID No:152) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA6" encoded by a nucleic acid that hybridizes to the "PSMA6" nucleic acid or its complement under low stringency conditions, and/or

(lv) "PSMB1" (SEQ ID No:153) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB1" encoded by a nucleic acid that hybridizes to the "PSMB1" nucleic acid or its complement under low stringency conditions, and/or

(lvi) "PSMB2" (SEQ ID No:154) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB2" encoded by a nucleic acid that hybridizes to the "PSMB2" nucleic acid or its complement under low stringency conditions, and/or

(lvii) "PSMB3" (SEQ ID No:155) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB3" encoded by a nucleic acid that hybridizes to the "PSMB3" nucleic acid or its complement under low stringency conditions, and/or

(lviii) "PSMB4" (SEQ ID No:156) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB4" encoded by a nucleic acid that hybridizes to the "PSMB4" nucleic acid or its complement under low stringency conditions, and/or

(lix) "PSMB5" (SEQ ID No:157) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB5" encoded by a nucleic acid that hybridizes to the "PSMB5" nucleic acid or its complement under low stringency conditions, and/or

- (Ix) "PSMB6" (SEQ ID No:158) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB6" encoded by a nucleic acid that hybridizes to the "PSMB6" nucleic acid or its complement under low stringency conditions, and/or
- (Ixi) "PSMC1" (SEQ ID No:159) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC1" encoded by a nucleic acid that hybridizes to the "PSMC1" nucleic acid or its complement under low stringency conditions, and/or
- (Ixii) "PSMC2" (SEQ ID No:160) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC2" encoded by a nucleic acid that hybridizes to the "PSMC2" nucleic acid or its complement under low stringency conditions, and/or
- (Ixiii) "PSMC3" (SEQ ID No:161) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC3" encoded by a nucleic acid that hybridizes to the "PSMC3" nucleic acid or its complement under low stringency conditions, and/or
- (Ixiv) "PSMC4" (SEQ ID No:162) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC4" encoded by a nucleic acid that hybridizes to the "PSMC4" nucleic acid or its complement under low stringency conditions, and/or
- (Ixv) "PSMC5" (SEQ ID No:163) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC5" encoded by a nucleic acid that hybridizes to the "PSMC5" nucleic acid or its complement under low stringency conditions, and/or
- (Ixvi) "PSMC6" (SEQ ID No:164) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC6" encoded by a nucleic acid that hybridizes to the "PSMC6" nucleic acid or its complement under low stringency conditions, and/or
- (Ixvii) "PSMD1" (SEQ ID No:165) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD1" encoded by a nucleic acid that hybridizes to the "PSMD1" nucleic acid or its complement under low stringency conditions, and/or
- (Ixviii) "PSMD11" (SEQ ID No:166) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD11"

- encoded by a nucleic acid that hybridizes to the "PSMD11" nucleic acid or its complement under low stringency conditions, and/or
- (Ixx) "PSMD12" (SEQ ID No:167) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD12" encoded by a nucleic acid that hybridizes to the "PSMD12" nucleic acid or its complement under low stringency conditions, and/or
- (Ixxi) "PSMD13" (SEQ ID No:168) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD13" encoded by a nucleic acid that hybridizes to the "PSMD13" nucleic acid or its complement under low stringency conditions, and/or
- (Ixxii) "PSMD2" (SEQ ID No:169) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD2" encoded by a nucleic acid that hybridizes to the "PSMD2" nucleic acid or its complement under low stringency conditions, and/or
- (Ixxiii) "PSMD3" (SEQ ID No:170) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD3" encoded by a nucleic acid that hybridizes to the "PSMD3" nucleic acid or its complement under low stringency conditions, and/or
- (Ixxiv) "PSMD4" (SEQ ID No:171) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD4" encoded by a nucleic acid that hybridizes to the "PSMD4" nucleic acid or its complement under low stringency conditions, and/or
- (Ixxv) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions, and/or
- (Ixxvi) "Prohibitin" (SEQ ID No:173) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Prohibitin" encoded by a nucleic acid that hybridizes to the "Prohibitin" nucleic acid or its complement under low stringency conditions, and/or
- (Ixxvii) "RPS6KA3" (SEQ ID No:174) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RPS6KA3" encoded by a nucleic acid that hybridizes to the "RPS6KA3" nucleic acid or its complement under low stringency conditions, and/or

(lxxvii) "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" (SEQ ID No:175) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" encoded by a nucleic acid that hybridizes to the "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" nucleic acid or its complement under low stringency conditions, and/or

(lxxviii) "STRA6 isoform 1" (SEQ ID No:176) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STRA6 isoform 1" encoded by a nucleic acid that hybridizes to the "STRA6 isoform 1" nucleic acid or its complement under low stringency conditions, and/or

(lxxix) "Serine/threonine protein phosphatase 6" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 6" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 6" nucleic acid or its complement under low stringency conditions, and/or

(lxxx) "Sortilin 1" (SEQ ID No:177) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin 1" encoded by a nucleic acid that hybridizes to the "Sortilin 1" nucleic acid or its complement under low stringency conditions, and/or

(lxxxii) "Stearoyl-CoA desaturase" (SEQ ID No:178) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "Stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or

(lxxxii) "Tpar1" (SEQ ID No:179) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tpar1" encoded by a nucleic acid that hybridizes to the "Tpar1" nucleic acid or its complement under low stringency conditions, and/or

(lxxxiii) "Ubiquitin-protein ligase EDD" (SEQ ID No:180) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase EDD" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase EDD" nucleic acid or its complement under low stringency conditions, and/or

(lxxxiv) "Voltage-dependent anion channel 2" (SEQ ID No:181) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "Voltage-dependent anion channel 2" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 2" nucleic acid or its complement under low stringency conditions, and/or

(lxxxv) "Wolframin" (SEQ ID No:182) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions, and/or

(lxxxvi) "cholinergic receptor, nicotinic, alpha polypeptide 3" (SEQ ID No:183) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "cholinergic receptor, nicotinic, alpha polypeptide 3" encoded by a nucleic acid that hybridizes to the "cholinergic receptor, nicotinic, alpha polypeptide 3" nucleic acid or its complement under low stringency conditions, and/or

(lxxxvii) "ensp00000297280 (hypothetical protein with p-loop)" (SEQ ID No:184) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ensp00000297280 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ensp00000297280 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi

(siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins
 (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
 (ii) "200 kDa proteasome activator" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "200 kDa proteasome activator" encoded by a nucleic acid that hybridizes to the "200 kDa proteasome activator" nucleic acid or its complement under low stringency conditions,
 (iii) "ABCB11" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCB11" encoded by a nucleic acid that hybridizes to the "ABCB11" nucleic acid or its complement under low stringency conditions,
 (iv) "ATM" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATM" encoded by a nucleic acid that hybridizes to the "ATM" nucleic acid or its complement under low stringency conditions,

- (v) "ATP-binding cassette protein, sub-family B, member 1" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette protein, sub-family B, member 1" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette protein, sub-family B, member 1" nucleic acid or its complement under low stringency conditions,
- (vi) "ATP-dependent metalloprotease FtsH1 homolog" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-dependent metalloprotease FtsH1 homolog" encoded by a nucleic acid that hybridizes to the "ATP-dependent metalloprotease FtsH1 homolog" nucleic acid or its complement under low stringency conditions,
- (vii) "ATP7A" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP7A" encoded by a nucleic acid that hybridizes to the "ATP7A" nucleic acid or its complement under low stringency conditions,
- (viii) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions,
- (ix) "Adrenoleukodystrophy protein" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Adrenoleukodystrophy protein" encoded by a nucleic acid that hybridizes to the "Adrenoleukodystrophy protein" nucleic acid or its complement under low stringency conditions,
- (x) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
- (xi) "BIG1" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BIG1" encoded by a nucleic acid that hybridizes to the "BIG1" nucleic acid or its complement under low stringency conditions,
- (xii) "BTAF1" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BTAF1" encoded by a

nucleic acid that hybridizes to the "BTAF1" nucleic acid or its complement under low stringency conditions,

(xiii) "CD97" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CD97" encoded by a nucleic acid that hybridizes to the "CD97" nucleic acid or its complement under low stringency conditions,

(xiv) "CDM_HUMAN" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDM_HUMAN" encoded by a nucleic acid that hybridizes to the "CDM_HUMAN" nucleic acid or its complement under low stringency conditions,

(xv) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(xvi) "CGI-51" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-51" encoded by a nucleic acid that hybridizes to the "CGI-51" nucleic acid or its complement under low stringency conditions,

(xvii) "CHRNA3" (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CHRNA3" encoded by a nucleic acid that hybridizes to the "CHRNA3" nucleic acid or its complement under low stringency conditions,

(xviii) "Calcium-binding protein P22" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calcium-binding protein P22" encoded by a nucleic acid that hybridizes to the "Calcium-binding protein P22" nucleic acid or its complement under low stringency conditions,

(xix) "Cation-chloride cotransporter-interacting protein" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cation-chloride cotransporter-interacting protein" encoded by a nucleic acid that hybridizes to the "Cation-chloride cotransporter-interacting protein" nucleic acid or its complement under low stringency conditions,

(xx) "Centromere/kinetochore protein ZW10 homolog" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Centromere/kinetochore protein ZW10 homolog" encoded by a nucleic

- acid that hybridizes to the "Centromere/kinetochore protein ZW10 homolog" nucleic acid or its complement under low stringency conditions,
- (xxi) "Cerebral protein 10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein 10" encoded by a nucleic acid that hybridizes to the "Cerebral protein 10" nucleic acid or its complement under low stringency conditions,
- (xxii) "DAAM1" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DAAM1" encoded by a nucleic acid that hybridizes to the "DAAM1" nucleic acid or its complement under low stringency conditions,
- (xxiii) "DAPK1" (SEQ ID No:122) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DAPK1" encoded by a nucleic acid that hybridizes to the "DAPK1" nucleic acid or its complement under low stringency conditions,
- (xxiv) "DKFZp586c1924" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DKFZp586c1924" encoded by a nucleic acid that hybridizes to the "DKFZp586c1924" nucleic acid or its complement under low stringency conditions,
- (xxv) "DOCK3" (SEQ ID No:123) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DOCK3" encoded by a nucleic acid that hybridizes to the "DOCK3" nucleic acid or its complement under low stringency conditions,
- (xxvi) "Down syndrome critical region protein 2" (SEQ ID No:124) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Down syndrome critical region protein 2" encoded by a nucleic acid that hybridizes to the "Down syndrome critical region protein 2" nucleic acid or its complement under low stringency conditions,
- (xxvii) "ECSIT" (SEQ ID No:125) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,
- (xxviii) "FACL1" (SEQ ID No:126) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL1"

encoded by a nucleic acid that hybridizes to the "FACL1" nucleic acid or its complement under low stringency conditions,

(xxix) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xxx) "FLJ20420" (SEQ ID No:128) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20420" encoded by a nucleic acid that hybridizes to the "FLJ20420" nucleic acid or its complement under low stringency conditions,

(xxxi) "FLJ22555" (SEQ ID No:129) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22555" encoded by a nucleic acid that hybridizes to the "FLJ22555" nucleic acid or its complement under low stringency conditions,

(xxxii) "FLJ22678" (SEQ ID No:130) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22678" encoded by a nucleic acid that hybridizes to the "FLJ22678" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" (SEQ ID No:131) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" encoded by a nucleic acid that hybridizes to the "Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3" nucleic acid or its complement under low stringency conditions,

(xxxiv) "HTRA2" (SEQ ID No:132) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HTRA2" encoded by a nucleic acid that hybridizes to the "HTRA2" nucleic acid or its complement under low stringency conditions,

(xxxv) "HU-K4 " (SEQ ID No:133) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HU-K4 " encoded by a nucleic acid that hybridizes to the "HU-K4 " nucleic acid or its complement under low stringency conditions,

(xxxvi) "HYPOTHETICAL PROTEIN XP_174405" (SEQ ID No:134) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof,

or a variant of "HYPOTHETICAL PROTEIN XP_174405" encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN XP_174405" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Hypothetical protein FLJ23356" (SEQ ID No:135) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23356" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23356" nucleic acid or its complement under low stringency conditions,

(xxxviii) "Hypothetical protein KIAA0455" (SEQ ID No:136) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0455" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0455" nucleic acid or its complement under low stringency conditions,

(xxxix) "Hypothetical protein KIAA0971-I" (SEQ ID No:137) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0971-I" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0971-I" nucleic acid or its complement under low stringency conditions,

(xl) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xli) "KIAA0090" (SEQ ID No:139) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,

(xlii) "KIAA0103" (SEQ ID No:140) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0103" encoded by a nucleic acid that hybridizes to the "KIAA0103" nucleic acid or its complement under low stringency conditions,

(xlili) "MGC4248" (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248" encoded by a nucleic acid that hybridizes to the "MGC4248" nucleic acid or its complement under low stringency conditions,

(xlv) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions,

(xlv) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xlvi) "NPC1" (SEQ ID No:144) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPC1" encoded by a nucleic acid that hybridizes to the "NPC1" nucleic acid or its complement under low stringency conditions,

(xlvii) "NPD002" (SEQ ID No:145) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPD002" encoded by a nucleic acid that hybridizes to the "NPD002" nucleic acid or its complement under low stringency conditions,

(xlviii) "NPL4, a component of the nuclear pore complex" (SEQ ID No:146) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NPL4, a component of the nuclear pore complex" encoded by a nucleic acid that hybridizes to the "NPL4, a component of the nuclear pore complex" nucleic acid or its complement under low stringency conditions,

(xlix) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(l) "P63 protein" (SEQ ID No:148) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "P63 protein" encoded by a nucleic acid that hybridizes to the "P63 protein" nucleic acid or its complement under low stringency conditions,

(li) "PSMA1" (SEQ ID No:149) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA1" encoded by a nucleic acid that hybridizes to the "PSMA1" nucleic acid or its complement under low stringency conditions,

- (lii) "PSMA3" (SEQ ID No:150) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA3" encoded by a nucleic acid that hybridizes to the "PSMA3" nucleic acid or its complement under low stringency conditions,
- (liii) "PSMA4" (SEQ ID No:151) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA4" encoded by a nucleic acid that hybridizes to the "PSMA4" nucleic acid or its complement under low stringency conditions,
- (liv) "PSMA6" (SEQ ID No:152) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMA6" encoded by a nucleic acid that hybridizes to the "PSMA6" nucleic acid or its complement under low stringency conditions,
- (lv) "PSMB1" (SEQ ID No:153) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB1" encoded by a nucleic acid that hybridizes to the "PSMB1" nucleic acid or its complement under low stringency conditions,
- (lvi) "PSMB2" (SEQ ID No:154) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB2" encoded by a nucleic acid that hybridizes to the "PSMB2" nucleic acid or its complement under low stringency conditions,
- (lvii) "PSMB3" (SEQ ID No:155) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB3" encoded by a nucleic acid that hybridizes to the "PSMB3" nucleic acid or its complement under low stringency conditions,
- (lviii) "PSMB4" (SEQ ID No:156) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB4" encoded by a nucleic acid that hybridizes to the "PSMB4" nucleic acid or its complement under low stringency conditions,
- (lix) "PSMB5" (SEQ ID No:157) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB5" encoded by a nucleic acid that hybridizes to the "PSMB5" nucleic acid or its complement under low stringency conditions,
- (lx) "PSMB6" (SEQ ID No:158) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMB6" encoded by a

nucleic acid that hybridizes to the "PSMB6" nucleic acid or its complement under low stringency conditions,

(lxi) "PSMC1" (SEQ ID No:159) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC1" encoded by a nucleic acid that hybridizes to the "PSMC1" nucleic acid or its complement under low stringency conditions,

(lxii) "PSMC2" (SEQ ID No:160) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC2" encoded by a nucleic acid that hybridizes to the "PSMC2" nucleic acid or its complement under low stringency conditions,

(lxiii) "PSMC3" (SEQ ID No:161) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC3" encoded by a nucleic acid that hybridizes to the "PSMC3" nucleic acid or its complement under low stringency conditions,

(lxiv) "PSMC4" (SEQ ID No:162) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC4" encoded by a nucleic acid that hybridizes to the "PSMC4" nucleic acid or its complement under low stringency conditions,

(lxv) "PSMC5" (SEQ ID No:163) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC5" encoded by a nucleic acid that hybridizes to the "PSMC5" nucleic acid or its complement under low stringency conditions,

(lxvi) "PSMC6" (SEQ ID No:164) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMC6" encoded by a nucleic acid that hybridizes to the "PSMC6" nucleic acid or its complement under low stringency conditions,

(lxvii) "PSMD1" (SEQ ID No:165) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD1" encoded by a nucleic acid that hybridizes to the "PSMD1" nucleic acid or its complement under low stringency conditions,

(lxviii) "PSMD11" (SEQ ID No:166) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD11" encoded by a nucleic acid that hybridizes to the "PSMD11" nucleic acid or its complement under low stringency conditions,

- (Ixxix) "PSMD12" (SEQ ID No:167) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD12" encoded by a nucleic acid that hybridizes to the "PSMD12" nucleic acid or its complement under low stringency conditions,
- (Ixix) "PSMD13" (SEQ ID No:168) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD13" encoded by a nucleic acid that hybridizes to the "PSMD13" nucleic acid or its complement under low stringency conditions,
- (Ixixi) "PSMD2" (SEQ ID No:169) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD2" encoded by a nucleic acid that hybridizes to the "PSMD2" nucleic acid or its complement under low stringency conditions,
- (Ixixii) "PSMD3" (SEQ ID No:170) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD3" encoded by a nucleic acid that hybridizes to the "PSMD3" nucleic acid or its complement under low stringency conditions,
- (Ixixiii) "PSMD4" (SEQ ID No:171) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PSMD4" encoded by a nucleic acid that hybridizes to the "PSMD4" nucleic acid or its complement under low stringency conditions,
- (Ixixiv) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions,
- (Ixixv) "Prohibitin" (SEQ ID No:173) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Prohibitin" encoded by a nucleic acid that hybridizes to the "Prohibitin" nucleic acid or its complement under low stringency conditions,
- (Ixixvi) "RPS6KA3" (SEQ ID No:174) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RPS6KA3" encoded by a nucleic acid that hybridizes to the "RPS6KA3" nucleic acid or its complement under low stringency conditions,
- (Ixixvii) "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" (SEQ ID No:175) or a functionally active derivative thereof, or a functionally active fragment thereof, or a

homolog thereof, or a variant of "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" encoded by a nucleic acid that hybridizes to the "SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10" nucleic acid or its complement under low stringency conditions,

(lxxviii) "STRA6 isoform 1" (SEQ ID No:176) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STRA6 isoform 1" encoded by a nucleic acid that hybridizes to the "STRA6 isoform 1" nucleic acid or its complement under low stringency conditions,

(lxxix) "Serine/threonine protein phosphatase 6" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Serine/threonine protein phosphatase 6" encoded by a nucleic acid that hybridizes to the "Serine/threonine protein phosphatase 6" nucleic acid or its complement under low stringency conditions,

(lxxx) "Sortilin 1" (SEQ ID No:177) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin 1" encoded by a nucleic acid that hybridizes to the "Sortilin 1" nucleic acid or its complement under low stringency conditions,

(lxxxii) "Stearoyl-CoA desaturase" (SEQ ID No:178) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "Stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(lxxxiii) "Tparl" (SEQ ID No:179) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tparl" encoded by a nucleic acid that hybridizes to the "Tparl" nucleic acid or its complement under low stringency conditions,

(lxxxiv) "Ubiquitin-protein ligase EDD" (SEQ ID No:180) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Ubiquitin-protein ligase EDD" encoded by a nucleic acid that hybridizes to the "Ubiquitin-protein ligase EDD" nucleic acid or its complement under low stringency conditions,

(lxxxv) "Voltage-dependent anion channel 2" (SEQ ID No:181) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Voltage-dependent anion channel 2" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 2" nucleic acid or its complement under low stringency conditions,

(lxxxv) "Wolframin" (SEQ ID No:182) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(lxxxvi) "cholinergic receptor, nicotinic, alpha polypeptide 3" (SEQ ID No:183) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "cholinergic receptor, nicotinic, alpha polypeptide 3" encoded by a nucleic acid that hybridizes to the "cholinergic receptor, nicotinic, alpha polypeptide 3" nucleic acid or its complement under low stringency conditions,

and/or(lxxxvii) "ensp00000297280 (hypothetical protein with p-loop)" (SEQ ID No:184) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ensp00000297280 (hypothetical protein with p-loop)" encoded by a nucleic acid that hybridizes to the "ensp00000297280 (hypothetical protein with p-loop)" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

The present invention further relates to the following embodiments of the Nicastrin-complex:

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein selected from the group consisting of:
 - (i) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
 - (ii) "BACE1" (SEQ ID No:187) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,
 - (iii) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin"

encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iv) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(v) "Presenilin-1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and

(vi) "Presenilin-2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and

(b) at least one second protein, which second protein is selected from the group consisting of:

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(iv) "BSCv protein (FRAGMENT)" (SEQ ID No:188) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

- "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (v) "CAMK4" (SEQ ID No:189) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,
- (vi) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (vii) "Casein kinase II beta chain" (SEQ ID No:190) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,
- (viii) "Cathepsin B" (SEQ ID No:191) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,
- (ix) "DCTN1" (SEQ ID No:192) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,
- (x) "Delta-6 fatty acid desaturase" (SEQ ID No:193) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,
- (xi) "ENSG00000144840" (SEQ ID No:194) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (xii) "FACL3" (SEQ ID No:195) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

- (xiii) "FACL4" (SEQ ID No:196) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,
- (xiv) "FLJ13977" (SEQ ID No:197) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,
- (xv) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (xvi) "FLJ20481" (SEQ ID No:198) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (xvii) "FLJ22390" (SEQ ID No:199) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (xviii) "ICAM-2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,
- (xix) "KIAA0095" (SEQ ID No:201) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,
- (xx) "KIAA0922" (SEQ ID No:202) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,
- (xxi) "KIAA1181 (FRAGMENT)" (SEQ ID No:203) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA1533 (FRAGMENT)" (SEQ ID No:204) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxiii) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xxiv) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxv) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxvi) "PAS domain containing serine/threonine kinase" (SEQ ID No:207) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,

(xxvii) "PP1, regulatory subunit 15B" (SEQ ID No:208) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xxviii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:211) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxix) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:212) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxx) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxi) "REP8 protein" (SEQ ID No:214) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxii) "RING finger protein 5" (SEQ ID No:215) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Stromal cell-derived factor 2-like 1" (SEQ ID No:217) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xxxv) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xxxvi) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:219) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and

(xxxvii) "tyrosine phosphatase ensg00000149185" (SEQ ID No:220) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein 'Nicastrin' (SEQ ID NO. 147), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'Nicastrin' encoded by a nucleic acid that hybridizes to the 'Nicastrin' under low stringency conditions.

3. The protein complex according to No. 1 selected from complex (I) and comprising the following proteins:

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid

that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(iv) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "BACE1" (SEQ ID No:187) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(vi) "BSCv protein (FRAGMENT)" (SEQ ID No:188) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(vii) "CAMK4" (SEQ ID No:189) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,

(viii) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(ix) "Casein kinase II beta chain" (SEQ ID No:190) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,

(x) "Cathepsin B" (SEQ ID No:191) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B"

encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(xi) "DCTN1" (SEQ ID No:192) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,

(xii) "Delta-6 fatty acid desaturase" (SEQ ID No:193) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,

(xiii) "ENSG00000144840" (SEQ ID No:194) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xiv) "FACL3" (SEQ ID No:195) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(xv) "FACL4" (SEQ ID No:196) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,

(xvi) "FLJ13977" (SEQ ID No:197) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

(xvii) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xviii) "FLJ20481" (SEQ ID No:198) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

- (xix) "FLJ22390" (SEQ ID No:199) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (xx) "ICAM-2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,
- (xxi) "KIAA0095" (SEQ ID No:201) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,
- (xxii) "KIAA0922" (SEQ ID No:202) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,
- (xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:203) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:204) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,
- (xxvi) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

- (xxvii) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,
- (xxviii) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:207) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,
- (xxx) "PP1, regulatory subunit 15B" (SEQ ID No:208) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,
- (xxxi) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,
- (xxxii) "Presenilin-1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,
- (xxxiii) "Presenilin-2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,
- (xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:211) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:212) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxvii) "REP8 protein" (SEQ ID No:214) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxviii) "RING finger protein 5" (SEQ ID No:215) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:217) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

- (xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:219) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or
- (xliii) "tyrosine phosphatase ensg00000149185" (SEQ ID No:220) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions,
- and a protein complex selected from complex (II) and comprising the following proteins:
- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
 - (ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
 - (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
 - (iv) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
 - (v) "BSCv protein (FRAGMENT)" (SEQ ID No:188) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(vi) "CAMK4" (SEQ ID No:189) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,

(vii) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(viii) "Casein kinase II beta chain" (SEQ ID No:190) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,

(ix) "Cathepsin B" (SEQ ID No:191) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(x) "DCTN1" (SEQ ID No:192) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,

(xi) "Delta-6 fatty acid desaturase" (SEQ ID No:193) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,

(xii) "ENSG00000144840" (SEQ ID No:194) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xiii) "FACL3" (SEQ ID No:195) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

- (xiv) "FACL4" (SEQ ID No:196) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,
- (xv) "FLJ13977" (SEQ ID No:197) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,
- (xvi) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (xvii) "FLJ20481" (SEQ ID No:198) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (xviii) "FLJ22390" (SEQ ID No:199) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (xix) "ICAM-2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,
- (xx) "KIAA0095" (SEQ ID No:201) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,
- (xxi) "KIAA0922" (SEQ ID No:202) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,
- (xxii) "KIAA1181 (FRAGMENT)" (SEQ ID No:203) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxiii) "KIAA1533 (FRAGMENT)" (SEQ ID No:204) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxiv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xxv) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxvi) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxvii) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xxviii) "PAS domain containing serine/threonine kinase" (SEQ ID No:207) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,

(xxix) "PP1, regulatory subunit 15B" (SEQ ID No:208) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xxx) "Presenilin-1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1"

encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxxix) "Presenilin-2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxxii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:211) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:212) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxv) "REP8 protein" (SEQ ID No:214) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxvi) "RING finger protein 5" (SEQ ID No:215) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xxxviii) "Stromal cell-derived factor 2-like 1" (SEQ ID No:217) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xxxix) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xl) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:219) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or

(xli) "tyrosine phosphatase ensg00000149185" (SEQ ID No:220) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 36 of the following proteins:

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (iv) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
- (v) "BACE1" (SEQ ID No:187) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,
- (vi) "BSCv protein (FRAGMENT)" (SEQ ID No:188) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (vii) "CAMK4" (SEQ ID No:189) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,
- (viii) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (ix) "Casein kinase II beta chain" (SEQ ID No:190) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,
- (x) "Cathepsin B" (SEQ ID No:191) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

- (xi) "DCTN1" (SEQ ID No:192) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,
- (xii) "Delta-6 fatty acid desaturase" (SEQ ID No:193) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,
- (xiii) "ENSG00000144840" (SEQ ID No:194) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (xiv) "FACL3" (SEQ ID No:195) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
- (xv) "FACL4" (SEQ ID No:196) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,
- (xvi) "FLJ13977" (SEQ ID No:197) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,
- (xvii) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (xviii) "FLJ20481" (SEQ ID No:198) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (xix) "FLJ22390" (SEQ ID No:199) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390"

encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xx) "ICAM-2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xxi) "KIAA0095" (SEQ ID No:201) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA0922" (SEQ ID No:202) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

(xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:203) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:204) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xxvi) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxvii) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin"

encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxviii) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:207) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,

(xxx) "PP1, regulatory subunit 15B" (SEQ ID No:208) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xxxi) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(xxxii) "Presenilin-1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Presenilin-2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:211) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:212) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof,

or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxvii) "REP8 protein" (SEQ ID No:214) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxviii) "RING finger protein 5" (SEQ ID No:215) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xli) "Stromal cell-derived factor 2-like 1" (SEQ ID No:217) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xlii) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xliii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:219) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein

yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions,

(xlili) "tyrosine phosphatase ensg00000149185" (SEQ ID No:220) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by

modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Nicastrin complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the Nicastrin complex selected from

(i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(ii) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(iii) "ENSG00000144840" (SEQ ID No:194) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"ENSG00000144840" encoded by a nucleic acid that hybridizes to the

"ENSG00000144840" nucleic acid or its complement under low stringency conditions,

- (iv) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (v) "FLJ20481" (SEQ ID No:198) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ22390" (SEQ ID No:199) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (vii) "KIAA0095" (SEQ ID No:201) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,
- (viii) "KIAA0922" (SEQ ID No:202) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,
- (ix) "KIAA1181 (FRAGMENT)" (SEQ ID No:203) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (x) "KIAA1533 (FRAGMENT)" (SEQ ID No:204) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xi) "PP1, regulatory subunit 15B" (SEQ ID No:208) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,
- (xii) "RING finger protein 5" (SEQ ID No:215) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING

finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xiii) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and

(xiv) "tyrosine phosphatase ensg00000149185" (SEQ ID No:220) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the

nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof; selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

(i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof,

- or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (ii) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (iii) "ENSG00000144840" (SEQ ID No:194) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (iv) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (v) "FLJ20481" (SEQ ID No:198) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ22390" (SEQ ID No:199) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (vii) "KIAA0095" (SEQ ID No:201) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,
- (viii) "KIAA0922" (SEQ ID No:202) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,
- (ix) "KIAA1181 (FRAGMENT)" (SEQ ID No:203) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

- (x) "KIAA1533 (FRAGMENT)" (SEQ ID No:204) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xi) "PP1, regulatory subunit 15B" (SEQ ID No:208) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,
- (xii) "RING finger protein 5" (SEQ ID No:215) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,
- (xiii) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "tyrosine phosphatase ensg00000149185" (SEQ ID No:220) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

- (i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (ii) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (iii) "ENSG00000144840" (SEQ ID No:194) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (iv) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (v) "FLJ20481" (SEQ ID No:198) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ22390" (SEQ ID No:199) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (vii) "KIAA0095" (SEQ ID No:201) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,
- (viii) "KIAA0922" (SEQ ID No:202) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

- (ix) "KIAA1181 (FRAGMENT)" (SEQ ID No:203) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (x) "KIAA1533 (FRAGMENT)" (SEQ ID No:204) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xi) "PP1, regulatory subunit 15B" (SEQ ID No:208) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,
- (xii) "RING finger protein 5" (SEQ ID No:215) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,
- (xiii) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "tyrosine phosphatase ensg00000149185" (SEQ ID No:220) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, comprising the steps of
 - (a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and
 - (b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of (a) exposing said complex, or a cell or organism containing Nicastrin complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof,

or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions, and/or

(iv) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or

(v) "BACE1" (SEQ ID No:187) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or

(vi) "BSCv protein (FRAGMENT)" (SEQ ID No:188) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(vii) "CAMK4" (SEQ ID No:189) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions, and/or

(viii) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or

(ix) "Casein kinase II beta chain" (SEQ ID No:190) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions, and/or

- (x) "Cathepsin B" (SEQ ID No:191) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "DCTN1" (SEQ ID No:192) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "Delta-6 fatty acid desaturase" (SEQ ID No:193) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "ENSG00000144840" (SEQ ID No:194) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "FACL3" (SEQ ID No:195) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "FACL4" (SEQ ID No:196) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "FLJ13977" (SEQ ID No:197) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions, and/or

- (xviii) "FLJ20481" (SEQ ID No:198) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "FLJ22390" (SEQ ID No:199) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions, and/or
- (xx) "ICAM-2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions, and/or
- (xxi) "KIAA0095" (SEQ ID No:201) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions, and/or
- (xxii) "KIAA0922" (SEQ ID No:202) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions, and/or
- (xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:203) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or
- (xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:204) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or
- (xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions, and/or

- (xxvi) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions, and/or
- (xxvii) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or
- (xxviii) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or
- (xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:207) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions, and/or
- (xxx) "PP1, regulatory subunit 15B" (SEQ ID No:208) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions, and/or
- (xxxi) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or
- (xxxii) "Presenilin-1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and/or
- (xxxiii) "Presenilin-2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2"

encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:211) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:212) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "REP8.protein" (SEQ ID No:214) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions, and/or

(xxxviii) "RING finger protein 5" (SEQ ID No:215) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions, and/or

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions, and/or

(xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:217) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes

to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions, and/or

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:219) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or

(xliii) "tyrosine phosphatase ensg00000149185" (SEQ ID No:220) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or

- (ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or
- (v) "BACE1" (SEQ ID No:187) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "BSCv protein (FRAGMENT)" (SEQ ID No:188) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "CAMK4" (SEQ ID No:189) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "Casein kinase II beta chain" (SEQ ID No:190) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein

kinase II beta chain" nucleic acid or its complement under low stringency conditions, and/or

(x) "Cathepsin B" (SEQ ID No:191) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions, and/or

(xi) "DCTN1" (SEQ ID No:192) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions, and/or

(xii) "Delta-6 fatty acid desaturase" (SEQ ID No:193) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "ENSG00000144840" (SEQ ID No:194) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "FACL3" (SEQ ID No:195) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or

(xv) "FACL4" (SEQ ID No:196) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "FLJ13977" (SEQ ID No:197) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342"

encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "FLJ20481" (SEQ ID No:198) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or

(xix) "FLJ22390" (SEQ ID No:199) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions, and/or

(xx) "ICAM-2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "KIAA0095" (SEQ ID No:201) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "KIAA0922" (SEQ ID No:202) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:203) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:204) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that

hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:207) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions, and/or

(xxx) "PP1, regulatory subunit 15B" (SEQ ID No:208) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "Presenilin-1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and/or

- (xxxiii) "Presenilin-2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and/or
- (xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:211) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions, and/or
- (xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:212) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions, and/or
- (xxxvi) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions, and/or
- (xxxvii) "REP8 protein" (SEQ ID No:214) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions, and/or
- (xxxviii) "RING finger protein 5" (SEQ ID No:215) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions, and/or
- (xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions, and/or
- (xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:217) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions, and/or

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:219) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or

(xlili) "tyrosine phosphatase ensg00000149185" (SEQ ID No:220) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by

modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins
 (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
 (ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
 (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
 (iv) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a

nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "BACE1" (SEQ ID No:187) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(vi) "BSCv protein (FRAGMENT)" (SEQ ID No:188) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(vii) "CAMK4" (SEQ ID No:189) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,

(viii) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(ix) "Casein kinase II beta chain" (SEQ ID No:190) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,

(x) "Cathepsin B" (SEQ ID No:191) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(xi) "DCTN1" (SEQ ID No:192) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,

(xii) "Delta-6 fatty acid desaturase" (SEQ ID No:193) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,

- (xiii) "ENSG00000144840" (SEQ ID No:194) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (xiv) "FACL3" (SEQ ID No:195) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
- (xv) "FACL4" (SEQ ID No:196) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,
- (xvi) "FLJ13977" (SEQ ID No:197) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,
- (xvii) "FLJ20342" (SEQ ID No:127) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (xviii) "FLJ20481" (SEQ ID No:198) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (xix) "FLJ22390" (SEQ ID No:199) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (xx) "ICAM-2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,
- (xxi) "KIAA0095" (SEQ ID No:201) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095"

encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA0922" (SEQ ID No:202) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

(xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:203) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:204) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xxvi) "NICE-3" (SEQ ID No:143) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxvii) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxviii) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:207) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase"

encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,

(xxx) "PP1, regulatory subunit 15B" (SEQ ID No:208) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xxxi) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(xxxii) "Presenilin-1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Presenilin-2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:211) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:212) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxvii) "REP8 protein" (SEQ ID No:214) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein"

encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxviii) "RING finger protein 5" (SEQ ID No:215) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:217) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:219) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or (xliii) "tyrosine phosphatase ensg00000149185" (SEQ ID No:220) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as

neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

The present invention further relates to the following embodiments of the Aph1a-complex

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein selected from the group consisting of:
 - (i) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
 - (ii) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
 - (iii) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,
 - (iv) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions, and
 - (v) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions, and
 - (b) at least one second protein, which second protein is selected from the group consisting of:
 - (i) "18 kDa microsomal signal peptidase subunit " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit " encoded by a nucleic acid

that hybridizes to the "18 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions,

(ii) "23 kDa microsomal signal peptidase" (SEQ ID No:221) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "23 kDa microsomal signal peptidase" encoded by a nucleic acid that hybridizes to the "23 kDa microsomal signal peptidase" nucleic acid or its complement under low stringency conditions,

(iii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(iv) "ABCC1" (SEQ ID No:222) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCC1" encoded by a nucleic acid that hybridizes to the "ABCC1" nucleic acid or its complement under low stringency conditions,

(v) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,

(vi) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(vii) "ATM" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATM" encoded by a nucleic acid that hybridizes to the "ATM" nucleic acid or its complement under low stringency conditions,

(viii) "ATP-binding cassette, sub-family A member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A member 3" nucleic acid or its complement under low stringency conditions,

- (ix) "ATP1B1" (SEQ ID No:223) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP1B1" encoded by a nucleic acid that hybridizes to the "ATP1B1" nucleic acid or its complement under low stringency conditions,
- (x) "ATP2C1" (SEQ ID No:224) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP2C1" encoded by a nucleic acid that hybridizes to the "ATP2C1" nucleic acid or its complement under low stringency conditions,
- (xi) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions,
- (xii) "Brain-specific GTP-binding protein" (SEQ ID No:225) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Brain-specific GTP-binding protein" encoded by a nucleic acid that hybridizes to the "Brain-specific GTP-binding protein" nucleic acid or its complement under low stringency conditions,
- (xiii) "CDW92" (SEQ ID No:226) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDW92" encoded by a nucleic acid that hybridizes to the "CDW92" nucleic acid or its complement under low stringency conditions,
- (xiv) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (xv) "CNTNAP1" (SEQ ID No:227) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CNTNAP1" encoded by a nucleic acid that hybridizes to the "CNTNAP1" nucleic acid or its complement under low stringency conditions,
- (xvi) "Cerebral protein-10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein-10" encoded by a nucleic acid that hybridizes to the "Cerebral protein-10" nucleic acid or its complement under low stringency conditions,

(xvii) "DNM1" (SEQ ID No:228) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNM1" encoded by a nucleic acid that hybridizes to the "DNM1" nucleic acid or its complement under low stringency conditions,

(xviii) "Dihydrofolate reductase" (SEQ ID No:229) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dihydrofolate reductase" encoded by a nucleic acid that hybridizes to the "Dihydrofolate reductase" nucleic acid or its complement under low stringency conditions,

(xix) "ENG" (SEQ ID No:230) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG" encoded by a nucleic acid that hybridizes to the "ENG" nucleic acid or its complement under low stringency conditions,

(xx) "EXT2" (SEQ ID No:231) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXT2" encoded by a nucleic acid that hybridizes to the "EXT2" nucleic acid or its complement under low stringency conditions,

(xxi) "EXTL3" (SEQ ID No:232) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXTL3" encoded by a nucleic acid that hybridizes to the "EXTL3" nucleic acid or its complement under low stringency conditions,

(xxii) "Endocytic receptor Endo180" (SEQ ID No:233) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Endocytic receptor Endo180" encoded by a nucleic acid that hybridizes to the "Endocytic receptor Endo180" nucleic acid or its complement under low stringency conditions,

(xxiii) "FLJ13660" (SEQ ID No:234) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13660" encoded by a nucleic acid that hybridizes to the "FLJ13660" nucleic acid or its complement under low stringency conditions,

(xxiv) "GPR49" (SEQ ID No:235) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,

- (xxv) "HK2" (SEQ ID No:236) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HK2" encoded by a nucleic acid that hybridizes to the "HK2" nucleic acid or its complement under low stringency conditions,
- (xxvi) "HU-K4" (SEQ ID No:133) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HU-K4" encoded by a nucleic acid that hybridizes to the "HU-K4" nucleic acid or its complement under low stringency conditions,
- (xxvii) "HUNC18a" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HUNC18a" encoded by a nucleic acid that hybridizes to the "HUNC18a" nucleic acid or its complement under low stringency conditions,
- (xxviii) "HYPOTHETICAL PROTEIN " (SEQ ID No:237) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN " encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN " nucleic acid or its complement under low stringency conditions,
- (xxix) "Hypothetical protein (Fragment)" (SEQ ID No:238) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein (Fragment)" encoded by a nucleic acid that hybridizes to the "Hypothetical protein (Fragment)" nucleic acid or its complement under low stringency conditions,
- (xxx) "Hypothetical protein FLJ14562" (SEQ ID No:239) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ14562" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ14562" nucleic acid or its complement under low stringency conditions,
- (xxxi) "Hypothetical protein FLJ23630" (SEQ ID No:240) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23630" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23630" nucleic acid or its complement under low stringency conditions,
- (xxxii) "Hypothetical protein KIAA0372" (SEQ ID No:241) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "Hypothetical protein KIAA0372" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0372" nucleic acid or its complement under low stringency conditions,

(xxxiii) "ICAM2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM2" encoded by a nucleic acid that hybridizes to the "ICAM2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "IGF2R" (SEQ ID No:242) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IGF2R" encoded by a nucleic acid that hybridizes to the "IGF2R" nucleic acid or its complement under low stringency conditions,

(xxxv) "ITPR1" (SEQ ID No:243) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,

(xxxviii) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxxix) "KIAA0251 (FRAGMENT)" (SEQ ID No:244) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0251 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0251 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

- (xi) "KIAA0363 (FRAGMENT)" (SEQ ID No:245) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0363 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xli) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,
- (xlii) "KIAA0971" (SEQ ID No:246) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0971" encoded by a nucleic acid that hybridizes to the "KIAA0971" nucleic acid or its complement under low stringency conditions,
- (xliii) "KIAA1250" (SEQ ID No:247) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,
- (xliv) "LRP5" (SEQ ID No:248) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LRP5" encoded by a nucleic acid that hybridizes to the "LRP5" nucleic acid or its complement under low stringency conditions,
- (xlv) "MGC4248 " (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248 " encoded by a nucleic acid that hybridizes to the "MGC4248 " nucleic acid or its complement under low stringency conditions,
- (xlvi) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,
- (xlvii) "NRP2" (SEQ ID No:249) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NRP2" encoded by a nucleic acid that hybridizes to the "NRP2" nucleic acid or its complement under low stringency conditions,

(xlviii) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xlix) "PCDHA10" (SEQ ID No:250) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHA10" encoded by a nucleic acid that hybridizes to the "PCDHA10" nucleic acid or its complement under low stringency conditions,

(l) "PCDHB12" (SEQ ID No:251) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB12" encoded by a nucleic acid that hybridizes to the "PCDHB12" nucleic acid or its complement under low stringency conditions,

(li) "PCDHB13: protocadherin beta 13" (SEQ ID No:252) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB13: protocadherin beta 13" encoded by a nucleic acid that hybridizes to the "PCDHB13: protocadherin beta 13" nucleic acid or its complement under low stringency conditions,

(lii) "PCDHB4" (SEQ ID No:253) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB4" encoded by a nucleic acid that hybridizes to the "PCDHB4" nucleic acid or its complement under low stringency conditions,

(liii) "PCDHGB1" (SEQ ID No:254) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB1" encoded by a nucleic acid that hybridizes to the "PCDHGB1" nucleic acid or its complement under low stringency conditions,

(liv) "PCDHGB6" (SEQ ID No:255) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB6" encoded by a nucleic acid that hybridizes to the "PCDHGB6" nucleic acid or its complement under low stringency conditions,

(lv) "PMPCB" (SEQ ID No:256) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PMPCB" encoded by a nucleic acid that hybridizes to the "PMPCB" nucleic acid or its complement under low stringency conditions,

- (lvi) "PP2C gamma" (SEQ ID No:257) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP2C gamma" encoded by a nucleic acid that hybridizes to the "PP2C gamma" nucleic acid or its complement under low stringency conditions,
- (lvii) "Pcdhb17" (SEQ ID No:258) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pcdhb17" encoded by a nucleic acid that hybridizes to the "Pcdhb17" nucleic acid or its complement under low stringency conditions,
- (lviii) "Protocadherin 7" (SEQ ID No:259) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin 7" encoded by a nucleic acid that hybridizes to the "Protocadherin 7" nucleic acid or its complement under low stringency conditions,
- (lix) "Protocadherin beta 16" (SEQ ID No:260) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 16" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 16" nucleic acid or its complement under low stringency conditions,
- (lx) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,
- (lxi) "RAB-18" (SEQ ID No:261) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB-18" encoded by a nucleic acid that hybridizes to the "RAB-18" nucleic acid or its complement under low stringency conditions,
- (lxii) "RNASEL" (SEQ ID No:262) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RNASEL" encoded by a nucleic acid that hybridizes to the "RNASEL" nucleic acid or its complement under low stringency conditions,
- (lxiii) "Rab3 GTPase-activating protein, non-catalytic subunit" (SEQ ID No:263) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Rab3 GTPase-activating protein, non-catalytic subunit" encoded by a nucleic acid that hybridizes to the "Rab3 GTPase-activating protein, non-catalytic subunit" nucleic acid or its complement under low stringency conditions,

(lxiv) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(lxv) "SMAP-1B" (SEQ ID No:264) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SMAP-1B" encoded by a nucleic acid that hybridizes to the "SMAP-1B" nucleic acid or its complement under low stringency conditions,

(lxvi) "SPTLC2" (SEQ ID No:265) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(lxvii) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions,

(lxviii) "Sideroflexin 1" (SEQ ID No:266) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sideroflexin 1" encoded by a nucleic acid that hybridizes to the "Sideroflexin 1" nucleic acid or its complement under low stringency conditions,

(lxix) "Signal transducer and activator of transcription-1" (SEQ ID No:267) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Signal transducer and activator of transcription-1" encoded by a nucleic acid that hybridizes to the "Signal transducer and activator of transcription-1" nucleic acid or its complement under low stringency conditions,

(lxx) "Similar to CGI-135 protein" (SEQ ID No:268) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to CGI-135 protein" encoded by a nucleic acid that hybridizes to the "Similar to CGI-135 protein" nucleic acid or its complement under low stringency conditions,

(lxxi) "Sterile alpha and HEAT/Armadillo motif protein" (SEQ ID No:269) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterile alpha and HEAT/Armadillo motif protein" encoded by a nucleic

acid that hybridizes to the "Sterile alpha and HEAT/Armadillo motif protein" nucleic acid or its complement under low stringency conditions,

(lxxii) "Sterol O-acyltransferase 1" (SEQ ID No:270) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterol O-acyltransferase 1" encoded by a nucleic acid that hybridizes to the "Sterol O-acyltransferase 1" nucleic acid or its complement under low stringency conditions,

(lxxiii) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(lxxiv) "Triple functional domain protein (PTPRF interacting)" (SEQ ID No:271) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Triple functional domain protein (PTPRF interacting)" encoded by a nucleic acid that hybridizes to the "Triple functional domain protein (PTPRF interacting)" nucleic acid or its complement under low stringency conditions,

(lxxv) "UNC5C" (SEQ ID No:272) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UNC5C" encoded by a nucleic acid that hybridizes to the "UNC5C" nucleic acid or its complement under low stringency conditions,

(lxxvi) "Vacuolar ATP synthase membrane sector associated protein m8-9" (SEQ ID No:273) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Vacuolar ATP synthase membrane sector associated protein m8-9" encoded by a nucleic acid that hybridizes to the "Vacuolar ATP synthase membrane sector associated protein m8-9" nucleic acid or its complement under low stringency conditions,

(lxxvii) "Y391_HUMAN" (SEQ ID No:274) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Y391_HUMAN" encoded by a nucleic acid that hybridizes to the "Y391_HUMAN" nucleic acid or its complement under low stringency conditions,

(lxxviii) "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" (SEQ ID No:275) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" encoded by a nucleic acid that hybridizes to the

"hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" nucleic acid or its complement under low stringency conditions,

(lxxix) "hypothetical protein MGC22916" (SEQ ID No:276) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC22916" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC22916" nucleic acid or its complement under low stringency conditions,

(lxxx) "integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(lxxxi) "tegt: testis enhanced gene transcript (bax inhibitor 1)" (SEQ ID No:278) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tegt: testis enhanced gene transcript (bax inhibitor 1)" encoded by a nucleic acid that hybridizes to the "tegt: testis enhanced gene transcript (bax inhibitor 1)" nucleic acid or its complement under low stringency conditions, and

(lxxxii) "vacuolar protein sorting protein 18" (SEQ ID No:279) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "vacuolar protein sorting protein 18" encoded by a nucleic acid that hybridizes to the "vacuolar protein sorting protein 18" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein 'Aph1a' (SEQ ID NO. 109), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'Aph1a' encoded by a nucleic acid that hybridizes to the 'Aph1a' under low stringency conditions.

3. The protein complex according to No. 1 selected from complex (I) and comprising the following proteins:

- (i) "18 kDa microsomal signal peptidase subunit " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions,
- (ii) "23 kDa microsomal signal peptidase" (SEQ ID No:221) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "23 kDa microsomal signal peptidase" encoded by a nucleic acid that hybridizes to the "23 kDa microsomal signal peptidase" nucleic acid or its complement under low stringency conditions,
- (iii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
- (iv) "ABCC1" (SEQ ID No:222) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCC1" encoded by a nucleic acid that hybridizes to the "ABCC1" nucleic acid or its complement under low stringency conditions,
- (v) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,
- (vi) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (vii) "ATM" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATM" encoded by a nucleic acid that hybridizes to the "ATM" nucleic acid or its complement under low stringency conditions,

- (viii) "ATP-binding cassette, sub-family A member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A member 3" nucleic acid or its complement under low stringency conditions,
- (ix) "ATP1B1" (SEQ ID No:223) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP1B1" encoded by a nucleic acid that hybridizes to the "ATP1B1" nucleic acid or its complement under low stringency conditions,
- (x) "ATP2C1" (SEQ ID No:224) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP2C1" encoded by a nucleic acid that hybridizes to the "ATP2C1" nucleic acid or its complement under low stringency conditions,
- (xi) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions,
- (xii) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
- (xiii) "Brain-specific GTP-binding protein" (SEQ ID No:225) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Brain-specific GTP-binding protein" encoded by a nucleic acid that hybridizes to the "Brain-specific GTP-binding protein" nucleic acid or its complement under low stringency conditions,
- (xiv) "CDW92" (SEQ ID No:226) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDW92" encoded by a nucleic acid that hybridizes to the "CDW92" nucleic acid or its complement under low stringency conditions,
- (xv) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a

nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(xvi) "CNTNAP1" (SEQ ID No:227) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CNTNAP1" encoded by a nucleic acid that hybridizes to the "CNTNAP1" nucleic acid or its complement under low stringency conditions,

(xvii) "Cerebral protein-10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein-10" encoded by a nucleic acid that hybridizes to the "Cerebral protein-10" nucleic acid or its complement under low stringency conditions,

(xviii) "DNM1" (SEQ ID No:228) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNM1" encoded by a nucleic acid that hybridizes to the "DNM1" nucleic acid or its complement under low stringency conditions,

(xix) "Dihydrofolate reductase" (SEQ ID No:229) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dihydrofolate reductase" encoded by a nucleic acid that hybridizes to the "Dihydrofolate reductase" nucleic acid or its complement under low stringency conditions,

(xx) "ENG" (SEQ ID No:230) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG" encoded by a nucleic acid that hybridizes to the "ENG" nucleic acid or its complement under low stringency conditions,

(xxi) "EXT2" (SEQ ID No:231) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXT2" encoded by a nucleic acid that hybridizes to the "EXT2" nucleic acid or its complement under low stringency conditions,

(xxii) "EXTL3" (SEQ ID No:232) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXTL3" encoded by a nucleic acid that hybridizes to the "EXTL3" nucleic acid or its complement under low stringency conditions,

(xxiii) "Endocytic receptor Endo180" (SEQ ID No:233) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Endocytic receptor Endo180" encoded by a nucleic acid that hybridizes to the

"Endocytic receptor Endo180" nucleic acid or its complement under low stringency conditions,

(xxiv) "FLJ13660" (SEQ ID No:234) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13660" encoded by a nucleic acid that hybridizes to the "FLJ13660" nucleic acid or its complement under low stringency conditions,

(xxv) "GPR49" (SEQ ID No:235) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,

(xxvi) "HK2" (SEQ ID No:236) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HK2" encoded by a nucleic acid that hybridizes to the "HK2" nucleic acid or its complement under low stringency conditions,

(xxvii) "HU-K4" (SEQ ID No:133) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HU-K4" encoded by a nucleic acid that hybridizes to the "HU-K4" nucleic acid or its complement under low stringency conditions,

(xxviii) "HUNC18a" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HUNC18a" encoded by a nucleic acid that hybridizes to the "HUNC18a" nucleic acid or its complement under low stringency conditions,

(xxix) "HYPOTHETICAL PROTEIN " (SEQ ID No:237) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN " encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN " nucleic acid or its complement under low stringency conditions,

(xxx) "Hypothetical protein (Fragment)" (SEQ ID No:238) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein (Fragment)" encoded by a nucleic acid that hybridizes to the "Hypothetical protein (Fragment)" nucleic acid or its complement under low stringency conditions,

(xxxi) "Hypothetical protein FLJ14562" (SEQ ID No:239) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "Hypothetical protein FLJ14562" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ14562" nucleic acid or its complement under low stringency conditions,

(xxxii) "Hypothetical protein FLJ23630" (SEQ ID No:240) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23630" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23630" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Hypothetical protein KIAA0372" (SEQ ID No:241) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0372" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0372" nucleic acid or its complement under low stringency conditions,

(xxxiv) "ICAM2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM2" encoded by a nucleic acid that hybridizes to the "ICAM2" nucleic acid or its complement under low stringency conditions,

(xxxv) "IGF2R" (SEQ ID No:242) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IGF2R" encoded by a nucleic acid that hybridizes to the "IGF2R" nucleic acid or its complement under low stringency conditions,

(xxxvi) "ITPR1" (SEQ ID No:243) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions,

(xxxviii) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that

hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,

(xxxix) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xl) "KIAA0251 (FRAGMENT)" (SEQ ID No:244) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0251 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0251 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xlii) "KIAA0363 (FRAGMENT)" (SEQ ID No:245) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0363 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xliii) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,

(xliv) "KIAA0971" (SEQ ID No:246) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0971" encoded by a nucleic acid that hybridizes to the "KIAA0971" nucleic acid or its complement under low stringency conditions,

(xlv) "KIAA1250" (SEQ ID No:247) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,

(xlvi) "LRP5" (SEQ ID No:248) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LRP5" encoded by a nucleic acid that hybridizes to the "LRP5" nucleic acid or its complement under low stringency conditions,

(xlvii) "MGC4248" (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248" encoded by a nucleic acid that hybridizes to the "MGC4248" nucleic acid or its complement under low stringency conditions,

- (xlvii) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,
- (xlviii) "NRP2" (SEQ ID No:249) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NRP2" encoded by a nucleic acid that hybridizes to the "NRP2" nucleic acid or its complement under low stringency conditions,
- (xlix) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,
- (l) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (li) "PCDHA10" (SEQ ID No:250) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHA10" encoded by a nucleic acid that hybridizes to the "PCDHA10" nucleic acid or its complement under low stringency conditions,
- (lii) "PCDHB12" (SEQ ID No:251) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB12" encoded by a nucleic acid that hybridizes to the "PCDHB12" nucleic acid or its complement under low stringency conditions,
- (liii) "PCDHB13: protocadherin beta 13" (SEQ ID No:252) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB13: protocadherin beta 13" encoded by a nucleic acid that hybridizes to the "PCDHB13: protocadherin beta 13" nucleic acid or its complement under low stringency conditions,
- (liv) "PCDHB4" (SEQ ID No:253) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB4" encoded by a nucleic acid that hybridizes to the "PCDHB4" nucleic acid or its complement under low stringency conditions,

- (iv) "PCDHGB1" (SEQ ID No:254) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB1" encoded by a nucleic acid that hybridizes to the "PCDHGB1" nucleic acid or its complement under low stringency conditions,
- (lvi) "PCDHGB6" (SEQ ID No:255) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB6" encoded by a nucleic acid that hybridizes to the "PCDHGB6" nucleic acid or its complement under low stringency conditions,
- (lvii) "PMPCB" (SEQ ID No:256) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PMPCB" encoded by a nucleic acid that hybridizes to the "PMPCB" nucleic acid or its complement under low stringency conditions,
- (lviii) "PP2C gamma" (SEQ ID No:257) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP2C gamma" encoded by a nucleic acid that hybridizes to the "PP2C gamma" nucleic acid or its complement under low stringency conditions,
- (lix) "Pcdhb17" (SEQ ID No:258) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pcdhb17" encoded by a nucleic acid that hybridizes to the "Pcdhb17" nucleic acid or its complement under low stringency conditions,
- (lx) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,
- (lxi) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions,
- (lxii) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions,
- (lxiii) "Protocadherin 7" (SEQ ID No:259) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin

- 7" encoded by a nucleic acid that hybridizes to the "Protocadherin 7" nucleic acid or its complement under low stringency conditions,
- (lxiv) "Protocadherin beta 16" (SEQ ID No:260) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 16" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 16" nucleic acid or its complement under low stringency conditions,
- (lxv) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,
- (lxvi) "RAB-18" (SEQ ID No:261) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB-18" encoded by a nucleic acid that hybridizes to the "RAB-18" nucleic acid or its complement under low stringency conditions,
- (lxvii) "RNASEL" (SEQ ID No:262) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RNASEL" encoded by a nucleic acid that hybridizes to the "RNASEL" nucleic acid or its complement under low stringency conditions,
- (lxviii) "Rab3 GTPase-activating protein, non-catalytic subunit" (SEQ ID No:263) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Rab3 GTPase-activating protein, non-catalytic subunit" encoded by a nucleic acid that hybridizes to the "Rab3 GTPase-activating protein, non-catalytic subunit" nucleic acid or its complement under low stringency conditions,
- (lxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,
- (lxx) "SMAP-1B" (SEQ ID No:264) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SMAP-1B" encoded by a nucleic acid that hybridizes to the "SMAP-1B" nucleic acid or its complement under low stringency conditions,

(lxxi) "SPTLC2" (SEQ ID No:265) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(lxxii) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions,

(lxxiii) "Sideroflexin 1" (SEQ ID No:266) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sideroflexin 1" encoded by a nucleic acid that hybridizes to the "Sideroflexin 1" nucleic acid or its complement under low stringency conditions,

(lxxiv) "Signal transducer and activator of transcription-1" (SEQ ID No:267) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Signal transducer and activator of transcription-1" encoded by a nucleic acid that hybridizes to the "Signal transducer and activator of transcription-1" nucleic acid or its complement under low stringency conditions,

(lxxv) "Similar to CGI-135 protein" (SEQ ID No:268) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to CGI-135 protein" encoded by a nucleic acid that hybridizes to the "Similar to CGI-135 protein" nucleic acid or its complement under low stringency conditions,

(lxxvi) "Sterile alpha and HEAT/Armadillo motif protein" (SEQ ID No:269) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterile alpha and HEAT/Armadillo motif protein" encoded by a nucleic acid that hybridizes to the "Sterile alpha and HEAT/Armadillo motif protein" nucleic acid or its complement under low stringency conditions,

(lxxvii) "Sterol O-acyltransferase 1" (SEQ ID No:270) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterol O-acyltransferase 1" encoded by a nucleic acid that hybridizes to the "Sterol O-acyltransferase 1" nucleic acid or its complement under low stringency conditions,

(lxxviii) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that

hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(lxxix) "Triple functional domain protein (PTPRF interacting)" (SEQ ID No:271) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Triple functional domain protein (PTPRF interacting)" encoded by a nucleic acid that hybridizes to the "Triple functional domain protein (PTPRF interacting)" nucleic acid or its complement under low stringency conditions,

(lxxx) "UNC5C" (SEQ ID No:272) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UNC5C" encoded by a nucleic acid that hybridizes to the "UNC5C" nucleic acid or its complement under low stringency conditions,

(lxxxi) "Vacuolar ATP synthase membrane sector associated protein m8-9" (SEQ ID No:273) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Vacuolar ATP synthase membrane sector associated protein m8-9" encoded by a nucleic acid that hybridizes to the "Vacuolar ATP synthase membrane sector associated protein m8-9" nucleic acid or its complement under low stringency conditions,

(lxxxii) "Y391_HUMAN" (SEQ ID No:274) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Y391_HUMAN" encoded by a nucleic acid that hybridizes to the "Y391_HUMAN" nucleic acid or its complement under low stringency conditions,

(lxxxiii) "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" (SEQ ID No:275) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" nucleic acid or its complement under low stringency conditions,

(lxxxiv) "hypothetical protein MGC22916" (SEQ ID No:276) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC22916" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC22916" nucleic acid or its complement under low stringency conditions,

(lxxxv) "integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(lxxxvi) "tegt: testis enhanced gene transcript (bax inhibitor 1)" (SEQ ID No:278) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tegt: testis enhanced gene transcript (bax inhibitor 1)" encoded by a nucleic acid that hybridizes to the "tegt: testis enhanced gene transcript (bax inhibitor 1)" nucleic acid or its complement under low stringency conditions, and/or (lxxxvii) "vacuolar protein sorting protein 18" (SEQ ID No:279) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "vacuolar protein sorting protein 18" encoded by a nucleic acid that hybridizes to the "vacuolar protein sorting protein 18" nucleic acid or its complement under low stringency conditions,

and a protein complex selected from complex (II) and comprising the following proteins:

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "23 kDa microsomal signal peptidase" (SEQ ID No:221) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "23 kDa microsomal signal peptidase" encoded by a nucleic acid that hybridizes to the "23 kDa microsomal signal peptidase" nucleic acid or its complement under low stringency conditions,

(iii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(iv) "ABCC1" (SEQ ID No:222) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCC1" encoded by a nucleic acid that hybridizes to the "ABCC1" nucleic acid or its complement under low stringency conditions,

- (v) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,
- (vi) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (vii) "ATM" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATM" encoded by a nucleic acid that hybridizes to the "ATM" nucleic acid or its complement under low stringency conditions,
- (viii) "ATP-binding cassette, sub-family A member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A member 3" nucleic acid or its complement under low stringency conditions,
- (ix) "ATP1B1" (SEQ ID No:223) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP1B1" encoded by a nucleic acid that hybridizes to the "ATP1B1" nucleic acid or its complement under low stringency conditions,
- (x) "ATP2C1" (SEQ ID No:224) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP2C1" encoded by a nucleic acid that hybridizes to the "ATP2C1" nucleic acid or its complement under low stringency conditions,
- (xi) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions,
- (xii) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

- (xiii) "Brain-specific GTP-binding protein" (SEQ ID No:225) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Brain-specific GTP-binding protein" encoded by a nucleic acid that hybridizes to the "Brain-specific GTP-binding protein" nucleic acid or its complement under low stringency conditions,
- (xiv) "CDW92" (SEQ ID No:226) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDW92" encoded by a nucleic acid that hybridizes to the "CDW92" nucleic acid or its complement under low stringency conditions,
- (xv) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (xvi) "CNTNAP1" (SEQ ID No:227) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CNTNAP1" encoded by a nucleic acid that hybridizes to the "CNTNAP1" nucleic acid or its complement under low stringency conditions,
- (xvii) "Cerebral protein-10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein-10" encoded by a nucleic acid that hybridizes to the "Cerebral protein-10" nucleic acid or its complement under low stringency conditions,
- (xviii) "DNM1" (SEQ ID No:228) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNM1" encoded by a nucleic acid that hybridizes to the "DNM1" nucleic acid or its complement under low stringency conditions,
- (xix) "Dihydrofolate reductase" (SEQ ID No:229) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dihydrofolate reductase" encoded by a nucleic acid that hybridizes to the "Dihydrofolate reductase" nucleic acid or its complement under low stringency conditions,
- (xx) "ENG" (SEQ ID No:230) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG" encoded by a nucleic acid that hybridizes to the "ENG" nucleic acid or its complement under low stringency conditions,

- (xxi) "EXT2" (SEQ ID No:231) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXT2" encoded by a nucleic acid that hybridizes to the "EXT2" nucleic acid or its complement under low stringency conditions,
- (xxii) "EXTL3" (SEQ ID No:232) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXTL3" encoded by a nucleic acid that hybridizes to the "EXTL3" nucleic acid or its complement under low stringency conditions,
- (xxiii) "Endocytic receptor Endo180" (SEQ ID No:233) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Endocytic receptor Endo180" encoded by a nucleic acid that hybridizes to the "Endocytic receptor Endo180" nucleic acid or its complement under low stringency conditions,
- (xxiv) "FLJ13660" (SEQ ID No:234) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13660" encoded by a nucleic acid that hybridizes to the "FLJ13660" nucleic acid or its complement under low stringency conditions,
- (xxv) "GPR49" (SEQ ID No:235) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,
- (xxvi) "HK2" (SEQ ID No:236) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HK2" encoded by a nucleic acid that hybridizes to the "HK2" nucleic acid or its complement under low stringency conditions,
- (xxvii) "HU-K4" (SEQ ID No:133) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HU-K4" encoded by a nucleic acid that hybridizes to the "HU-K4" nucleic acid or its complement under low stringency conditions,
- (xxviii) "HUNC18a" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HUNC18a" encoded by a nucleic acid that hybridizes to the "HUNC18a" nucleic acid or its complement under low stringency conditions,

(xxix) "HYPOTHETICAL PROTEIN " (SEQ ID No:237) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN " encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN " nucleic acid or its complement under low stringency conditions,

(xxx) "Hypothetical protein (Fragment)" (SEQ ID No:238) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein (Fragment)" encoded by a nucleic acid that hybridizes to the "Hypothetical protein (Fragment)" nucleic acid or its complement under low stringency conditions,

(xxxi) "Hypothetical protein FLJ14562" (SEQ ID No:239) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ14562" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ14562" nucleic acid or its complement under low stringency conditions,

(xxxii) "Hypothetical protein FLJ23630" (SEQ ID No:240) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23630" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23630" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Hypothetical protein KIAA0372" (SEQ ID No:241) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0372" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0372" nucleic acid or its complement under low stringency conditions,

(xxxiv) "ICAM2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM2" encoded by a nucleic acid that hybridizes to the "ICAM2" nucleic acid or its complement under low stringency conditions,

(xxxv) "IGF2R" (SEQ ID No:242) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IGF2R" encoded by a nucleic acid that hybridizes to the "IGF2R" nucleic acid or its complement under low stringency conditions,

- (xxxvi) "ITPR1" (SEQ ID No:243) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,
- (xxxvii) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions,
- (xxxviii) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,
- (xxxix) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xi) "KIAA0251 (FRAGMENT)" (SEQ ID No:244) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0251 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0251 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xli) "KIAA0363 (FRAGMENT)" (SEQ ID No:245) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0363 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xlii) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,
- (xlili) "KIAA0971" (SEQ ID No:246) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0971" encoded by a nucleic acid that hybridizes to the "KIAA0971" nucleic acid or its complement under low stringency conditions,

- (xliv) "KIAA1250" (SEQ ID No:247) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,
- (xlv) "LRP5" (SEQ ID No:248) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LRP5" encoded by a nucleic acid that hybridizes to the "LRP5" nucleic acid or its complement under low stringency conditions,
- (xlvi) "MGC4248 " (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248 " encoded by a nucleic acid that hybridizes to the "MGC4248 " nucleic acid or its complement under low stringency conditions,
- (xlvii) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,
- (xlviii) "NRP2" (SEQ ID No:249) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NRP2" encoded by a nucleic acid that hybridizes to the "NRP2" nucleic acid or its complement under low stringency conditions,
- (xlix) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,
- (l) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (li) "PCDHA10" (SEQ ID No:250) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHA10" encoded by a nucleic acid that hybridizes to the "PCDHA10" nucleic acid or its complement under low stringency conditions,

- (lii) "PCDHB12" (SEQ ID No:251) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB12" encoded by a nucleic acid that hybridizes to the "PCDHB12" nucleic acid or its complement under low stringency conditions,
- (liii) "PCDHB13: protocadherin beta 13" (SEQ ID No:252) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB13: protocadherin beta 13" encoded by a nucleic acid that hybridizes to the "PCDHB13: protocadherin beta 13" nucleic acid or its complement under low stringency conditions,
- (liv) "PCDHB4" (SEQ ID No:253) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB4" encoded by a nucleic acid that hybridizes to the "PCDHB4" nucleic acid or its complement under low stringency conditions,
- (lv) "PCDHGB1" (SEQ ID No:254) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB1" encoded by a nucleic acid that hybridizes to the "PCDHGB1" nucleic acid or its complement under low stringency conditions,
- (lvi) "PCDHGB6" (SEQ ID No:255) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB6" encoded by a nucleic acid that hybridizes to the "PCDHGB6" nucleic acid or its complement under low stringency conditions,
- (lvii) "PMPCB" (SEQ ID No:256) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PMPCB" encoded by a nucleic acid that hybridizes to the "PMPCB" nucleic acid or its complement under low stringency conditions,
- (lviii) "PP2C gamma" (SEQ ID No:257) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP2C gamma" encoded by a nucleic acid that hybridizes to the "PP2C gamma" nucleic acid or its complement under low stringency conditions,
- (lix) "Pcdhb17" (SEQ ID No:258) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pcdhb17" encoded by a nucleic acid that hybridizes to the "Pcdhb17" nucleic acid or its complement under low stringency conditions,

- (lx) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions,
- (lxi) "Protocadherin 7" (SEQ ID No:259) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin 7" encoded by a nucleic acid that hybridizes to the "Protocadherin 7" nucleic acid or its complement under low stringency conditions,
- (lxii) "Protocadherin beta 16" (SEQ ID No:260) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 16" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 16" nucleic acid or its complement under low stringency conditions,
- (lxiii) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,
- (lxiv) "RAB-18" (SEQ ID No:261) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB-18" encoded by a nucleic acid that hybridizes to the "RAB-18" nucleic acid or its complement under low stringency conditions,
- (lxv) "RNASEL" (SEQ ID No:262) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RNASEL" encoded by a nucleic acid that hybridizes to the "RNASEL" nucleic acid or its complement under low stringency conditions,
- (lxvi) "Rab3 GTPase-activating protein, non-catalytic subunit" (SEQ ID No:263) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Rab3 GTPase-activating protein, non-catalytic subunit" encoded by a nucleic acid that hybridizes to the "Rab3 GTPase-activating protein, non-catalytic subunit" nucleic acid or its complement under low stringency conditions,
- (lxvii) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain

dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(Ixxviii) "SMAP-1B" (SEQ ID No:264) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SMAP-1B" encoded by a nucleic acid that hybridizes to the "SMAP-1B" nucleic acid or its complement under low stringency conditions,

(Ixxix) "SPTLC2" (SEQ ID No:265) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(Ixxx) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions,

(Ixxxi) "Sideroflexin 1" (SEQ ID No:266) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sideroflexin 1" encoded by a nucleic acid that hybridizes to the "Sideroflexin 1" nucleic acid or its complement under low stringency conditions,

(Ixxxii) "Signal transducer and activator of transcription-1" (SEQ ID No:267) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Signal transducer and activator of transcription-1" encoded by a nucleic acid that hybridizes to the "Signal transducer and activator of transcription-1" nucleic acid or its complement under low stringency conditions,

(Ixxxiii) "Similar to CGI-135 protein" (SEQ ID No:268) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to CGI-135 protein" encoded by a nucleic acid that hybridizes to the "Similar to CGI-135 protein" nucleic acid or its complement under low stringency conditions,

(Ixxxiv) "Sterile alpha and HEAT/Armadillo motif protein" (SEQ ID No:269) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterile alpha and HEAT/Armadillo motif protein" encoded by a nucleic acid that hybridizes to the "Sterile alpha and HEAT/Armadillo motif protein" nucleic acid or its complement under low stringency conditions,

(Ixxxv) "Sterol O-acyltransferase 1" (SEQ ID No:270) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"Sterol O-acyltransferase 1" encoded by a nucleic acid that hybridizes to the "Sterol O-acyltransferase 1" nucleic acid or its complement under low stringency conditions,
 (lxxvi) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(lxxvii) "Triple functional domain protein (PTPRF interacting)" (SEQ ID No:271) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Triple functional domain protein (PTPRF interacting)" encoded by a nucleic acid that hybridizes to the "Triple functional domain protein (PTPRF interacting)" nucleic acid or its complement under low stringency conditions,
 (lxxviii) "UNC5C" (SEQ ID No:272) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UNC5C" encoded by a nucleic acid that hybridizes to the "UNC5C" nucleic acid or its complement under low stringency conditions,

(lxxix) "Vacuolar ATP synthase membrane sector associated protein m8-9" (SEQ ID No:273) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Vacuolar ATP synthase membrane sector associated protein m8-9" encoded by a nucleic acid that hybridizes to the "Vacuolar ATP synthase membrane sector associated protein m8-9" nucleic acid or its complement under low stringency conditions,

(lxxx) "Y391_HUMAN" (SEQ ID No:274) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Y391_HUMAN" encoded by a nucleic acid that hybridizes to the "Y391_HUMAN" nucleic acid or its complement under low stringency conditions,

(lxxxi) "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" (SEQ ID No:275) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" nucleic acid or its complement under low stringency conditions,

(lxxxii) "hypothetical protein MGC22916" (SEQ ID No:276) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "hypothetical protein MGC22916" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC22916" nucleic acid or its complement under low stringency conditions,

(lxxxiii) "integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(lxxxiv) "tegt: testis enhanced gene transcript (bax inhibitor 1)" (SEQ ID No:278) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tegt: testis enhanced gene transcript (bax inhibitor 1)" encoded by a nucleic acid that hybridizes to the "tegt: testis enhanced gene transcript (bax inhibitor 1)" nucleic acid or its complement under low stringency conditions, and/or

(lxxxv) "vacuolar protein sorting protein 18" (SEQ ID No:279) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "vacuolar protein sorting protein 18" encoded by a nucleic acid that hybridizes to the "vacuolar protein sorting protein 18" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 81 of the following proteins:

(i) "18 kDa microsomal signal peptidase subunit " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions,

(ii) "23 kDa microsomal signal peptidase" (SEQ ID No:221) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "23 kDa microsomal signal peptidase" encoded by a nucleic acid that hybridizes to the "23 kDa microsomal signal peptidase" nucleic acid or its complement under low stringency conditions,

(iii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid

that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(iv) "ABCC1" (SEQ ID No:222) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCC1" encoded by a nucleic acid that hybridizes to the "ABCC1" nucleic acid or its complement under low stringency conditions,

(v) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,

(vi) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(vii) "ATM" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATM" encoded by a nucleic acid that hybridizes to the "ATM" nucleic acid or its complement under low stringency conditions,

(viii) "ATP-binding cassette, sub-family A member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A member 3" nucleic acid or its complement under low stringency conditions,

(ix) "ATP1B1" (SEQ ID No:223) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP1B1" encoded by a nucleic acid that hybridizes to the "ATP1B1" nucleic acid or its complement under low stringency conditions,

(x) "ATP2C1" (SEQ ID No:224) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP2C1" encoded by a nucleic acid that hybridizes to the "ATP2C1" nucleic acid or its complement under low stringency conditions,

(xi) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the

"Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions,

(xii) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(xiii) "Brain-specific GTP-binding protein" (SEQ ID No:225) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Brain-specific GTP-binding protein" encoded by a nucleic acid that hybridizes to the "Brain-specific GTP-binding protein" nucleic acid or its complement under low stringency conditions,

(xiv) "CDW92" (SEQ ID No:226) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDW92" encoded by a nucleic acid that hybridizes to the "CDW92" nucleic acid or its complement under low stringency conditions,

(xv) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(xvi) "CNTNAP1" (SEQ ID No:227) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CNTNAP1" encoded by a nucleic acid that hybridizes to the "CNTNAP1" nucleic acid or its complement under low stringency conditions,

(xvii) "Cerebral protein-10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein-10" encoded by a nucleic acid that hybridizes to the "Cerebral protein-10" nucleic acid or its complement under low stringency conditions,

(xviii) "DNM1" (SEQ ID No:228) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNM1" encoded by a nucleic acid that hybridizes to the "DNM1" nucleic acid or its complement under low stringency conditions,

(xix) "Dihydrofolate reductase" (SEQ ID No:229) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"Dihydrofolate reductase" encoded by a nucleic acid that hybridizes to the "Dihydrofolate reductase" nucleic acid or its complement under low stringency conditions,

(xx) "ENG" (SEQ ID No:230) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG" encoded by a nucleic acid that hybridizes to the "ENG" nucleic acid or its complement under low stringency conditions,

(xxi) "EXT2" (SEQ ID No:231) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXT2" encoded by a nucleic acid that hybridizes to the "EXT2" nucleic acid or its complement under low stringency conditions,

(xxii) "EXTL3" (SEQ ID No:232) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXTL3" encoded by a nucleic acid that hybridizes to the "EXTL3" nucleic acid or its complement under low stringency conditions,

(xxiii) "Endocytic receptor Endo180" (SEQ ID No:233) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Endocytic receptor Endo180" encoded by a nucleic acid that hybridizes to the "Endocytic receptor Endo180" nucleic acid or its complement under low stringency conditions,

(xxiv) "FLJ13660" (SEQ ID No:234) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13660" encoded by a nucleic acid that hybridizes to the "FLJ13660" nucleic acid or its complement under low stringency conditions,

(xxv) "GPR49" (SEQ ID No:235) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,

(xxvi) "HK2" (SEQ ID No:236) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HK2" encoded by a nucleic acid that hybridizes to the "HK2" nucleic acid or its complement under low stringency conditions,

(xxvii) "HU-K4" (SEQ ID No:133) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HU-K4"

encoded by a nucleic acid that hybridizes to the "HU-K4" nucleic acid or its complement under low stringency conditions,

(xxviii) "HUNC18a" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HUNC18a" encoded by a nucleic acid that hybridizes to the "HUNC18a" nucleic acid or its complement under low stringency conditions,

(xxix) "HYPOTHETICAL PROTEIN " (SEQ ID No:237) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN " encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN " nucleic acid or its complement under low stringency conditions,

(xxx) "Hypothetical protein (Fragment)" (SEQ ID No:238) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein (Fragment)" encoded by a nucleic acid that hybridizes to the "Hypothetical protein (Fragment)" nucleic acid or its complement under low stringency conditions,

(xxxi) "Hypothetical protein FLJ14562" (SEQ ID No:239) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ14562" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ14562" nucleic acid or its complement under low stringency conditions,

(xxxii) "Hypothetical protein FLJ23630" (SEQ ID No:240) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23630" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23630" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Hypothetical protein KIAA0372" (SEQ ID No:241) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0372" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0372" nucleic acid or its complement under low stringency conditions,

(xxxiv) "ICAM2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM2"

encoded by a nucleic acid that hybridizes to the "ICAM2" nucleic acid or its complement under low stringency conditions,

(xxxv) "IGF2R" (SEQ ID No:242) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IGF2R" encoded by a nucleic acid that hybridizes to the "IGF2R" nucleic acid or its complement under low stringency conditions,

(xxxvi) "ITPR1" (SEQ ID No:243) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions,

(xxxviii) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,

(xxxix) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xl) "KIAA0251 (FRAGMENT)" (SEQ ID No:244) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0251 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0251 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xli) "KIAA0363 (FRAGMENT)" (SEQ ID No:245) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0363 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xlii) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763"

encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,

(xlili) "KIAA0971" (SEQ ID No:246) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0971" encoded by a nucleic acid that hybridizes to the "KIAA0971" nucleic acid or its complement under low stringency conditions,

(xliv) "KIAA1250" (SEQ ID No:247) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,

(xlv) "LRP5" (SEQ ID No:248) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LRP5" encoded by a nucleic acid that hybridizes to the "LRP5" nucleic acid or its complement under low stringency conditions,

(xlvi) "MGC4248 " (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248 " encoded by a nucleic acid that hybridizes to the "MGC4248 " nucleic acid or its complement under low stringency conditions,

(xlvii) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xlviii) "NRP2" (SEQ ID No:249) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NRP2" encoded by a nucleic acid that hybridizes to the "NRP2" nucleic acid or its complement under low stringency conditions,

(xlix) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(l) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a

nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(li) "PCDHA10" (SEQ ID No:250) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHA10" encoded by a nucleic acid that hybridizes to the "PCDHA10" nucleic acid or its complement under low stringency conditions,

(lii) "PCDHB12" (SEQ ID No:251) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB12" encoded by a nucleic acid that hybridizes to the "PCDHB12" nucleic acid or its complement under low stringency conditions,

(liii) "PCDHB13: protocadherin beta 13" (SEQ ID No:252) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB13: protocadherin beta 13" encoded by a nucleic acid that hybridizes to the "PCDHB13: protocadherin beta 13" nucleic acid or its complement under low stringency conditions,

(liv) "PCDHB4" (SEQ ID No:253) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB4" encoded by a nucleic acid that hybridizes to the "PCDHB4" nucleic acid or its complement under low stringency conditions,

(lv) "PCDHGB1" (SEQ ID No:254) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB1" encoded by a nucleic acid that hybridizes to the "PCDHGB1" nucleic acid or its complement under low stringency conditions,

(lvi) "PCDHGB6" (SEQ ID No:255) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB6" encoded by a nucleic acid that hybridizes to the "PCDHGB6" nucleic acid or its complement under low stringency conditions,

(lvii) "PMPCB" (SEQ ID No:256) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PMPCB" encoded by a nucleic acid that hybridizes to the "PMPCB" nucleic acid or its complement under low stringency conditions,

(lviii) "PP2C gamma" (SEQ ID No:257) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP2C gamma"

encoded by a nucleic acid that hybridizes to the "PP2C gamma" nucleic acid or its complement under low stringency conditions,

(lix) "Pcdhb17" (SEQ ID No:258) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pcdhb17" encoded by a nucleic acid that hybridizes to the "Pcdhb17" nucleic acid or its complement under low stringency conditions,

(lx) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(lxi) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions,

(lxii) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions,

(lxiii) "Protocadherin 7" (SEQ ID No:259) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin 7" encoded by a nucleic acid that hybridizes to the "Protocadherin 7" nucleic acid or its complement under low stringency conditions,

(lxiv) "Protocadherin beta 16" (SEQ ID No:260) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 16" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 16" nucleic acid or its complement under low stringency conditions,

(lxv) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(lxvi) "RAB-18" (SEQ ID No:261) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB-18" encoded by a nucleic acid that hybridizes to the "RAB-18" nucleic acid or its complement under low stringency conditions,

(Ixxvii) "RNASEL" (SEQ ID No:262) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RNASEL" encoded by a nucleic acid that hybridizes to the "RNASEL" nucleic acid or its complement under low stringency conditions,

(Ixxviii) "Rab3 GTPase-activating protein, non-catalytic subunit" (SEQ ID No:263) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Rab3 GTPase-activating protein, non-catalytic subunit" encoded by a nucleic acid that hybridizes to the "Rab3 GTPase-activating protein, non-catalytic subunit" nucleic acid or its complement under low stringency conditions,

(Ixxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(Ixxx) "SMAP-1B" (SEQ ID No:264) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SMAP-1B" encoded by a nucleic acid that hybridizes to the "SMAP-1B" nucleic acid or its complement under low stringency conditions,

(Ixxxi) "SPTLC2" (SEQ ID No:265) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(Ixxxii) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions,

(Ixxxiii) "Sideroflexin 1" (SEQ ID No:266) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sideroflexin 1" encoded by a nucleic acid that hybridizes to the "Sideroflexin 1" nucleic acid or its complement under low stringency conditions,

(Ixxxiv) "Signal transducer and activator of transcription-1" (SEQ ID No:267) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Signal transducer and activator of transcription-1"

encoded by a nucleic acid that hybridizes to the "Signal transducer and activator of transcription-1" nucleic acid or its complement under low stringency conditions,

(lxxv) "Similar to CGI-135 protein" (SEQ ID No:268) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to CGI-135 protein" encoded by a nucleic acid that hybridizes to the "Similar to CGI-135 protein" nucleic acid or its complement under low stringency conditions,

(lxxvi) "Sterile alpha and HEAT/Armadillo motif protein" (SEQ ID No:269) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterile alpha and HEAT/Armadillo motif protein" encoded by a nucleic acid that hybridizes to the "Sterile alpha and HEAT/Armadillo motif protein" nucleic acid or its complement under low stringency conditions,

(lxxvii) "Sterol O-acyltransferase 1" (SEQ ID No:270) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterol O-acyltransferase 1" encoded by a nucleic acid that hybridizes to the "Sterol O-acyltransferase 1" nucleic acid or its complement under low stringency conditions,

(lxxviii) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(lxxix) "Triple functional domain protein (PTPRF interacting)" (SEQ ID No:271) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Triple functional domain protein (PTPRF interacting)" encoded by a nucleic acid that hybridizes to the "Triple functional domain protein (PTPRF interacting)" nucleic acid or its complement under low stringency conditions,

(lxxx) "UNC5C" (SEQ ID No:272) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UNC5C" encoded by a nucleic acid that hybridizes to the "UNC5C" nucleic acid or its complement under low stringency conditions,

(lxxxi) "Vacuolar ATP synthase membrane sector associated protein m8-9" (SEQ ID No:273) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Vacuolar ATP synthase membrane sector associated protein m8-9" encoded by a nucleic acid that hybridizes to the "Vacuolar ATP

synthase membrane sector, associated protein m8-9" nucleic acid or its complement under low stringency conditions,

(lxxxii) "Y391_HUMAN" (SEQ ID No:274) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Y391_HUMAN" encoded by a nucleic acid that hybridizes to the "Y391_HUMAN" nucleic acid or its complement under low stringency conditions,

(lxxxiii) "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" (SEQ ID No:275) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" nucleic acid or its complement under low stringency conditions,

(lxxxiv) "hypothetical protein MGC22916" (SEQ ID No:276) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC22916" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC22916" nucleic acid or its complement under low stringency conditions,

(lxxxv) "integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(lxxxvi) "tegt: testis enhanced gene transcript (bax inhibitor 1)" (SEQ ID No:278) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tegt: testis enhanced gene transcript (bax inhibitor 1)" encoded by a nucleic acid that hybridizes to the "tegt: testis enhanced gene transcript (bax inhibitor 1)" nucleic acid or its complement under low stringency conditions,

(lxxxvii) "vacuolar protein sorting protein 18" (SEQ ID No:279) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "vacuolar protein sorting protein 18" encoded by a nucleic acid that hybridizes to the "vacuolar protein sorting protein 18" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.
6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.
7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of No. 1 - 7 that is involved in the the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).
9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Aph-1a complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the Aph-1a complex selected from

- (i) "ABCC1" (SEQ ID No:222) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCC1" encoded by a nucleic acid that hybridizes to the "ABCC1" nucleic acid or its complement under low stringency conditions,
- (ii) "ATP-binding cassette, sub-family A member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A member 3" nucleic acid or its complement under low stringency conditions,
- (iii) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions,
- (iv) "CDW92" (SEQ ID No:226) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDW92" encoded by a nucleic acid that hybridizes to the "CDW92" nucleic acid or its complement under low stringency conditions,
- (v) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (vi) "Cerebral protein-10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral

protein-10" encoded by a nucleic acid that hybridizes to the "Cerebral protein-10" nucleic acid or its complement under low stringency conditions,

(vii) "GPR49" (SEQ ID No:235) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,

(viii) "HYPOTHETICAL PROTEIN " (SEQ ID No:237) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN " encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN " nucleic acid or its complement under low stringency conditions,

(ix) "Hypothetical protein (Fragment)" (SEQ ID No:238) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein (Fragment)" encoded by a nucleic acid that hybridizes to the "Hypothetical protein (Fragment)" nucleic acid or its complement under low stringency conditions,

(x) "Hypothetical protein FLJ14562" (SEQ ID No:239) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ14562" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ14562" nucleic acid or its complement under low stringency conditions,

(xi) "Hypothetical protein FLJ23630" (SEQ ID No:240) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23630" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23630" nucleic acid or its complement under low stringency conditions,

(xii) "Hypothetical protein KIAA0372" (SEQ ID No:241) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0372" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0372" nucleic acid or its complement under low stringency conditions,

(xiii) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xiv) "KIAA0251 (FRAGMENT)" (SEQ ID No:244) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0251 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0251 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xv) "KIAA0363 (FRAGMENT)" (SEQ ID No:245) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0363 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xvi) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,

(xvii) "KIAA0971" (SEQ ID No:246) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0971" encoded by a nucleic acid that hybridizes to the "KIAA0971" nucleic acid or its complement under low stringency conditions,

(xviii) "KIAA1250" (SEQ ID No:247) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,

(xix) "MGC4248 " (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248 " encoded by a nucleic acid that hybridizes to the "MGC4248 " nucleic acid or its complement under low stringency conditions,

(xx) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xxi) "PCDHA10" (SEQ ID No:250) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHA10"

encoded by a nucleic acid that hybridizes to the "PCDHA10" nucleic acid or its complement under low stringency conditions,

(xxii) "PCDHB12" (SEQ ID No:251) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB12" encoded by a nucleic acid that hybridizes to the "PCDHB12" nucleic acid or its complement under low stringency conditions,

(xxiii) "PCDHB13: protocadherin beta 13" (SEQ ID No:252) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB13: protocadherin beta 13" encoded by a nucleic acid that hybridizes to the "PCDHB13: protocadherin beta 13" nucleic acid or its complement under low stringency conditions,

(xxiv) "PCDHB4" (SEQ ID No:253) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB4" encoded by a nucleic acid that hybridizes to the "PCDHB4" nucleic acid or its complement under low stringency conditions,

(xxv) "PCDHGB1" (SEQ ID No:254) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB1" encoded by a nucleic acid that hybridizes to the "PCDHGB1" nucleic acid or its complement under low stringency conditions,

(xxvi) "PCDHGB6" (SEQ ID No:255) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB6" encoded by a nucleic acid that hybridizes to the "PCDHGB6" nucleic acid or its complement under low stringency conditions,

(xxvii) "Pcdhb17" (SEQ ID No:258) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pcdhb17" encoded by a nucleic acid that hybridizes to the "Pcdhb17" nucleic acid or its complement under low stringency conditions,

(xxviii) "Protocadherin 7" (SEQ ID No:259) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin 7" encoded by a nucleic acid that hybridizes to the "Protocadherin 7" nucleic acid or its complement under low stringency conditions,

(xxix) "Protocadherin beta 16" (SEQ ID No:260) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"Protocadherin beta 16" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 16" nucleic acid or its complement under low stringency conditions,

(xxx) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxi) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xxxii) "Similar to CGI-135 protein" (SEQ ID No:268) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to CGI-135 protein" encoded by a nucleic acid that hybridizes to the "Similar to CGI-135 protein" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Sterile alpha and HEAT/Armadillo motif protein" (SEQ ID No:269) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterile alpha and HEAT/Armadillo motif protein" encoded by a nucleic acid that hybridizes to the "Sterile alpha and HEAT/Armadillo motif protein" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xxxv) "Vacuolar ATP synthase membrane sector associated protein m8-9" (SEQ ID No:273) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Vacuolar ATP synthase membrane sector associated protein m8-9" encoded by a nucleic acid that hybridizes to the "Vacuolar ATP synthase membrane sector associated protein m8-9" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Y391_HUMAN" (SEQ ID No:274) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"Y391_HUMAN" encoded by a nucleic acid that hybridizes to the "Y391_HUMAN" nucleic acid or its complement under low stringency conditions,

(xxxvii) "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" (SEQ ID No:275) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" nucleic acid or its complement under low stringency conditions,

(xxxviii) "hypothetical protein MGC22916" (SEQ ID No:276) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC22916" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC22916" nucleic acid or its complement under low stringency conditions,

(xxxix) "integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and

(xl) "tegt: testis enhanced gene transcript (bax inhibitor 1)" (SEQ ID No:278) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tegt: testis enhanced gene transcript (bax inhibitor 1)" encoded by a nucleic acid that hybridizes to the "tegt: testis enhanced gene transcript (bax inhibitor 1)" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.
22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.
23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:
- (i) "ABCC1" (SEQ ID No:222) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCC1" encoded by a nucleic acid that hybridizes to the "ABCC1" nucleic acid or its complement under low stringency conditions,
 - (ii) "ATP-binding cassette, sub-family A member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A member 3" nucleic acid or its complement under low stringency conditions,
 - (iii) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions,
 - (iv) "CDW92" (SEQ ID No:226) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDW92" encoded by a nucleic acid that hybridizes to the "CDW92" nucleic acid or its complement under low stringency conditions,
 - (v) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

- (vi) "Cerebral protein-10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein-10" encoded by a nucleic acid that hybridizes to the "Cerebral protein-10" nucleic acid or its complement under low stringency conditions,
- (vii) "GPR49" (SEQ ID No:235) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,
- (viii) "HYPOTHETICAL PROTEIN " (SEQ ID No:237) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN " encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN " nucleic acid or its complement under low stringency conditions,
- (ix) "Hypothetical protein (Fragment)" (SEQ ID No:238) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein (Fragment)" encoded by a nucleic acid that hybridizes to the "Hypothetical protein (Fragment)" nucleic acid or its complement under low stringency conditions,
- (x) "Hypothetical protein FLJ14562" (SEQ ID No:239) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ14562" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ14562" nucleic acid or its complement under low stringency conditions,
- (xi) "Hypothetical protein FLJ23630" (SEQ ID No:240) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23630" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23630" nucleic acid or its complement under low stringency conditions,
- (xii) "Hypothetical protein KIAA0372" (SEQ ID No:241) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0372" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0372" nucleic acid or its complement under low stringency conditions,

- (xiii) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xiv) "KIAA0251 (FRAGMENT)" (SEQ ID No:244) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0251 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0251 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xv) "KIAA0363 (FRAGMENT)" (SEQ ID No:245) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0363 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xvi) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,
- (xvii) "KIAA0971" (SEQ ID No:246) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0971" encoded by a nucleic acid that hybridizes to the "KIAA0971" nucleic acid or its complement under low stringency conditions,
- (xviii) "KIAA1250" (SEQ ID No:247) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,
- (xix) "MGC4248 " (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248 " encoded by a nucleic acid that hybridizes to the "MGC4248 " nucleic acid or its complement under low stringency conditions,
- (xx) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xxi) "PCDHA10" (SEQ ID No:250) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHA10" encoded by a nucleic acid that hybridizes to the "PCDHA10" nucleic acid or its complement under low stringency conditions,

(xxii) "PCDHB12" (SEQ ID No:251) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB12" encoded by a nucleic acid that hybridizes to the "PCDHB12" nucleic acid or its complement under low stringency conditions,

(xxiii) "PCDHB13: protocadherin beta 13" (SEQ ID No:252) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB13: protocadherin beta 13" encoded by a nucleic acid that hybridizes to the "PCDHB13: protocadherin beta 13" nucleic acid or its complement under low stringency conditions,

(xxiv) "PCDHB4" (SEQ ID No:253) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB4" encoded by a nucleic acid that hybridizes to the "PCDHB4" nucleic acid or its complement under low stringency conditions,

(xxv) "PCDHGB1" (SEQ ID No:254) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB1" encoded by a nucleic acid that hybridizes to the "PCDHGB1" nucleic acid or its complement under low stringency conditions,

(xxvi) "PCDHGB6" (SEQ ID No:255) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB6" encoded by a nucleic acid that hybridizes to the "PCDHGB6" nucleic acid or its complement under low stringency conditions,

(xxvii) "Pcdhb17" (SEQ ID No:258) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pcdhb17" encoded by a nucleic acid that hybridizes to the "Pcdhb17" nucleic acid or its complement under low stringency conditions,

(xxviii) "Protocadherin 7" (SEQ ID No:259) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin 7" encoded by a nucleic acid that hybridizes to the "Protocadherin 7" nucleic acid or its complement under low stringency conditions,

- (xxix) "Protocadherin beta 16" (SEQ ID No:260) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 16" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 16" nucleic acid or its complement under low stringency conditions,
- (xxx) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,
- (xxxi) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,
- (xxxii) "Similar to CGI-135 protein" (SEQ ID No:268) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to CGI-135 protein" encoded by a nucleic acid that hybridizes to the "Similar to CGI-135 protein" nucleic acid or its complement under low stringency conditions,
- (xxxiii) "Sterile alpha and HEAT/Armadillo motif protein" (SEQ ID No:269) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterile alpha and HEAT/Armadillo motif protein" encoded by a nucleic acid that hybridizes to the "Sterile alpha and HEAT/Armadillo motif protein" nucleic acid or its complement under low stringency conditions,
- (xxxiv) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,
- (xxxv) "Vacuolar ATP synthase membrane sector associated protein m8-9" (SEQ ID No:273) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Vacuolar ATP synthase membrane sector associated protein m8-9" encoded by a nucleic acid that hybridizes to the "Vacuolar ATP synthase membrane sector associated protein m8-9" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Y391_HUMAN" (SEQ ID No:274) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"Y391_HUMAN" encoded by a nucleic acid that hybridizes to the "Y391_HUMAN" nucleic acid or its complement under low stringency conditions,

(xxxvii) "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" (SEQ ID No:275) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" encoded by a nucleic acid that hybridizes to the

"hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" nucleic acid or its complement under low stringency conditions,

(xxxviii) "hypothetical protein MGC22916" (SEQ ID No:276) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC22916" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC22916" nucleic acid or its complement under low stringency conditions,

(xxxix) "integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or

(xl) "tegt: testis enhanced gene transcript (bax inhibitor 1)" (SEQ ID No:278) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tegt: testis enhanced gene transcript (bax inhibitor 1)" encoded by a nucleic acid that hybridizes to the "tegt: testis enhanced gene transcript (bax inhibitor 1)" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

- (i) "ABCC1" (SEQ ID No:222) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCC1" encoded by a nucleic acid that hybridizes to the "ABCC1" nucleic acid or its complement under low stringency conditions,
- (ii) "ATP-binding cassette, sub-family A member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A member 3" nucleic acid or its complement under low stringency conditions,
- (iii) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions,
- (iv) "CDW92" (SEQ ID No:226) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDW92" encoded by a nucleic acid that hybridizes to the "CDW92" nucleic acid or its complement under low stringency conditions,
- (v) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (vi) "Cerebral protein-10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein-10" encoded by a nucleic acid that hybridizes to the "Cerebral protein-10" nucleic acid or its complement under low stringency conditions,
- (vii) "GPR49" (SEQ ID No:235) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,
- (viii) "HYPOTHETICAL PROTEIN " (SEQ ID No:237) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN " encoded by a nucleic acid that hybridizes to the

"HYPOTHETICAL PROTEIN " nucleic acid or its complement under low stringency conditions,

(ix) "Hypothetical protein (Fragment)" (SEQ ID No:238) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein (Fragment)" encoded by a nucleic acid that hybridizes to the "Hypothetical protein (Fragment)" nucleic acid or its complement under low stringency conditions,

(x) "Hypothetical protein FLJ14562" (SEQ ID No:239) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ14562" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ14562" nucleic acid or its complement under low stringency conditions,

(xi) "Hypothetical protein FLJ23630" (SEQ ID No:240) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23630" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23630" nucleic acid or its complement under low stringency conditions,

(xii) "Hypothetical protein KIAA0372" (SEQ ID No:241) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0372" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0372" nucleic acid or its complement under low stringency conditions,

(xiii) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xiv) "KIAA0251 (FRAGMENT)" (SEQ ID No:244) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0251 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0251 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xv) "KIAA0363 (FRAGMENT)" (SEQ ID No:245) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0363 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

- (xvi) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,
- (xvii) "KIAA0971" (SEQ ID No:246) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0971" encoded by a nucleic acid that hybridizes to the "KIAA0971" nucleic acid or its complement under low stringency conditions,
- (xviii) "KIAA1250" (SEQ ID No:247) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,
- (xix) "MGC4248 " (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248 " encoded by a nucleic acid that hybridizes to the "MGC4248 " nucleic acid or its complement under low stringency conditions,
- (xx) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,
- (xxi) "PCDHA10" (SEQ ID No:250) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHA10" encoded by a nucleic acid that hybridizes to the "PCDHA10" nucleic acid or its complement under low stringency conditions,
- (xxii) "PCDHB12" (SEQ ID No:251) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB12" encoded by a nucleic acid that hybridizes to the "PCDHB12" nucleic acid or its complement under low stringency conditions,
- (xxiii) "PCDHB13: protocadherin beta 13" (SEQ ID No:252) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB13: protocadherin beta 13" encoded by a nucleic acid that hybridizes to the "PCDHB13: protocadherin beta 13" nucleic acid or its complement under low stringency conditions,

- (xxiv) "PCDHB4" (SEQ ID No:253) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB4" encoded by a nucleic acid that hybridizes to the "PCDHB4" nucleic acid or its complement under low stringency conditions,
- (xxv) "PCDHGB1" (SEQ ID No:254) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB1" encoded by a nucleic acid that hybridizes to the "PCDHGB1" nucleic acid or its complement under low stringency conditions,
- (xxvi) "PCDHGB6" (SEQ ID No:255) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB6" encoded by a nucleic acid that hybridizes to the "PCDHGB6" nucleic acid or its complement under low stringency conditions,
- (xxvii) "Pcdhb17" (SEQ ID No:258) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pcdhb17" encoded by a nucleic acid that hybridizes to the "Pcdhb17" nucleic acid or its complement under low stringency conditions,
- (xxviii) "Protocadherin 7" (SEQ ID No:259) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin 7" encoded by a nucleic acid that hybridizes to the "Protocadherin 7" nucleic acid or its complement under low stringency conditions,
- (xxix) "Protocadherin beta 16" (SEQ ID No:260) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 16" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 16" nucleic acid or its complement under low stringency conditions,
- (xxx) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,
- (xxxi) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

- (xxxii) "Similar to CGI-135 protein" (SEQ ID No:268) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to CGI-135 protein" encoded by a nucleic acid that hybridizes to the "Similar to CGI-135 protein" nucleic acid or its complement under low stringency conditions,
- (xxxiii) "Sterile alpha and HEAT/Armadillo motif protein" (SEQ ID No:269) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterile alpha and HEAT/Armadillo motif protein" encoded by a nucleic acid that hybridizes to the "Sterile alpha and HEAT/Armadillo motif protein" nucleic acid or its complement under low stringency conditions,
- (xxxiv) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,
- (xxxv) "Vacuolar ATP synthase membrane sector associated protein m8-9" (SEQ ID No:273) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Vacuolar ATP synthase membrane sector associated protein m8-9" encoded by a nucleic acid that hybridizes to the "Vacuolar ATP synthase membrane sector associated protein m8-9" nucleic acid or its complement under low stringency conditions,
- (xxxvi) "Y391_HUMAN" (SEQ ID No:274) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Y391_HUMAN" encoded by a nucleic acid that hybridizes to the "Y391_HUMAN" nucleic acid or its complement under low stringency conditions,
- (xxxvii) "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" (SEQ ID No:275) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" nucleic acid or its complement under low stringency conditions,
- (xxxviii) "hypothetical protein MGC22916" (SEQ ID No:276) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC22916" encoded by a nucleic acid that hybridizes to

the "hypothetical protein MGC22916" nucleic acid or its complement under low stringency conditions,

(xxxix) "integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or

(xl) "tegt: testis enhanced gene transcript (bax inhibitor 1)" (SEQ ID No:278) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tegt: testis enhanced gene transcript (bax inhibitor 1)" encoded by a nucleic acid that hybridizes to the "tegt: testis enhanced gene transcript (bax inhibitor 1)" nucleic acid or its complement under low stringency conditions, comprising the steps of

- (a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and
- (b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of (a) exposing said complex, or a cell or organism containing Aph-1a complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.
28. The method of No. 26, wherein the activity of said complex is determined.
29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.
30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.
31. The method of No. 30, wherein said determining step comprises determining whether
- (i) "18 kDa microsomal signal-peptidase subunit " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions, and/or
 - (ii) "23 kDa microsomal signal peptidase" (SEQ ID No:221) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "23 kDa microsomal signal peptidase" encoded by a nucleic acid that hybridizes to the "23 kDa microsomal signal peptidase" nucleic acid or its complement under low stringency conditions, and/or
 - (iii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or
 - (iv) "ABCC1" (SEQ ID No:222) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCC1" encoded by a nucleic acid that hybridizes to the "ABCC1" nucleic acid or its complement under low stringency conditions, and/or

- (v) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "ATM" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATM" encoded by a nucleic acid that hybridizes to the "ATM" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "ATP-binding cassette, sub-family A member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A member 3" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "ATP1B1" (SEQ ID No:223) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP1B1" encoded by a nucleic acid that hybridizes to the "ATP1B1" nucleic acid or its complement under low stringency conditions, and/or
- (x) "ATP2C1" (SEQ ID No:224) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP2C1" encoded by a nucleic acid that hybridizes to the "ATP2C1" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or

- (xiii) "Brain-specific GTP-binding protein" (SEQ ID No:225) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Brain-specific GTP-binding protein" encoded by a nucleic acid that hybridizes to the "Brain-specific GTP-binding protein" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "CDW92" (SEQ ID No:226) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDW92" encoded by a nucleic acid that hybridizes to the "CDW92" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "CNTNAP1" (SEQ ID No:227) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CNTNAP1" encoded by a nucleic acid that hybridizes to the "CNTNAP1" nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "Cerebral protein-10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein-10" encoded by a nucleic acid that hybridizes to the "Cerebral protein-10" nucleic acid or its complement under low stringency conditions, and/or
- (xviii) "DNM1" (SEQ ID No:228) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNM1" encoded by a nucleic acid that hybridizes to the "DNM1" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "Dihydrofolate reductase" (SEQ ID No:229) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dihydrofolate reductase" encoded by a nucleic acid that hybridizes to the "Dihydrofolate reductase" nucleic acid or its complement under low stringency conditions, and/or
- (xx) "ENG" (SEQ ID No:230) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG" encoded by a nucleic acid that hybridizes to the "ENG" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "EXT2" (SEQ ID No:231) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXT2" encoded by a nucleic acid that hybridizes to the "EXT2" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "EXTL3" (SEQ ID No:232) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXTL3" encoded by a nucleic acid that hybridizes to the "EXTL3" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "Endocytic receptor Endo180" (SEQ ID No:233) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Endocytic receptor Endo180" encoded by a nucleic acid that hybridizes to the "Endocytic receptor Endo180" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "FLJ13660" (SEQ ID No:234) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13660" encoded by a nucleic acid that hybridizes to the "FLJ13660" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "GPR49" (SEQ ID No:235) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "HK2" (SEQ ID No:236) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HK2" encoded by a nucleic acid that hybridizes to the "HK2" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "HU-K4" (SEQ ID No:133) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HU-K4" encoded by a nucleic acid that hybridizes to the "HU-K4" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "HUNC18a" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HUNC18a" encoded by a nucleic acid that hybridizes to the "HUNC18a" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "HYPOTHETICAL PROTEIN " (SEQ ID No:237) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN " encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN " nucleic acid or its complement under low stringency conditions, and/or

(xxx) "Hypothetical protein (Fragment)" (SEQ ID No:238) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein (Fragment)" encoded by a nucleic acid that hybridizes to the "Hypothetical protein (Fragment)" nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "Hypothetical protein FLJ14562" (SEQ ID No:239) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ14562" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ14562" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "Hypothetical protein FLJ23630" (SEQ ID No:240) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23630" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23630" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "Hypothetical protein KIAA0372" (SEQ ID No:241) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0372" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0372" nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "ICAM2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM2" encoded by a nucleic acid that hybridizes to the "ICAM2" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "IGF2R" (SEQ ID No:242) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IGF2R" encoded by a nucleic acid that hybridizes to the "IGF2R" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "ITPR1" (SEQ ID No:243) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions, and/or

(xxxviii) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions, and/or

(xxxix) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xl) "KIAA0251 (FRAGMENT)" (SEQ ID No:244) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0251 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0251 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xli) "KIAA0363 (FRAGMENT)" (SEQ ID No:245) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0363 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xlii) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions, and/or

(xliii) "KIAA0971" (SEQ ID No:246) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0971" encoded by a nucleic acid that hybridizes to the "KIAA0971" nucleic acid or its complement under low stringency conditions, and/or

- (xlv) "KIAA1250" (SEQ ID No:247) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions, and/or
- (xlv) "LRP5" (SEQ ID No:248) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LRP5" encoded by a nucleic acid that hybridizes to the "LRP5" nucleic acid or its complement under low stringency conditions, and/or
- (xlvi) "MGC4248 " (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248 " encoded by a nucleic acid that hybridizes to the "MGC4248 " nucleic acid or its complement under low stringency conditions, and/or
- (xlvii) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions, and/or
- (xlviii) "NRP2" (SEQ ID No:249) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NRP2" encoded by a nucleic acid that hybridizes to the "NRP2" nucleic acid or its complement under low stringency conditions, and/or
- (xlix) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or
- (l) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or
- (li) "PCDHA10" (SEQ ID No:250) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHA10" encoded by a nucleic acid that hybridizes to the "PCDHA10" nucleic acid or its complement under low stringency conditions, and/or

- (lii) "PCDHB12" (SEQ ID No:251) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB12" encoded by a nucleic acid that hybridizes to the "PCDHB12" nucleic acid or its complement under low stringency conditions, and/or
- (liii) "PCDHB13: protocadherin beta 13" (SEQ ID No:252) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB13: protocadherin beta 13" encoded by a nucleic acid that hybridizes to the "PCDHB13: protocadherin beta 13" nucleic acid or its complement under low stringency conditions, and/or
- (liv) "PCDHB4" (SEQ ID No:253) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB4" encoded by a nucleic acid that hybridizes to the "PCDHB4" nucleic acid or its complement under low stringency conditions, and/or
- (lv) "PCDHGB1" (SEQ ID No:254) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB1" encoded by a nucleic acid that hybridizes to the "PCDHGB1" nucleic acid or its complement under low stringency conditions, and/or
- (lvi) "PCDHGB6" (SEQ ID No:255) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB6" encoded by a nucleic acid that hybridizes to the "PCDHGB6" nucleic acid or its complement under low stringency conditions, and/or
- (lvii) "PMPCB" (SEQ ID No:256) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PMPCB" encoded by a nucleic acid that hybridizes to the "PMPCB" nucleic acid or its complement under low stringency conditions, and/or
- (lviii) "PP2C gamma" (SEQ ID No:257) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP2C gamma" encoded by a nucleic acid that hybridizes to the "PP2C gamma" nucleic acid or its complement under low stringency conditions, and/or
- (lix) "Pcdhb17" (SEQ ID No:258) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pcdhb17" encoded by a nucleic acid that hybridizes to the "Pcdhb17" nucleic acid or its complement under low stringency conditions, and/or

- (lx) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or
- (lxi) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions, and/or
- (lxii) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions, and/or
- (lxiii) "Protocadherin 7" (SEQ ID No:259) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin 7" encoded by a nucleic acid that hybridizes to the "Protocadherin 7" nucleic acid or its complement under low stringency conditions, and/or
- (lxiv) "Protocadherin beta 16" (SEQ ID No:260) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 16" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 16" nucleic acid or its complement under low stringency conditions, and/or
- (lxv) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions, and/or
- (lxvi) "RAB-18" (SEQ ID No:261) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB-18" encoded by a nucleic acid that hybridizes to the "RAB-18" nucleic acid or its complement under low stringency conditions, and/or
- (lxvii) "RNASEL" (SEQ ID No:262) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RNASEL" encoded by a nucleic acid that hybridizes to the "RNASEL" nucleic acid or its complement under low stringency conditions, and/or
- (lxviii) "Rab3 GTPase-activating protein, non-catalytic subunit" (SEQ ID No:263) or a functionally active derivative thereof, or a functionally active fragment thereof, or a

homolog thereof, or a variant of "Rab3 GTPase-activating protein, non-catalytic subunit" encoded by a nucleic acid that hybridizes to the "Rab3 GTPase-activating protein, non-catalytic subunit" nucleic acid or its complement under low stringency conditions, and/or (Ixx) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions, and/or

(Ixx) "SMAP-1B" (SEQ ID No:264) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SMAP-1B" encoded by a nucleic acid that hybridizes to the "SMAP-1B" nucleic acid or its complement under low stringency conditions, and/or

(Ixxi) "SPTLC2" (SEQ ID No:265) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions, and/or

(Ixxii) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions, and/or

(Ixxiii) "Sideroflexin 1" (SEQ ID No:266) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sideroflexin 1" encoded by a nucleic acid that hybridizes to the "Sideroflexin 1" nucleic acid or its complement under low stringency conditions, and/or

(Ixxiv) "Signal transducer and activator of transcription-1" (SEQ ID No:267) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Signal transducer and activator of transcription-1" encoded by a nucleic acid that hybridizes to the "Signal transducer and activator of transcription-1" nucleic acid or its complement under low stringency conditions, and/or

(Ixxv) "Similar to CGI-135 protein" (SEQ ID No:268) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to CGI-135 protein" encoded by a nucleic acid that hybridizes to the "Similar to CGI-135 protein" nucleic acid or its complement under low stringency conditions, and/or

(lxxvi) "Sterile alpha and HEAT/Armadillo motif protein" (SEQ ID No:269) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterile alpha and HEAT/Armadillo motif protein" encoded by a nucleic acid that hybridizes to the "Sterile alpha and HEAT/Armadillo motif protein" nucleic acid or its complement under low stringency conditions, and/or

(lxxvii) "Sterol O-acyltransferase 1" (SEQ ID No:270) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterol O-acyltransferase 1" encoded by a nucleic acid that hybridizes to the "Sterol O-acyltransferase 1" nucleic acid or its complement under low stringency conditions, and/or

(lxxviii) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(lxxix) "Triple functional domain protein (PTPRF interacting)" (SEQ ID No:271) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Triple functional domain protein (PTPRF interacting)" encoded by a nucleic acid that hybridizes to the "Triple functional domain protein (PTPRF interacting)" nucleic acid or its complement under low stringency conditions, and/or

(lxxx) "UNC5C" (SEQ ID No:272) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UNC5C" encoded by a nucleic acid that hybridizes to the "UNC5C" nucleic acid or its complement under low stringency conditions, and/or

(lxxxi) "Vacuolar ATP synthase membrane sector associated protein m8-9" (SEQ ID No:273) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Vacuolar ATP synthase membrane sector associated protein m8-9" encoded by a nucleic acid that hybridizes to the "Vacuolar ATP synthase membrane sector associated protein m8-9" nucleic acid or its complement under low stringency conditions, and/or

(lxxxii) "Y391_HUMAN" (SEQ ID No:274) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Y391_HUMAN" encoded by a nucleic acid that hybridizes to the "Y391_HUMAN" nucleic acid or its complement under low stringency conditions, and/or

(lxxxiii) "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" (SEQ ID No:275) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" nucleic acid or its complement under low stringency conditions, and/or

(lxxxiv) "hypothetical protein MGC22916" (SEQ ID No:276) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC22916" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC22916" nucleic acid or its complement under low stringency conditions, and/or

(lxxxv) "integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or

(lxxxvi) "tegt: testis enhanced gene transcript (bax inhibitor 1)" (SEQ ID No:278) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tegt: testis enhanced gene transcript (bax inhibitor 1)" encoded by a nucleic acid that hybridizes to the "tegt: testis enhanced gene transcript (bax inhibitor 1)" nucleic acid or its complement under low stringency conditions, and/or

(lxxxvii) "vacuolar protein sorting protein 18" (SEQ ID No:279) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "vacuolar protein sorting protein 18" encoded by a nucleic acid that hybridizes to the "vacuolar protein sorting protein 18" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament

for the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether
- (i) "18 kDa microsomal signal peptidase subunit " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions, and/or
 - (ii) "23 kDa microsomal signal peptidase" (SEQ ID No:221) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "23 kDa microsomal signal peptidase" encoded by a nucleic acid that hybridizes to the "23 kDa microsomal signal peptidase" nucleic acid or its complement under low stringency conditions, and/or
 - (iii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or
 - (iv) "ABCC1" (SEQ ID No:222) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCC1" encoded by a nucleic acid that hybridizes to the "ABCC1" nucleic acid or its complement under low stringency conditions, and/or
 - (v) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions, and/or
 - (vi) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or
 - (vii) "ATM" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATM" encoded by a nucleic acid that hybridizes to the "ATM" nucleic acid or its complement under low stringency conditions, and/or

- (viii) "ATP-binding cassette, sub-family A member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A member 3" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "ATP1B1" (SEQ ID No:223) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP1B1" encoded by a nucleic acid that hybridizes to the "ATP1B1" nucleic acid or its complement under low stringency conditions, and/or
- (x) "ATP2C1" (SEQ ID No:224) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP2C1" encoded by a nucleic acid that hybridizes to the "ATP2C1" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "Brain-specific GTP-binding protein" (SEQ ID No:225) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Brain-specific GTP-binding protein" encoded by a nucleic acid that hybridizes to the "Brain-specific GTP-binding protein" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "CDW92" (SEQ ID No:226) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDW92" encoded by a nucleic acid that hybridizes to the "CDW92" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a

nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "CNTNAP1" (SEQ ID No:227) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CNTNAP1" encoded by a nucleic acid that hybridizes to the "CNTNAP1" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "Cerebral protein-10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein-10" encoded by a nucleic acid that hybridizes to the "Cerebral protein-10" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "DNM1" (SEQ ID No:228) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNM1" encoded by a nucleic acid that hybridizes to the "DNM1" nucleic acid or its complement under low stringency conditions, and/or

(xix) "Dihydrofolate reductase" (SEQ ID No:229) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dihydrofolate reductase" encoded by a nucleic acid that hybridizes to the "Dihydrofolate reductase" nucleic acid or its complement under low stringency conditions, and/or

(xx) "ENG" (SEQ ID No:230) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG" encoded by a nucleic acid that hybridizes to the "ENG" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "EXT2" (SEQ ID No:231) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXT2" encoded by a nucleic acid that hybridizes to the "EXT2" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "EXTL3" (SEQ ID No:232) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXTL3" encoded by a nucleic acid that hybridizes to the "EXTL3" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "Endocytic receptor Endo180" (SEQ ID No:233) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Endocytic receptor Endo180" encoded by a nucleic acid that hybridizes to the

"Endocytic receptor Endo180" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "FLJ13660" (SEQ ID No:234) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13660" encoded by a nucleic acid that hybridizes to the "FLJ13660" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "GPR49" (SEQ ID No:235) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "HK2" (SEQ ID No:236) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HK2" encoded by a nucleic acid that hybridizes to the "HK2" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "HU-K4" (SEQ ID No:133) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HU-K4" encoded by a nucleic acid that hybridizes to the "HU-K4" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "HUNC18a" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HUNC18a" encoded by a nucleic acid that hybridizes to the "HUNC18a" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "HYPOTHETICAL PROTEIN " (SEQ ID No:237) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN " encoded by a nucleic acid that hybridizes to the "HYPOTHETICAL PROTEIN " nucleic acid or its complement under low stringency conditions, and/or

(xxx) "Hypothetical protein (Fragment)" (SEQ ID No:238) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein (Fragment)" encoded by a nucleic acid that hybridizes to the "Hypothetical protein (Fragment)" nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "Hypothetical protein FLJ14562" (SEQ ID No:239) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "Hypothetical protein FLJ14562" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ14562" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "Hypothetical protein FLJ23630" (SEQ ID No:240) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23630" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23630" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "Hypothetical protein KIAA0372" (SEQ ID No:241) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0372" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0372" nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "ICAM2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM2" encoded by a nucleic acid that hybridizes to the "ICAM2" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "IGF2R" (SEQ ID No:242) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IGF2R" encoded by a nucleic acid that hybridizes to the "IGF2R" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "ITPR1" (SEQ ID No:243) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions, and/or

(xxxviii) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that

hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions, and/or

(xxxix) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xi) "KIAA0251 (FRAGMENT)" (SEQ ID No:244) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0251 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0251 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xli) "KIAA0363 (FRAGMENT)" (SEQ ID No:245) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0363 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(xlii) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions, and/or

(xlili) "KIAA0971" (SEQ ID No:246) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0971" encoded by a nucleic acid that hybridizes to the "KIAA0971" nucleic acid or its complement under low stringency conditions, and/or

(xliv) "KIAA1250" (SEQ ID No:247) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions, and/or

(xlv) "LRP5" (SEQ ID No:248) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LRP5" encoded by a nucleic acid that hybridizes to the "LRP5" nucleic acid or its complement under low stringency conditions, and/or

(xlvi) "MGC4248 " (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248 " encoded by a nucleic acid that hybridizes to the "MGC4248 " nucleic acid or its complement under low stringency conditions, and/or

(xlvii) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions, and/or

(xlviii) "NRP2" (SEQ ID No:249) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NRP2" encoded by a nucleic acid that hybridizes to the "NRP2" nucleic acid or its complement under low stringency conditions, and/or

(xlix) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or

(i) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(ii) "PCDHA10" (SEQ ID No:250) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHA10" encoded by a nucleic acid that hybridizes to the "PCDHA10" nucleic acid or its complement under low stringency conditions, and/or

(iii) "PCDHB12" (SEQ ID No:251) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB12" encoded by a nucleic acid that hybridizes to the "PCDHB12" nucleic acid or its complement under low stringency conditions, and/or

(liii) "PCDHB13: protocadherin beta 13" (SEQ ID No:252) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB13: protocadherin beta 13" encoded by a nucleic acid that hybridizes to the "PCDHB13: protocadherin beta 13" nucleic acid or its complement under low stringency conditions, and/or

(liv) "PCDHB4" (SEQ ID No:253) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB4" encoded by a nucleic acid that hybridizes to the "PCDHB4" nucleic acid or its complement under low stringency conditions, and/or

- (lv) "PCDHGB1" (SEQ ID No:254) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB1" encoded by a nucleic acid that hybridizes to the "PCDHGB1" nucleic acid or its complement under low stringency conditions, and/or
- (lvi) "PCDHGB6" (SEQ ID No:255) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB6" encoded by a nucleic acid that hybridizes to the "PCDHGB6" nucleic acid or its complement under low stringency conditions, and/or
- (lvii) "PMPCB" (SEQ ID No:256) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PMPCB" encoded by a nucleic acid that hybridizes to the "PMPCB" nucleic acid or its complement under low stringency conditions, and/or
- (lviii) "PP2C gamma" (SEQ ID No:257) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP2C gamma" encoded by a nucleic acid that hybridizes to the "PP2C gamma" nucleic acid or its complement under low stringency conditions, and/or
- (lix) "Pcdhb17" (SEQ ID No:258) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pcdhb17" encoded by a nucleic acid that hybridizes to the "Pcdhb17" nucleic acid or its complement under low stringency conditions, and/or
- (lx) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or
- (lxi) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions, and/or
- (lxii) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions, and/or
- (lxiii) "Protocadherin 7" (SEQ ID No:259) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin

7" encoded by a nucleic acid that hybridizes to the "Protocadherin 7" nucleic acid or its complement under low stringency conditions, and/or

(lxiv) "Protocadherin beta 16" (SEQ ID No:260) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"Protocadherin beta 16" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 16" nucleic acid or its complement under low stringency conditions, and/or

(lxv) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions, and/or

(lxvi) "RAB-18" (SEQ ID No:261) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB-18" encoded by a nucleic acid that hybridizes to the "RAB-18" nucleic acid or its complement under low stringency conditions, and/or

(lxvii) "RNASEL" (SEQ ID No:262) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RNASEL" encoded by a nucleic acid that hybridizes to the "RNASEL" nucleic acid or its complement under low stringency conditions, and/or

(lxviii) "Rab3 GTPase-activating protein, non-catalytic subunit" (SEQ ID No:263) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Rab3 GTPase-activating protein, non-catalytic subunit" encoded by a nucleic acid that hybridizes to the "Rab3 GTPase-activating protein, non-catalytic subunit" nucleic acid or its complement under low stringency conditions, and/or

(lxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions, and/or

(lxx) "SMAP-1B" (SEQ ID No:264) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SMAP-1B" encoded by a nucleic acid that hybridizes to the "SMAP-1B" nucleic acid or its complement under low stringency conditions, and/or

- (lxxi) "SPTLC2" (SEQ ID No:265) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions, and/or
- (lxxii) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions, and/or
- (lxxiii) "Sideroflexin 1" (SEQ ID No:266) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sideroflexin 1" encoded by a nucleic acid that hybridizes to the "Sideroflexin 1" nucleic acid or its complement under low stringency conditions, and/or
- (lxxiv) "Signal transducer and activator of transcription-1" (SEQ ID No:267) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Signal transducer and activator of transcription-1" encoded by a nucleic acid that hybridizes to the "Signal transducer and activator of transcription-1" nucleic acid or its complement under low stringency conditions, and/or
- (lxxv) "Similar to CGI-135 protein" (SEQ ID No:268) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to CGI-135 protein" encoded by a nucleic acid that hybridizes to the "Similar to CGI-135 protein" nucleic acid or its complement under low stringency conditions, and/or
- (lxxvi) "Sterile alpha and HEAT/Armadillo motif protein" (SEQ ID No:269) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterile alpha and HEAT/Armadillo motif protein" encoded by a nucleic acid that hybridizes to the "Sterile alpha and HEAT/Armadillo motif protein" nucleic acid or its complement under low stringency conditions, and/or
- (lxxvii) "Sterol O-acyltransferase 1" (SEQ ID No:270) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterol O-acyltransferase 1" encoded by a nucleic acid that hybridizes to the "Sterol O-acyltransferase 1" nucleic acid or its complement under low stringency conditions, and/or
- (lxxviii) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that

hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(lxxxix) "Triple functional domain protein (PTPRF interacting)" (SEQ ID No:271) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Triple functional domain protein (PTPRF interacting)" encoded by a nucleic acid that hybridizes to the "Triple functional domain protein (PTPRF interacting)" nucleic acid or its complement under low stringency conditions, and/or

(lxxx) "UNC5C" (SEQ ID No:272) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UNC5C" encoded by a nucleic acid that hybridizes to the "UNC5C" nucleic acid or its complement under low stringency conditions, and/or

(lxxxi) "Vacuolar ATP synthase membrane sector associated protein m8-9" (SEQ ID No:273) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Vacuolar ATP synthase membrane sector associated protein m8-9" encoded by a nucleic acid that hybridizes to the "Vacuolar ATP synthase membrane sector associated protein m8-9" nucleic acid or its complement under low stringency conditions, and/or

(lxxxii) "Y391_HUMAN" (SEQ ID No:274) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Y391_HUMAN" encoded by a nucleic acid that hybridizes to the "Y391_HUMAN" nucleic acid or its complement under low stringency conditions, and/or

(lxxxiii) "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" (SEQ ID No:275) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" nucleic acid or its complement under low stringency conditions, and/or

(lxxxiv) "hypothetical protein MGC22916" (SEQ ID No:276) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC22916" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC22916" nucleic acid or its complement under low stringency conditions, and/or

(lxxxv) "integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or

(lxxxvi) "tegt: testis enhanced gene transcript (bax inhibitor 1)" (SEQ ID No:278) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tegt: testis enhanced gene transcript (bax inhibitor 1)" encoded by a nucleic acid that hybridizes to the "tegt: testis enhanced gene transcript (bax inhibitor 1)" nucleic acid or its complement under low stringency conditions, and/or

(lxxxvii) "vacuolar protein sorting protein 18" (SEQ ID No:279) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "vacuolar protein sorting protein 18" encoded by a nucleic acid that hybridizes to the "vacuolar protein sorting protein 18" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of

RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins

(i) "18 kDa microsomal signal peptidase subunit " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions,

(ii) "23 kDa microsomal signal peptidase" (SEQ ID No:221) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "23 kDa microsomal signal peptidase" encoded by a nucleic acid that hybridizes to the "23 kDa microsomal signal peptidase" nucleic acid or its complement under low stringency conditions,

(iii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:185) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(iv) "ABCC1" (SEQ ID No:222) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ABCC1" encoded by a nucleic acid that hybridizes to the "ABCC1" nucleic acid or its complement under low stringency conditions,

(v) "APLP2" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a

nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,

(vi) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(vii) "ATM" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATM" encoded by a nucleic acid that hybridizes to the "ATM" nucleic acid or its complement under low stringency conditions,

(viii) "ATP-binding cassette, sub-family A member 3" (SEQ ID No:186) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A member 3" nucleic acid or its complement under low stringency conditions,

(ix) "ATP1B1" (SEQ ID No:223) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP1B1" encoded by a nucleic acid that hybridizes to the "ATP1B1" nucleic acid or its complement under low stringency conditions,

(x) "ATP2C1" (SEQ ID No:224) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP2C1" encoded by a nucleic acid that hybridizes to the "ATP2C1" nucleic acid or its complement under low stringency conditions,

(xi) "Acetolactate synthase homolog" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Acetolactate synthase homolog" encoded by a nucleic acid that hybridizes to the "Acetolactate synthase homolog" nucleic acid or its complement under low stringency conditions,

(xii) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(xiii) "Brain-specific GTP-binding protein" (SEQ ID No:225) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "Brain-specific GTP-binding protein" encoded by a nucleic acid that hybridizes to the "Brain-specific GTP-binding protein" nucleic acid or its complement under low stringency conditions,

(xiv) "CDW92" (SEQ ID No:226) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CDW92" encoded by a nucleic acid that hybridizes to the "CDW92" nucleic acid or its complement under low stringency conditions,

(xv) "CGI-13" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(xvi) "CNTNAP1" (SEQ ID No:227) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CNTNAP1" encoded by a nucleic acid that hybridizes to the "CNTNAP1" nucleic acid or its complement under low stringency conditions,

(xvii) "Cerebral protein-10" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cerebral protein-10" encoded by a nucleic acid that hybridizes to the "Cerebral protein-10" nucleic acid or its complement under low stringency conditions,

(xviii) "DNM1" (SEQ ID No:228) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DNM1" encoded by a nucleic acid that hybridizes to the "DNM1" nucleic acid or its complement under low stringency conditions,

(xix) "Dihydrofolate reductase" (SEQ ID No:229) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dihydrofolate reductase" encoded by a nucleic acid that hybridizes to the "Dihydrofolate reductase" nucleic acid or its complement under low stringency conditions,

(xx) "ENG" (SEQ ID No:230) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENG" encoded by a nucleic acid that hybridizes to the "ENG" nucleic acid or its complement under low stringency conditions,

(xxi) "EXT2" (SEQ ID No:231) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXT2" encoded by a

nucleic acid that hybridizes to the "EXT2" nucleic acid or its complement under low stringency conditions,

(xxii) "EXTL3" (SEQ ID No:232) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "EXTL3" encoded by a nucleic acid that hybridizes to the "EXTL3" nucleic acid or its complement under low stringency conditions,

(xxiii) "Endocytic receptor Endo180" (SEQ ID No:233) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Endocytic receptor Endo180" encoded by a nucleic acid that hybridizes to the "Endocytic receptor Endo180" nucleic acid or its complement under low stringency conditions,

(xxiv) "FLJ13660" (SEQ ID No:234) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13660" encoded by a nucleic acid that hybridizes to the "FLJ13660" nucleic acid or its complement under low stringency conditions,

(xxv) "GPR49" (SEQ ID No:235) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,

(xxvi) "HK2" (SEQ ID No:236) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HK2" encoded by a nucleic acid that hybridizes to the "HK2" nucleic acid or its complement under low stringency conditions,

(xxvii) "HU-K4" (SEQ ID No:133) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HU-K4" encoded by a nucleic acid that hybridizes to the "HU-K4" nucleic acid or its complement under low stringency conditions,

(xxviii) "HUNC18a" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HUNC18a" encoded by a nucleic acid that hybridizes to the "HUNC18a" nucleic acid or its complement under low stringency conditions,

(xxix) "HYPOTHETICAL PROTEIN " (SEQ ID No:237) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HYPOTHETICAL PROTEIN " encoded by a nucleic acid that hybridizes to the

"HYPOTHETICAL PROTEIN " nucleic acid or its complement under low stringency conditions,

(xxx) "Hypothetical protein (Fragment)" (SEQ ID No:238) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein (Fragment)" encoded by a nucleic acid that hybridizes to the "Hypothetical protein (Fragment)" nucleic acid or its complement under low stringency conditions,

(xxxi) "Hypothetical protein FLJ14562" (SEQ ID No:239) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ14562" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ14562" nucleic acid or its complement under low stringency conditions,

(xxxii) "Hypothetical protein FLJ23630" (SEQ ID No:240) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein FLJ23630" encoded by a nucleic acid that hybridizes to the "Hypothetical protein FLJ23630" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Hypothetical protein KIAA0372" (SEQ ID No:241) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Hypothetical protein KIAA0372" encoded by a nucleic acid that hybridizes to the "Hypothetical protein KIAA0372" nucleic acid or its complement under low stringency conditions,

(xxxiv) "ICAM2" (SEQ ID No:200) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM2" encoded by a nucleic acid that hybridizes to the "ICAM2" nucleic acid or its complement under low stringency conditions,

(xxxv) "IGF2R" (SEQ ID No:242) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IGF2R" encoded by a nucleic acid that hybridizes to the "IGF2R" nucleic acid or its complement under low stringency conditions,

(xxxvi) "ITPR1" (SEQ ID No:243) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Insulinoma-glucagonoma protein 20" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Insulinoma-glucagonoma protein 20" encoded by a nucleic acid that hybridizes to the "Insulinoma-glucagonoma protein 20" nucleic acid or its complement under low stringency conditions,

(xxxviii) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,

(xxxix) "KIAA0062 (FRAGMENT)" (SEQ ID No:138) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0062 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0062 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xl) "KIAA0251 (FRAGMENT)" (SEQ ID No:244) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0251 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0251 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xli) "KIAA0363 (FRAGMENT)" (SEQ ID No:245) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA0363 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xlii) "KIAA0763" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0763" encoded by a nucleic acid that hybridizes to the "KIAA0763" nucleic acid or its complement under low stringency conditions,

(xliii) "KIAA0971" (SEQ ID No:246) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0971" encoded by a nucleic acid that hybridizes to the "KIAA0971" nucleic acid or its complement under low stringency conditions,

(xliv) "KIAA1250" (SEQ ID No:247) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,

(xlv) "LRP5" (SEQ ID No:248) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LRP5" encoded by a nucleic acid that hybridizes to the "LRP5" nucleic acid or its complement under low stringency conditions,

(xlvi) "MGC4248 " (SEQ ID No:141) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4248 " encoded by a nucleic acid that hybridizes to the "MGC4248 " nucleic acid or its complement under low stringency conditions,

(xlvii) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:205) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xlviii) "NRP2" (SEQ ID No:249) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NRP2" encoded by a nucleic acid that hybridizes to the "NRP2" nucleic acid or its complement under low stringency conditions,

(xlix) "Neurotrypsin" (SEQ ID No:206) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(l) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(li) "PCDHA10" (SEQ ID No:250) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHA10" encoded by a nucleic acid that hybridizes to the "PCDHA10" nucleic acid or its complement under low stringency conditions,

(lii) "PCDHB12" (SEQ ID No:251) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB12" encoded by a nucleic acid that hybridizes to the "PCDHB12" nucleic acid or its complement under low stringency conditions,

- (liii) "PCDHB13: protocadherin beta 13" (SEQ ID No:252) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB13: protocadherin beta 13" encoded by a nucleic acid that hybridizes to the "PCDHB13: protocadherin beta 13" nucleic acid or its complement under low stringency conditions,
- (liv) "PCDHB4" (SEQ ID No:253) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHB4" encoded by a nucleic acid that hybridizes to the "PCDHB4" nucleic acid or its complement under low stringency conditions,
- (lv) "PCDHGB1" (SEQ ID No:254) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB1" encoded by a nucleic acid that hybridizes to the "PCDHGB1" nucleic acid or its complement under low stringency conditions,
- (lvi) "PCDHGB6" (SEQ ID No:255) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PCDHGB6" encoded by a nucleic acid that hybridizes to the "PCDHGB6" nucleic acid or its complement under low stringency conditions,
- (lvii) "PMPCB" (SEQ ID No:256) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PMPCB" encoded by a nucleic acid that hybridizes to the "PMPCB" nucleic acid or its complement under low stringency conditions,
- (lviii) "PP2C gamma" (SEQ ID No:257) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP2C gamma" encoded by a nucleic acid that hybridizes to the "PP2C gamma" nucleic acid or its complement under low stringency conditions,
- (lix) "Pcdhb17" (SEQ ID No:258) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pcdhb17" encoded by a nucleic acid that hybridizes to the "Pcdhb17" nucleic acid or its complement under low stringency conditions,
- (lx) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(Ixi) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions,

(Ixii) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions,

(Ixiii) "Protocadherin 7" (SEQ ID No:259) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin 7" encoded by a nucleic acid that hybridizes to the "Protocadherin 7" nucleic acid or its complement under low stringency conditions,

(Ixiv) "Protocadherin beta 16" (SEQ ID No:260) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 16" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 16" nucleic acid or its complement under low stringency conditions,

(Ixv) "Protocadherin beta 8" (SEQ ID No:213) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(Ixvi) "RAB-18" (SEQ ID No:261) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RAB-18" encoded by a nucleic acid that hybridizes to the "RAB-18" nucleic acid or its complement under low stringency conditions,

(Ixvii) "RNASEL" (SEQ ID No:262) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RNASEL" encoded by a nucleic acid that hybridizes to the "RNASEL" nucleic acid or its complement under low stringency conditions,

(Ixviii) "Rab3 GTPase-activating protein, non-catalytic subunit" (SEQ ID No:263) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Rab3 GTPase-activating protein, non-catalytic subunit" encoded by a nucleic acid that hybridizes to the "Rab3 GTPase-activating protein, non-catalytic subunit" nucleic acid or its complement under low stringency conditions,

(Ixxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:216) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(Ixix) "SMAP-1B" (SEQ ID No:264) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SMAP-1B" encoded by a nucleic acid that hybridizes to the "SMAP-1B" nucleic acid or its complement under low stringency conditions,

(Ixixi) "SPTLC2" (SEQ ID No:265) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(Ixixii) "STMN3" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STMN3" encoded by a nucleic acid that hybridizes to the "STMN3" nucleic acid or its complement under low stringency conditions,

(Ixixiii) "Sideroflexin 1" (SEQ ID No:266) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sideroflexin 1" encoded by a nucleic acid that hybridizes to the "Sideroflexin 1" nucleic acid or its complement under low stringency conditions,

(Ixixiv) "Signal transducer and activator of transcription-1" (SEQ ID No:267) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Signal transducer and activator of transcription-1" encoded by a nucleic acid that hybridizes to the "Signal transducer and activator of transcription-1" nucleic acid or its complement under low stringency conditions,

(Ixixv) "Similar to CGI-135 protein" (SEQ ID No:268) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Similar to CGI-135 protein" encoded by a nucleic acid that hybridizes to the "Similar to CGI-135 protein" nucleic acid or its complement under low stringency conditions,

(Ixixvi) "Sterile alpha and HEAT/Armadillo motif protein" (SEQ ID No:269) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterile alpha and HEAT/Armadillo motif protein" encoded by a nucleic

acid that hybridizes to the "Sterile alpha and HEAT/Armadillo motif protein" nucleic acid or its complement under low stringency conditions,

(lxxvii) "Sterol O-acyltransferase 1" (SEQ ID No:270) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sterol O-acyltransferase 1" encoded by a nucleic acid that hybridizes to the "Sterol O-acyltransferase 1" nucleic acid or its complement under low stringency conditions,

(lxxviii) "Thioredoxin domain-containing protein" (SEQ ID No:218) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(lxxix) "Triple functional domain protein (PTPRF interacting)" (SEQ ID No:271) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Triple functional domain protein (PTPRF interacting)" encoded by a nucleic acid that hybridizes to the "Triple functional domain protein (PTPRF interacting)" nucleic acid or its complement under low stringency conditions,

(lxxx) "UNC5C" (SEQ ID No:272) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UNC5C" encoded by a nucleic acid that hybridizes to the "UNC5C" nucleic acid or its complement under low stringency conditions,

(lxxxi) "Vacuolar ATP synthase membrane sector associated protein m8-9" (SEQ ID No:273) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Vacuolar ATP synthase membrane sector associated protein m8-9" encoded by a nucleic acid that hybridizes to the "Vacuolar ATP synthase membrane sector associated protein m8-9" nucleic acid or its complement under low stringency conditions,

(lxxxii) "Y391_HUMAN" (SEQ ID No:274) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Y391_HUMAN" encoded by a nucleic acid that hybridizes to the "Y391_HUMAN" nucleic acid or its complement under low stringency conditions,

(lxxxiii) "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" (SEQ ID No:275) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" encoded by a nucleic acid that hybridizes to the

"hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5" nucleic acid or its complement under low stringency conditions,

(lxxxiv) "hypothetical protein MGC22916" (SEQ ID No:276) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "hypothetical protein MGC22916" encoded by a nucleic acid that hybridizes to the "hypothetical protein MGC22916" nucleic acid or its complement under low stringency conditions,

(lxxxv) "integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(lxxxvi) "tegt: testis enhanced gene transcript (bax inhibitor 1)" (SEQ ID No:278) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tegt: testis enhanced gene transcript (bax inhibitor 1)" encoded by a nucleic acid that hybridizes to the "tegt: testis enhanced gene transcript (bax inhibitor 1)" nucleic acid or its complement under low stringency conditions,

and/or(lxxxvii) "vacuolar protein sorting protein 18" (SEQ ID No:279) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "vacuolar protein sorting protein 18" encoded by a nucleic acid that hybridizes to the "vacuolar protein sorting protein 18" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

The present invention further relates to the following embodiments of the Pen-2 complex

1. A protein complex selected from complex (I) and comprising

(a) at least one first protein selected from the group consisting of:

(i) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a

nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(ii) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iii) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and

(iv) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions, and

(b) at least one second protein, which second protein is selected from the group consisting of:

(i) "Alpha-2 catenin" (SEQ ID No:280) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Alpha-2 catenin" encoded by a nucleic acid that hybridizes to the "Alpha-2 catenin" nucleic acid or its complement under low stringency conditions,

(ii) "COPINE FAMILY MEMBER" (SEQ ID No:281) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "COPINE FAMILY MEMBER" encoded by a nucleic acid that hybridizes to the "COPINE FAMILY MEMBER" nucleic acid or its complement under low stringency conditions,

(iii) "Copine III" (SEQ ID No:282) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Copine III" encoded by a nucleic acid that hybridizes to the "Copine III" nucleic acid or its complement under low stringency conditions,

(iv) "Dachshund 2" (SEQ ID No:283) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dachshund 2" encoded by a nucleic acid that hybridizes to the "Dachshund 2" nucleic acid or its complement under low stringency conditions,

(v) "Delta-1 catenin" (SEQ ID No:284) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-1

catenin" encoded by a nucleic acid that hybridizes to the "Delta-1 catenin" nucleic acid or its complement under low stringency conditions,

(vi) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,

(vii) "MGC2803" (SEQ ID No:286) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC2803" encoded by a nucleic acid that hybridizes to the "MGC2803" nucleic acid or its complement under low stringency conditions,

(viii) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions,

(ix) "TNRC15" (SEQ ID No:287) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TNRC15" encoded by a nucleic acid that hybridizes to the "TNRC15" nucleic acid or its complement under low stringency conditions,

(x) "TPST1" (SEQ ID No:288) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TPST1" encoded by a nucleic acid that hybridizes to the "TPST1" nucleic acid or its complement under low stringency conditions, and

(xi) "ZIP kinase" (SEQ ID No:289) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ZIP kinase" encoded by a nucleic acid that hybridizes to the "ZIP kinase" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein 'Pen-2' (SEQ ID NO. 209), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'Pen-2' encoded by a nucleic acid that hybridizes to the 'Pen-2' under low stringency conditions.

3. The protein complex according to No. 1 selected from complex (I) and comprising the following proteins:

- (i) "Alpha-2 catenin" (SEQ ID No:280) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Alpha-2 catenin" encoded by a nucleic acid that hybridizes to the "Alpha-2 catenin" nucleic acid or its complement under low stringency conditions,
- (ii) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
- (iii) "COPINE FAMILY MEMBER" (SEQ ID No:281) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "COPINE FAMILY MEMBER" encoded by a nucleic acid that hybridizes to the "COPINE FAMILY MEMBER" nucleic acid or its complement under low stringency conditions,
- (iv) "Copine III" (SEQ ID No:282) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Copine III" encoded by a nucleic acid that hybridizes to the "Copine III" nucleic acid or its complement under low stringency conditions,
- (v) "Dachshund 2" (SEQ ID No:283) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dachshund 2" encoded by a nucleic acid that hybridizes to the "Dachshund 2" nucleic acid or its complement under low stringency conditions,
- (vi) "Delta-1 catenin" (SEQ ID No:284) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-1 catenin" encoded by a nucleic acid that hybridizes to the "Delta-1 catenin" nucleic acid or its complement under low stringency conditions,
- (vii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102

- (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,
- (viii) "MGC2803" (SEQ ID No:286) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC2803" encoded by a nucleic acid that hybridizes to the "MGC2803" nucleic acid or its complement under low stringency conditions,
- (ix) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (x) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,
- (xi) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions,
- (xii) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions,
- (xiii) "TNRC15" (SEQ ID No:287) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TNRC15" encoded by a nucleic acid that hybridizes to the "TNRC15" nucleic acid or its complement under low stringency conditions,
- (xiv) "TPST1" (SEQ ID No:288) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TPST1" encoded by a nucleic acid that hybridizes to the "TPST1" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "ZIP kinase" (SEQ ID No:289) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ZIP kinase" encoded by a nucleic acid that hybridizes to the "ZIP kinase" nucleic acid or its complement under low stringency conditions,

and a protein complex selected from complex (II) and comprising the following proteins:

- (i) "Alpha-2 catenin" (SEQ ID No:280) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Alpha-2 catenin" encoded by a nucleic acid that hybridizes to the "Alpha-2 catenin" nucleic acid or its complement under low stringency conditions,
- (ii) "COPINE FAMILY MEMBER" (SEQ ID No:281) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "COPINE FAMILY MEMBER" encoded by a nucleic acid that hybridizes to the "COPINE FAMILY MEMBER" nucleic acid or its complement under low stringency conditions,
- (iii) "Copine III" (SEQ ID No:282) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Copine III" encoded by a nucleic acid that hybridizes to the "Copine III" nucleic acid or its complement under low stringency conditions,
- (iv) "Dachshund 2" (SEQ ID No:283) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dachshund 2" encoded by a nucleic acid that hybridizes to the "Dachshund 2" nucleic acid or its complement under low stringency conditions,
- (v) "Delta-1 catenin" (SEQ ID No:284) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-1 catenin" encoded by a nucleic acid that hybridizes to the "Delta-1 catenin" nucleic acid or its complement under low stringency conditions,
- (vi) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,
- (vii) "MGC2803" (SEQ ID No:286) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC2803" encoded by a nucleic acid that hybridizes to the "MGC2803" nucleic acid or its complement under low stringency conditions,
- (viii) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(ix) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(x) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions,

(xi) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions,

(xii) "TNRC15" (SEQ ID No:287) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TNRC15" encoded by a nucleic acid that hybridizes to the "TNRC15" nucleic acid or its complement under low stringency conditions,

(xiii) "TPST1" (SEQ ID No:288) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TPST1" encoded by a nucleic acid that hybridizes to the "TPST1" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "ZIP kinase" (SEQ ID No:289) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ZIP kinase" encoded by a nucleic acid that hybridizes to the "ZIP kinase" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 10 of the following proteins:

(i) "Alpha-2 catenin" (SEQ ID No:280) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Alpha-2 catenin" encoded by a nucleic acid that hybridizes to the "Alpha-2 catenin" nucleic acid or its complement under low stringency conditions,

(ii) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a

nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(iii) "COPINE FAMILY MEMBER" (SEQ ID No:281) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "COPINE FAMILY MEMBER" encoded by a nucleic acid that hybridizes to the "COPINE FAMILY MEMBER" nucleic acid or its complement under low stringency conditions,

(iv) "Copine III" (SEQ ID No:282) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Copine III" encoded by a nucleic acid that hybridizes to the "Copine III" nucleic acid or its complement under low stringency conditions,

(v) "Dachshund 2" (SEQ ID No:283) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dachshund 2" encoded by a nucleic acid that hybridizes to the "Dachshund 2" nucleic acid or its complement under low stringency conditions,

(vi) "Delta-1 catenin" (SEQ ID No:284) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-1 catenin" encoded by a nucleic acid that hybridizes to the "Delta-1 catenin" nucleic acid or its complement under low stringency conditions,

(vii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,

(viii) "MGC2803" (SEQ ID No:286) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC2803" encoded by a nucleic acid that hybridizes to the "MGC2803" nucleic acid or its complement under low stringency conditions,

(ix) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(x) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

- (xi) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions,
- (xii) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions,
- (xiii) "TNRC15" (SEQ ID No:287) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TNRC15" encoded by a nucleic acid that hybridizes to the "TNRC15" nucleic acid or its complement under low stringency conditions,
- (xiv) "TPST1" (SEQ ID No:288) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TPST1" encoded by a nucleic acid that hybridizes to the "TPST1" nucleic acid or its complement under low stringency conditions,
- (xv) "ZIP kinase" (SEQ ID No:289) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ZIP kinase" encoded by a nucleic acid that hybridizes to the "ZIP kinase" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps:expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Pen-2 complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the Pen-2 complex selected from

(i) "COPINE FAMILY MEMBER" (SEQ ID No:281) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"COPINE FAMILY MEMBER" encoded by a nucleic acid that hybridizes to the "COPINE FAMILY MEMBER" nucleic acid or its complement under low stringency conditions,

(ii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,

(iii) "MGC2803" (SEQ ID No:286) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC2803" encoded by a nucleic acid that hybridizes to the "MGC2803" nucleic acid or its complement under low stringency conditions, and

(iv) "TNRC15" (SEQ ID No:287) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TNRC15" encoded by a nucleic acid that hybridizes to the "TNRC15" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

- (i) "COPINE FAMILY MEMBER" (SEQ ID No:281) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "COPINE FAMILY MEMBER" encoded by a nucleic acid that hybridizes to the "COPINE FAMILY MEMBER" nucleic acid or its complement under low stringency conditions,
- (ii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,
- (iii) "MGC2803" (SEQ ID No:286) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC2803" encoded by a nucleic acid that hybridizes to the "MGC2803" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "TNRC15" (SEQ ID No:287) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TNRC15" encoded by a nucleic acid that hybridizes to the "TNRC15" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

- (i) "COPINE FAMILY MEMBER" (SEQ ID No:281) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "COPINE FAMILY MEMBER" encoded by a nucleic acid that hybridizes to the "COPINE FAMILY MEMBER" nucleic acid or its complement under low stringency conditions,
- (ii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,

(iii) "MGC2803" (SEQ ID No:286) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC2803" encoded by a nucleic acid that hybridizes to the "MGC2803" nucleic acid or its complement under low stringency conditions, and/or

(iv) "TNRC15" (SEQ ID No:287) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TNRC15" encoded by a nucleic acid that hybridizes to the "TNRC15" nucleic acid or its complement under low stringency conditions, comprising the steps of

(a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and

(b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of (a) exposing said complex, or a cell or organism containing Pen-2 complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether

- (i) "Alpha-2 catenin" (SEQ ID No:280) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Alpha-2 catenin" encoded by a nucleic acid that hybridizes to the "Alpha-2 catenin" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "COPINE FAMILY MEMBER" (SEQ ID No:281) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "COPINE FAMILY MEMBER" encoded by a nucleic acid that hybridizes to the "COPINE FAMILY MEMBER" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "Copine III" (SEQ ID No:282) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Copine III" encoded by a nucleic acid that hybridizes to the "Copine III" nucleic acid or its complement under low stringency conditions, and/or
- (v) "Dachshund 2" (SEQ ID No:283) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dachshund 2" encoded by a nucleic acid that hybridizes to the "Dachshund 2" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "Delta-1 catenin" (SEQ ID No:284) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-1

catenin" encoded by a nucleic acid that hybridizes to the "Delta-1 catenin" nucleic acid or its complement under low stringency conditions, and/or

(vii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions, and/or

(viii) "MGC2803" (SEQ ID No:286) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC2803" encoded by a nucleic acid that hybridizes to the "MGC2803" nucleic acid or its complement under low stringency conditions, and/or

(ix) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(x) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or

(xi) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions, and/or

(xii) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "TNRC15" (SEQ ID No:287) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TNRC15" encoded by a nucleic acid that hybridizes to the "TNRC15" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "TPST1" (SEQ ID No:288) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TPST1" encoded by a nucleic acid that hybridizes to the "TPST1" nucleic acid or its complement under low stringency conditions, and/or

(xv) "ZIP kinase" (SEQ ID No:289) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ZIP kinase" encoded by a nucleic acid that hybridizes to the "ZIP kinase" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether

- (i) "Alpha-2 catenin" (SEQ ID No:280) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Alpha-2 catenin" encoded by a nucleic acid that hybridizes to the "Alpha-2 catenin" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "COPINE FAMILY MEMBER" (SEQ ID No:281) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "COPINE FAMILY MEMBER" encoded by a nucleic acid that hybridizes to the "COPINE FAMILY MEMBER" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "Copine III" (SEQ ID No:282) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Copine III" encoded by a nucleic acid that hybridizes to the "Copine III" nucleic acid or its complement under low stringency conditions, and/or
- (v) "Dachshund 2" (SEQ ID No:283) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dachshund 2" encoded by a nucleic acid that hybridizes to the "Dachshund 2" nucleic acid or its complement under low stringency conditions, and/or

- (vi) "Delta-1 catenin" (SEQ ID No:284) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-1 catenin" encoded by a nucleic acid that hybridizes to the "Delta-1 catenin" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "MGC2803" (SEQ ID No:286) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC2803" encoded by a nucleic acid that hybridizes to the "MGC2803" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or
- (x) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "TNRC15" (SEQ ID No:287) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TNRC15" encoded by a nucleic acid that hybridizes to the "TNRC15" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "TPST1" (SEQ ID No:288) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TPST1"

encoded by a nucleic acid that hybridizes to the "TPST1" nucleic acid or its complement under low stringency conditions, and/or

(xv) "ZIP kinase" (SEQ ID No:289) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ZIP kinase" encoded by a nucleic acid that hybridizes to the "ZIP kinase" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42 , wherein said disease or disorder involves increased levels of the amount or activity of said complex.
45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins
- (i) "Alpha-2 catenin" (SEQ ID No:280) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Alpha-2 catenin" encoded by a nucleic acid that hybridizes to the "Alpha-2 catenin" nucleic acid or its complement under low stringency conditions,
 - (ii) "Aph-1a" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
 - (iii) "COPINE FAMILY MEMBER" (SEQ ID No:281) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "COPINE FAMILY MEMBER" encoded by a nucleic acid that hybridizes to the "COPINE FAMILY MEMBER" nucleic acid or its complement under low stringency conditions,
 - (iv) "Copine III" (SEQ ID No:282) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Copine III" encoded by a nucleic acid that hybridizes to the "Copine III" nucleic acid or its complement under low stringency conditions,
 - (v) "Dachshund 2" (SEQ ID No:283) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dachshund 2" encoded by a nucleic acid that hybridizes to the "Dachshund 2" nucleic acid or its complement under low stringency conditions,
 - (vi) "Delta-1 catenin" (SEQ ID No:284) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-1 catenin" encoded by a nucleic acid that hybridizes to the "Delta-1 catenin" nucleic acid or its complement under low stringency conditions,
 - (vii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,
 - (viii) "MGC2803" (SEQ ID No:286) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC2803"

encoded by a nucleic acid that hybridizes to the "MGC2803" nucleic acid or its complement under low stringency conditions,

(ix) "Nicastrin" (SEQ ID No:147) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(x) "Pen-2" (SEQ ID No:209) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(xi) "Presenilin 1" (SEQ ID No:210) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 1" encoded by a nucleic acid that hybridizes to the "Presenilin 1" nucleic acid or its complement under low stringency conditions,

(xii) "Presenilin 2" (SEQ ID No:172) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin 2" encoded by a nucleic acid that hybridizes to the "Presenilin 2" nucleic acid or its complement under low stringency conditions,

(xiii) "TNRC15" (SEQ ID No:287) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TNRC15" encoded by a nucleic acid that hybridizes to the "TNRC15" nucleic acid or its complement under low stringency conditions,

(xiv) "TPST1" (SEQ ID No:288) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TPST1" encoded by a nucleic acid that hybridizes to the "TPST1" nucleic acid or its complement under low stringency conditions, and/or (xv) "ZIP kinase" (SEQ ID No:289) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ZIP kinase" encoded by a nucleic acid that hybridizes to the "ZIP kinase" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

The present invention further relates to the following embodiments of the APP695SW-complex

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein selected from the group consisting of:
 - (i) "APP695SW" (SEQ ID No:290) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP695SW" encoded by a nucleic acid that hybridizes to the "APP695SW" nucleic acid or its complement under low stringency conditions,
 - (ii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,
 - (iii) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions,
 - (iv) "JIP-1" (SEQ ID No:295) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JIP-1" encoded by a nucleic acid that hybridizes to the "JIP-1" nucleic acid or its complement under low stringency conditions, and
 - (v) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions, and
 - (b) at least one second protein, which second protein is selected from the group consisting of:
 - (i) "FLJ10773" (SEQ ID No:291) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10773" encoded by a nucleic acid that hybridizes to the "FLJ10773" nucleic acid or its complement under low stringency conditions,
 - (ii) "GTF2I" (SEQ ID No:293) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTF2I" encoded by a

nucleic acid that hybridizes to the "GTF2I" nucleic acid or its complement under low stringency conditions,

(iii) "IL13RA2" (SEQ ID No:294) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IL13RA2" encoded by a nucleic acid that hybridizes to the "IL13RA2" nucleic acid or its complement under low stringency conditions,

(iv) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,

(v) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and

(vi) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha" encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein 'APP695SW' (SEQ ID NO. 290), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'APP695SW' encoded by a nucleic acid that hybridizes to the 'APP695SW' under low stringency conditions.

3. The protein complex according to No. 1 selected from complex (I) and comprising the following proteins:

- (i) "APP695SW" (SEQ ID No:290) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP695SW" encoded by a nucleic acid that hybridizes to the "APP695SW" nucleic acid or its complement under low stringency conditions,
- (ii) "FLJ10773" (SEQ ID No:291) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10773" encoded by a nucleic acid that hybridizes to the "FLJ10773" nucleic acid or its complement under low stringency conditions,
- (iii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,
- (iv) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions,
- (v) "GTF2I" (SEQ ID No:293) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTF2I" encoded by a nucleic acid that hybridizes to the "GTF2I" nucleic acid or its complement under low stringency conditions,
- (vi) "IL13RA2" (SEQ ID No:294) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IL13RA2" encoded by a nucleic acid that hybridizes to the "IL13RA2" nucleic acid or its complement under low stringency conditions,
- (vii) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,
- (viii) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that

hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(ix) "JIP-1" (SEQ ID No:295) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JIP-1" encoded by a nucleic acid that hybridizes to the "JIP-1" nucleic acid or its complement under low stringency conditions,

(x) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha" encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions, and/or

(xi) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions,

and a protein complex selected from complex (II) and comprising the following proteins:

(i) "APP695SW" (SEQ ID No:290) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP695SW" encoded by a nucleic acid that hybridizes to the "APP695SW" nucleic acid or its complement under low stringency conditions,

(ii) "FLJ10773" (SEQ ID No:291) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10773" encoded by a nucleic acid that hybridizes to the "FLJ10773" nucleic acid or its complement under low stringency conditions,

(iii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,

(iv) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions,

(v) "GTF2I" (SEQ ID No:293) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTF2I" encoded by a

nucleic acid that hybridizes to the "GTF2I" nucleic acid or its complement under low stringency conditions,

(vi) "IL13RA2" (SEQ ID No:294) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IL13RA2" encoded by a nucleic acid that hybridizes to the "IL13RA2" nucleic acid or its complement under low stringency conditions,

(vii) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,

(viii) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(ix) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha" encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions, and/or

(x) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 5 of the following proteins:

(i) "APP695SW" (SEQ ID No:290) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP695SW" encoded by a nucleic acid that hybridizes to the "APP695SW" nucleic acid or its complement under low stringency conditions,

(ii) "FLJ10773" (SEQ ID No:291) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10773"

encoded by a nucleic acid that hybridizes to the "FLJ10773" nucleic acid or its complement under low stringency conditions,

(iii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,

(iv) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions,

(v) "GTF2I" (SEQ ID No:293) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTF2I" encoded by a nucleic acid that hybridizes to the "GTF2I" nucleic acid or its complement under low stringency conditions,

(vi) "IL13RA2" (SEQ ID No:294) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IL13RA2" encoded by a nucleic acid that hybridizes to the "IL13RA2" nucleic acid or its complement under low stringency conditions,

(vii) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,

(viii) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(ix) "JIP-1" (SEQ ID No:295) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JIP-1" encoded by a nucleic acid that hybridizes to the "JIP-1" nucleic acid or its complement under low stringency conditions,

(x) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha"

encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions,

(xi) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the APP695SW complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the APP695SW complex selected from

(i) "FLJ10773" (SEQ ID No:291) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10773" encoded by a nucleic acid that hybridizes to the "FLJ10773" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

(i) "FLJ10773" (SEQ ID No:291) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10773" encoded by a nucleic acid that hybridizes to the "FLJ10773" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

(i) "FLJ10773" (SEQ ID No:291) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10773" encoded by a nucleic acid that hybridizes to the "FLJ10773" nucleic acid or its complement under low stringency conditions, comprising the steps of

(a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and

(b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8

comprising the steps of (a) exposing said complex, or a cell or organism containing APP695SW complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether (i) "APP695SW" (SEQ ID No:290) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP695SW" encoded by a nucleic acid that hybridizes to the "APP695SW" nucleic acid or its complement under low stringency conditions, and/or

- (ii) "FLJ10773" (SEQ ID No:291) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10773" encoded by a nucleic acid that hybridizes to the "FLJ10773" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions, and/or
- (v) "GTF2I" (SEQ ID No:293) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTF2I" encoded by a nucleic acid that hybridizes to the "GTF2I" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "IL13RA2" (SEQ ID No:294) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IL13RA2" encoded by a nucleic acid that hybridizes to the "IL13RA2" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "JIP-1" (SEQ ID No:295) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JIP-1" encoded by a nucleic acid that hybridizes to the "JIP-1" nucleic acid or its complement under low stringency conditions, and/or

- (x) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha" encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not

having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether (i) "APP695SW" (SEQ ID No:290) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP695SW" encoded by a nucleic acid that hybridizes to the "APP695SW" nucleic acid or its complement under low stringency conditions, and/or

(ii) "FLJ10773" (SEQ ID No:291) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10773" encoded by a nucleic acid that hybridizes to the "FLJ10773" nucleic acid or its complement under low stringency conditions, and/or

(iii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions, and/or

(iv) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions, and/or

- (v) "GTF2I" (SEQ ID No:293) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTF2I" encoded by a nucleic acid that hybridizes to the "GTF2I" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "IL13RA2" (SEQ ID No:294) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IL13RA2" encoded by a nucleic acid that hybridizes to the "IL13RA2" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "JIP-1" (SEQ ID No:295) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JIP-1" encoded by a nucleic acid that hybridizes to the "JIP-1" nucleic acid or its complement under low stringency conditions, and/or
- (x) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha" encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as

neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins
(i) "APP695SW" (SEQ ID No:290) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP695SW" encoded by a nucleic acid that hybridizes to the "APP695SW" nucleic acid or its complement under low stringency conditions,
(ii) "FLJ10773" (SEQ ID No:291) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10773"

encoded by a nucleic acid that hybridizes to the "FLJ10773" nucleic acid or its complement under low stringency conditions,

(iii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,

(iv) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions,

(v) "GTF2I" (SEQ ID No:293) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GTF2I" encoded by a nucleic acid that hybridizes to the "GTF2I" nucleic acid or its complement under low stringency conditions,

(vi) "IL13RA2" (SEQ ID No:294) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "IL13RA2" encoded by a nucleic acid that hybridizes to the "IL13RA2" nucleic acid or its complement under low stringency conditions,

(vii) "Integral membrane protein 2B (ITM2B)" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane protein 2B (ITM2B)" encoded by a nucleic acid that hybridizes to the "Integral membrane protein 2B (ITM2B)" nucleic acid or its complement under low stringency conditions,

(viii) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(ix) "JIP-1" (SEQ ID No:295) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JIP-1" encoded by a nucleic acid that hybridizes to the "JIP-1" nucleic acid or its complement under low stringency conditions,

(x) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha"

encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions, and/or (xi) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

The present invention further relates to the following embodiments of the APP-C99-complex

1. A protein complex selected from complex (I) and comprising

(a) at least one first protein selected from the group consisting of:

(i) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,

(ii) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,

(iii) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions, and

(iv) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions, and

(b) at least one second protein, which second protein is selected from the group consisting of:

(i) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid

that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(ii) "CAMK2D" (SEQ ID No:297) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK2D" encoded by a nucleic acid that hybridizes to the "CAMK2D" nucleic acid or its complement under low stringency conditions,

(iii) "Delta-like homolog" (SEQ ID No:298) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions,

(iv) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(v) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,

(vi) "KIAA1949" (SEQ ID No:299) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1949" encoded by a nucleic acid that hybridizes to the "KIAA1949" nucleic acid or its complement under low stringency conditions,

(vii) "MGC4022" (SEQ ID No:300) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4022" encoded by a nucleic acid that hybridizes to the "MGC4022" nucleic acid or its complement under low stringency conditions,

(viii) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions,

(ix) "NAP-1 related protein" (SEQ ID No:301) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NAP-1

related protein" encoded by a nucleic acid that hybridizes to the "NAP-1 related protein" nucleic acid or its complement under low stringency conditions,

(x) "Neurocalcin delta" (SEQ ID No:302) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurocalcin delta" encoded by a nucleic acid that hybridizes to the "Neurocalcin delta" nucleic acid or its complement under low stringency conditions,

(xi) "REST corepressor" (SEQ ID No:303) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REST corepressor" encoded by a nucleic acid that hybridizes to the "REST corepressor" nucleic acid or its complement under low stringency conditions,

(xii) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha" encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions, and

(xiii) "S-100 beta" (SEQ ID No:304) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 beta" encoded by a nucleic acid that hybridizes to the "S-100 beta" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein APP-C99 (SEQ ID NO. 10), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'APP-C99' encoded by a nucleic acid that hybridizes to the 'APP-C99' under low stringency conditions.

3. The protein complex according to No. 1 selected from complex (I) and comprising the following proteins:

- (i) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (ii) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,
- (iii) "CAMK2D" (SEQ ID No:297) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK2D" encoded by a nucleic acid that hybridizes to the "CAMK2D" nucleic acid or its complement under low stringency conditions,
- (iv) "Delta-like homolog" (SEQ ID No:298) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions,
- (v) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,
- (vi) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions,
- (vii) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,
- (viii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,

- (ix) "KIAA1949" (SEQ ID No:299) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1949" encoded by a nucleic acid that hybridizes to the "KIAA1949" nucleic acid or its complement under low stringency conditions,
- (x) "MGC4022" (SEQ ID No:300) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4022" encoded by a nucleic acid that hybridizes to the "MGC4022" nucleic acid or its complement under low stringency conditions,
- (xi) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions,
- (xii) "NAP-1 related protein" (SEQ ID No:301) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NAP-1 related protein" encoded by a nucleic acid that hybridizes to the "NAP-1 related protein" nucleic acid or its complement under low stringency conditions,
- (xiii) "Neurocalcin delta" (SEQ ID No:302) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurocalcin delta" encoded by a nucleic acid that hybridizes to the "Neurocalcin delta" nucleic acid or its complement under low stringency conditions,
- (xiv) "REST corepressor" (SEQ ID No:303) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REST corepressor" encoded by a nucleic acid that hybridizes to the "REST corepressor" nucleic acid or its complement under low stringency conditions,
- (xv) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha" encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions,
- (xvi) "S-100 beta" (SEQ ID No:304) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 beta" encoded by a nucleic acid that hybridizes to the "S-100 beta" nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta"

encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions,

and a protein complex selected from complex (II) and comprising the following proteins:

(i) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(ii) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,

(iii) "CAMK2D" (SEQ ID No:297) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK2D" encoded by a nucleic acid that hybridizes to the "CAMK2D" nucleic acid or its complement under low stringency conditions,

(iv) "Delta-like homolog" (SEQ ID No:298) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions,

(v) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,

(vi) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions,

(vii) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(viii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102

(Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,

(ix) "KIAA1949" (SEQ ID No:299) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1949" encoded by a nucleic acid that hybridizes to the "KIAA1949" nucleic acid or its complement under low stringency conditions,

(x) "MGC4022" (SEQ ID No:300) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4022" encoded by a nucleic acid that hybridizes to the "MGC4022" nucleic acid or its complement under low stringency conditions,

(xi) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions,

(xii) "NAP-1 related protein" (SEQ ID No:301) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NAP-1 related protein" encoded by a nucleic acid that hybridizes to the "NAP-1 related protein" nucleic acid or its complement under low stringency conditions,

(xiii) "Neurocalcin delta" (SEQ ID No:302) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurocalcin delta" encoded by a nucleic acid that hybridizes to the "Neurocalcin delta" nucleic acid or its complement under low stringency conditions,

(xiv) "REST corepressor" (SEQ ID No:303) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REST corepressor" encoded by a nucleic acid that hybridizes to the "REST corepressor" nucleic acid or its complement under low stringency conditions,

(xv) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha" encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions,

(xvi) "S-100 beta" (SEQ ID No:304) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 beta" encoded by a nucleic acid that hybridizes to the "S-100 beta" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 12 of the following proteins:

(i) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(ii) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,

(iii) "CAMK2D" (SEQ ID No:297) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK2D" encoded by a nucleic acid that hybridizes to the "CAMK2D" nucleic acid or its complement under low stringency conditions,

(iv) "Delta-like homolog" (SEQ ID No:298) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions,

(v) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,

(vi) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions,

(vii) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that

hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(viii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,

(ix) "KIAA1949" (SEQ ID No:299) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1949" encoded by a nucleic acid that hybridizes to the "KIAA1949" nucleic acid or its complement under low stringency conditions,

(x) "MGC4022" (SEQ ID No:300) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4022" encoded by a nucleic acid that hybridizes to the "MGC4022" nucleic acid or its complement under low stringency conditions,

(xi) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions,

(xii) "NAP-1 related protein" (SEQ ID No:301) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NAP-1 related protein" encoded by a nucleic acid that hybridizes to the "NAP-1 related protein" nucleic acid or its complement under low stringency conditions,

(xiii) "Neurocalcin delta" (SEQ ID No:302) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurocalcin delta" encoded by a nucleic acid that hybridizes to the "Neurocalcin delta" nucleic acid or its complement under low stringency conditions,

(xiv) "REST corepressor" (SEQ ID No:303) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REST corepressor" encoded by a nucleic acid that hybridizes to the "REST corepressor" nucleic acid or its complement under low stringency conditions,

(xv) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha" encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions,

(xvi) "S-100 beta" (SEQ ID No:304) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 beta" encoded by a nucleic acid that hybridizes to the "S-100 beta" nucleic acid or its complement under low stringency conditions,

(xvii) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by

modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the APP-C99 complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the APP-C99 complex selected from

(i) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,

(ii) "KIAA1949" (SEQ ID No:299) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1949" encoded by a nucleic acid that hybridizes to the "KIAA1949" nucleic acid or its complement under low stringency conditions,

(iii) "MGC4022" (SEQ ID No:300) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4022" encoded by a nucleic acid that hybridizes to the "MGC4022" nucleic acid or its complement under low stringency conditions, and

(iv) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442"

encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and

an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

(i) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,

(ii) "KIAA1949" (SEQ ID No:299) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1949" encoded by a nucleic acid that hybridizes to the "KIAA1949" nucleic acid or its complement under low stringency conditions,

(iii) "MGC4022" (SEQ ID No:300) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4022"

encoded by a nucleic acid that hybridizes to the "MGC4022" nucleic acid or its complement under low stringency conditions, and/or
 (iv) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

(i) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,

(ii) "KIAA1949" (SEQ ID No:299) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1949" encoded by a nucleic acid that hybridizes to the "KIAA1949" nucleic acid or its complement under low stringency conditions,

(iii) "MGC4022" (SEQ ID No:300) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4022" encoded by a nucleic acid that hybridizes to the "MGC4022" nucleic acid or its complement under low stringency conditions, and/or

(iv) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions, comprising the steps of

(a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and

(b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex, of any one of No. 1 - 8 comprising the steps of (a) exposing said complex, or a cell or organism containing APP-C99 complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether (i) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid

that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or

(ii) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions, and/or

(iii) "CAMK2D" (SEQ ID No:297) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK2D" encoded by a nucleic acid that hybridizes to the "CAMK2D" nucleic acid or its complement under low stringency conditions, and/or

(iv) "Delta-like homolog" (SEQ ID No:298) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions, and/or

(v) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions, and/or

(vi) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions, and/or

(vii) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or

(viii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions, and/or

(ix) "KIAA1949" (SEQ ID No:299) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1949"

encoded by a nucleic acid that hybridizes to the "KIAA1949" nucleic acid or its complement under low stringency conditions, and/or

(x) "MGC4022" (SEQ ID No:300) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4022" encoded by a nucleic acid that hybridizes to the "MGC4022" nucleic acid or its complement under low stringency conditions, and/or

(xi) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions, and/or

(xii) "NAP-1 related protein" (SEQ ID No:301) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NAP-1 related protein" encoded by a nucleic acid that hybridizes to the "NAP-1 related protein" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "Neurocalcin delta" (SEQ ID No:302) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurocalcin delta" encoded by a nucleic acid that hybridizes to the "Neurocalcin delta" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "REST corepressor" (SEQ ID No:303) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REST corepressor" encoded by a nucleic acid that hybridizes to the "REST corepressor" nucleic acid or its complement under low stringency conditions, and/or

(xv) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha" encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "S-100 beta" (SEQ ID No:304) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 beta" encoded by a nucleic acid that hybridizes to the "S-100 beta" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated

complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether (i) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or

(ii) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions, and/or

(iii) "CAMK2D" (SEQ ID No:297) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK2D" encoded by a nucleic acid that hybridizes to the "CAMK2D" nucleic acid or its complement under low stringency conditions, and/or

(iv) "Delta-like homolog" (SEQ ID No:298) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions, and/or

(v) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions, and/or

(vi) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions, and/or

- (vii) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "KIAA1949" (SEQ ID No:299) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1949" encoded by a nucleic acid that hybridizes to the "KIAA1949" nucleic acid or its complement under low stringency conditions, and/or
- (x) "MGC4022" (SEQ ID No:300) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4022" encoded by a nucleic acid that hybridizes to the "MGC4022" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "NAP-1 related protein" (SEQ ID No:301) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NAP-1 related protein" encoded by a nucleic acid that hybridizes to the "NAP-1 related protein" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "Neurocalcin delta" (SEQ ID No:302) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurocalcin delta" encoded by a nucleic acid that hybridizes to the "Neurocalcin delta" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "REST corepressor" (SEQ ID No:303) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REST corepressor" encoded by a nucleic acid that hybridizes to the "REST corepressor" nucleic acid or its complement under low stringency conditions, and/or

(xv) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha" encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "S-100 beta" (SEQ ID No:304) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 beta" encoded by a nucleic acid that hybridizes to the "S-100 beta" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting

proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins
(i) "APP" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(ii) "APP-C99" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,

(iii) "CAMK2D" (SEQ ID No:297) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK2D" encoded by a nucleic acid that hybridizes to the "CAMK2D" nucleic acid or its complement under low stringency conditions,

(iv) "Delta-like homolog" (SEQ ID No:298) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions,

(v) "Fe65" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65" encoded by a nucleic acid that hybridizes to the "Fe65" nucleic acid or its complement under low stringency conditions,

(vi) "Fe65L1" (SEQ ID No:292) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Fe65L1" encoded by a nucleic acid that hybridizes to the "Fe65L1" nucleic acid or its complement under low stringency conditions,

- (vii) "Integral membrane transporter protein" (SEQ ID No:277) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "Integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,
- (viii) "KIAA1102 (Fragment)" (SEQ ID No:285) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1102 (Fragment)" encoded by a nucleic acid that hybridizes to the "KIAA1102 (Fragment)" nucleic acid or its complement under low stringency conditions,
- (ix) "KIAA1949" (SEQ ID No:299) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1949" encoded by a nucleic acid that hybridizes to the "KIAA1949" nucleic acid or its complement under low stringency conditions,
- (x) "MGC4022" (SEQ ID No:300) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC4022" encoded by a nucleic acid that hybridizes to the "MGC4022" nucleic acid or its complement under low stringency conditions,
- (xi) "MGC5442" (SEQ ID No:142) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MGC5442" encoded by a nucleic acid that hybridizes to the "MGC5442" nucleic acid or its complement under low stringency conditions,
- (xii) "NAP-1 related protein" (SEQ ID No:301) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NAP-1 related protein" encoded by a nucleic acid that hybridizes to the "NAP-1 related protein" nucleic acid or its complement under low stringency conditions,
- (xiii) "Neurocalcin delta" (SEQ ID No:302) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurocalcin delta" encoded by a nucleic acid that hybridizes to the "Neurocalcin delta" nucleic acid or its complement under low stringency conditions,
- (xiv) "REST corepressor" (SEQ ID No:303) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REST corepressor" encoded by a nucleic acid that hybridizes to the "REST corepressor" nucleic acid or its complement under low stringency conditions,

(xv) "S-100 alpha" (SEQ ID No:296) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 alpha" encoded by a nucleic acid that hybridizes to the "S-100 alpha" nucleic acid or its complement under low stringency conditions,

(xvi) "S-100 beta" (SEQ ID No:304) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 beta" encoded by a nucleic acid that hybridizes to the "S-100 beta" nucleic acid or its complement under low stringency conditions, and/or (xvii) "X11beta" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "X11beta" encoded by a nucleic acid that hybridizes to the "X11beta" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

The invention further relates to the following embodiments of the Tau-complex

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein selected from the group consisting of:
 - (i) "14-3-3 protein zeta/delta" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein zeta/delta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein zeta/delta" nucleic acid or its complement under low stringency conditions,
 - (ii) "Actin" (SEQ ID No:305) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Actin" encoded by a nucleic acid that hybridizes to the "Actin" nucleic acid or its complement under low stringency conditions,
 - (iii) "Alpha tubulin" (SEQ ID No:306) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Alpha tubulin" encoded by a nucleic acid that hybridizes to the "Alpha tubulin" nucleic acid or its complement under low stringency conditions,
 - (iv) "Beta tubulin" (SEQ ID No:307) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Beta tubulin"

encoded by a nucleic acid that hybridizes to the "Beta tubulin" nucleic acid or its complement under low stringency conditions,

(v) "PPP2CA (PP2A, catalytic subunit, alpha)" (SEQ ID No:312) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2CA (PP2A, catalytic subunit, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2CA (PP2A, catalytic subunit, alpha)" nucleic acid or its complement under low stringency conditions,

(vi) "PPP2CB (PP2A, catalytic subunit, beta)" (SEQ ID No:313) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2CB (PP2A, catalytic subunit, beta)" encoded by a nucleic acid that hybridizes to the "PPP2CB (PP2A, catalytic subunit, beta)" nucleic acid or its complement under low stringency conditions,

(vii) "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" (SEQ ID No:314) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" nucleic acid or its complement under low stringency conditions,

(viii) "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" nucleic acid or its complement under low stringency conditions, and

(ix) "Tau" (SEQ ID No:315) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tau" encoded by a nucleic acid that hybridizes to the "Tau" nucleic acid or its complement under low stringency conditions, and

(b) at least one second protein, which second protein is selected from the group consisting of:

(i) "Deoxyhypusine synthase" (SEQ ID No:308) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Deoxyhypusine synthase" encoded by a nucleic acid that hybridizes to the "Deoxyhypusine synthase" nucleic acid or its complement under low stringency conditions,

- (ii) "Dynactin 2" (SEQ ID No:309) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynactin 2" encoded by a nucleic acid that hybridizes to the "Dynactin 2" nucleic acid or its complement under low stringency conditions,
- (iii) "MEP50" (SEQ ID No:310) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEP50" encoded by a nucleic acid that hybridizes to the "MEP50" nucleic acid or its complement under low stringency conditions,
- (iv) "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" (SEQ ID No:311) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" encoded by a nucleic acid that hybridizes to the "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" nucleic acid or its complement under low stringency conditions, and
- (v) "S-100 beta" (SEQ ID No:304) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 beta" encoded by a nucleic acid that hybridizes to the "S-100 beta" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein Tau (SEQ ID NO. 315), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'Tau' encoded by a nucleic acid that hybridizes to the 'Tau' under low stringency conditions.

3. The protein complex according to No. 1 selected from complex (I) and comprising the following proteins:

- (i) "14-3-3 protein zeta/delta" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein zeta/delta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein zeta/delta" nucleic acid or its complement under low stringency conditions,
- (ii) "Actin" (SEQ ID No:305) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Actin" encoded by a nucleic acid that hybridizes to the "Actin" nucleic acid or its complement under low stringency conditions,
- (iii) "Alpha tubulin" (SEQ ID No:306) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Alpha tubulin" encoded by a nucleic acid that hybridizes to the "Alpha tubulin" nucleic acid or its complement under low stringency conditions,
- (iv) "Beta tubulin" (SEQ ID No:307) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Beta tubulin" encoded by a nucleic acid that hybridizes to the "Beta tubulin" nucleic acid or its complement under low stringency conditions,
- (v) "Deoxyhypusine synthase" (SEQ ID No:308) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Deoxyhypusine synthase" encoded by a nucleic acid that hybridizes to the "Deoxyhypusine synthase" nucleic acid or its complement under low stringency conditions,
- (vi) "Dynactin 2" (SEQ ID No:309) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynactin 2" encoded by a nucleic acid that hybridizes to the "Dynactin 2" nucleic acid or its complement under low stringency conditions,
- (vii) "MEP50" (SEQ ID No:310) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEP50" encoded by a nucleic acid that hybridizes to the "MEP50" nucleic acid or its complement under low stringency conditions,
- (viii) "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" (SEQ ID No:311) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" encoded by a nucleic acid that hybridizes to the "Nuclear receptor co-

repressor/HDAC3 complex subunit TBLR1" nucleic acid or its complement under low stringency conditions,

(ix) "PPP2CA (PP2A, catalytic subunit, alpha)" (SEQ ID No:312) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2CA (PP2A, catalytic subunit, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2CA (PP2A, catalytic subunit, alpha)" nucleic acid or its complement under low stringency conditions,

(x) "PPP2CB (PP2A, catalytic subunit, beta)" (SEQ ID No:313) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2CB (PP2A, catalytic subunit, beta)" encoded by a nucleic acid that hybridizes to the "PPP2CB (PP2A, catalytic subunit, beta)" nucleic acid or its complement under low stringency conditions,

(xi) "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" (SEQ ID No:314) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" nucleic acid or its complement under low stringency conditions,

(xii) "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" nucleic acid or its complement under low stringency conditions,

(xiii) "S-100 beta" (SEQ ID No:304) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 beta" encoded by a nucleic acid that hybridizes to the "S-100 beta" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "Tau" (SEQ ID No:315) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tau" encoded by a nucleic acid that hybridizes to the "Tau" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 4 of the following proteins:

- (i) "14-3-3 protein zeta/delta" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein zeta/delta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein zeta/delta" nucleic acid or its complement under low stringency conditions,
- (ii) "Actin" (SEQ ID No:305) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Actin" encoded by a nucleic acid that hybridizes to the "Actin" nucleic acid or its complement under low stringency conditions,
- (iii) "Alpha tubulin" (SEQ ID No:306) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Alpha tubulin" encoded by a nucleic acid that hybridizes to the "Alpha tubulin" nucleic acid or its complement under low stringency conditions,
- (iv) "Beta tubulin" (SEQ ID No:307) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Beta tubulin" encoded by a nucleic acid that hybridizes to the "Beta tubulin" nucleic acid or its complement under low stringency conditions,
- (v) "Deoxyhypusine synthase" (SEQ ID No:308) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Deoxyhypusine synthase" encoded by a nucleic acid that hybridizes to the "Deoxyhypusine synthase" nucleic acid or its complement under low stringency conditions,
- (vi) "Dynactin 2" (SEQ ID No:309) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynactin 2" encoded by a nucleic acid that hybridizes to the "Dynactin 2" nucleic acid or its complement under low stringency conditions,
- (vii) "MEP50" (SEQ ID No:310) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEP50" encoded by a nucleic acid that hybridizes to the "MEP50" nucleic acid or its complement under low stringency conditions,
- (viii) "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" (SEQ ID No:311) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" encoded by a nucleic acid that hybridizes to the "Nuclear receptor co-

repressor/HDAC3 complex subunit TBLR1" nucleic acid or its complement under low stringency conditions,

(ix) "PPP2CA (PP2A, catalytic subunit, alpha)" (SEQ ID No:312) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2CA (PP2A, catalytic subunit, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2CA (PP2A, catalytic subunit, alpha)" nucleic acid or its complement under low stringency conditions,

(x) "PPP2CB (PP2A, catalytic subunit, beta)" (SEQ ID No:313) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2CB (PP2A, catalytic subunit, beta)" encoded by a nucleic acid that hybridizes to the "PPP2CB (PP2A, catalytic subunit, beta)" nucleic acid or its complement under low stringency conditions,

(xi) "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" (SEQ ID No:314) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" nucleic acid or its complement under low stringency conditions,

(xii) "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" nucleic acid or its complement under low stringency conditions,

(xiii) "S-100 beta" (SEQ ID No:304) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 beta" encoded by a nucleic acid that hybridizes to the "S-100 beta" nucleic acid or its complement under low stringency conditions,

(xiv) "Tau" (SEQ ID No:315) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tau" encoded by a nucleic acid that hybridizes to the "Tau" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.
6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.
7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of No. 1 - 7 that is involved in the the phosphorylation of tau proteins in vitro or in cells (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the aggregation of tau proteins into filaments or tangles in vitro or in cells (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).
9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.
10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Tau complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the Tau complex selected from

(i) "MEP50" (SEQ ID No:310) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEP50" encoded by a nucleic acid that hybridizes to the "MEP50" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or

functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

(i) "MEP50" (SEQ ID No:310) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEP50" encoded by a nucleic acid that hybridizes to the "MEP50" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

(i) "MEP50" (SEQ ID No:310) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEP50" encoded by a nucleic acid that hybridizes to the "MEP50" nucleic acid or its complement under low stringency conditions, comprising the steps of

(a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and

(b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of (a) exposing said complex, or a cell or organism containing Tau complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether

- (i) "14-3-3 protein zeta/delta" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein zeta/delta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein zeta/delta" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "Actin" (SEQ ID No:305) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Actin" encoded by a nucleic acid that hybridizes to the "Actin" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "Alpha tubulin" (SEQ ID No:306) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Alpha tubulin" encoded by a nucleic acid that hybridizes to the "Alpha tubulin" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "Beta tubulin" (SEQ ID No:307) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Beta tubulin" encoded by a nucleic acid that hybridizes to the "Beta tubulin" nucleic acid or its complement under low stringency conditions, and/or
- (v) "Deoxyhypusine synthase" (SEQ ID No:308) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Deoxyhypusine synthase" encoded by a nucleic acid that hybridizes to the "Deoxyhypusine synthase" nucleic acid or its complement under low stringency conditions, and/or

- (vi) "Dynactin 2" (SEQ ID No:309) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynactin 2" encoded by a nucleic acid that hybridizes to the "Dynactin 2" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "MEP50" (SEQ ID No:310) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEP50" encoded by a nucleic acid that hybridizes to the "MEP50" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" (SEQ ID No:311) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" encoded by a nucleic acid that hybridizes to the "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "PPP2CA (PP2A, catalytic subunit, alpha)" (SEQ ID No:312) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2CA (PP2A, catalytic subunit, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2CA (PP2A, catalytic subunit, alpha)" nucleic acid or its complement under low stringency conditions, and/or
- (x) "PPP2CB (PP2A, catalytic subunit, beta)" (SEQ ID No:313) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2CB (PP2A, catalytic subunit, beta)" encoded by a nucleic acid that hybridizes to the "PPP2CB (PP2A, catalytic subunit, beta)" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" (SEQ ID No:314) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2RBA, (PP2A, 55 KDA

regulatory subunit B, alpha)" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "S-100 beta" (SEQ ID No:304) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 beta" encoded by a nucleic acid that hybridizes to the "S-100 beta" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "Tau" (SEQ ID No:315) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tau" encoded by a nucleic acid that hybridizes to the "Tau" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity,

or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether

- (i) "14-3-3 protein zeta/delta" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein zeta/delta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein zeta/delta" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "Actin" (SEQ ID No:305) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Actin" encoded by a nucleic acid that hybridizes to the "Actin" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "Alpha tubulin" (SEQ ID No:306) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Alpha tubulin" encoded by a nucleic acid that hybridizes to the "Alpha tubulin" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "Beta tubulin" (SEQ ID No:307) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Beta tubulin"

encoded by a nucleic acid that hybridizes to the "Beta tubulin" nucleic acid or its complement under low stringency conditions, and/or

(v) "Deoxyhypusine synthase" (SEQ ID No:308) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Deoxyhypusine synthase" encoded by a nucleic acid that hybridizes to the "Deoxyhypusine synthase" nucleic acid or its complement under low stringency conditions, and/or

(vi) "Dynactin 2" (SEQ ID No:309) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynactin 2" encoded by a nucleic acid that hybridizes to the "Dynactin 2" nucleic acid or its complement under low stringency conditions, and/or

(vii) "MEP50" (SEQ ID No:310) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEP50" encoded by a nucleic acid that hybridizes to the "MEP50" nucleic acid or its complement under low stringency conditions, and/or

(viii) "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" (SEQ ID No:311) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" encoded by a nucleic acid that hybridizes to the "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" nucleic acid or its complement under low stringency conditions, and/or

(ix) "PPP2CA (PP2A, catalytic subunit, alpha)" (SEQ ID No:312) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2CA (PP2A, catalytic subunit, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2CA (PP2A, catalytic subunit, alpha)" nucleic acid or its complement under low stringency conditions, and/or

(x) "PPP2CB (PP2A, catalytic subunit, beta)" (SEQ ID No:313) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2CB (PP2A, catalytic subunit, beta)" encoded by a nucleic acid that hybridizes to the "PPP2CB (PP2A, catalytic subunit, beta)" nucleic acid or its complement under low stringency conditions, and/or

(xi) "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" (SEQ ID No:314) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)"

encoded by a nucleic acid that hybridizes to the "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" nucleic acid or its complement under low stringency conditions, and/or (xii) "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "S-100 beta" (SEQ ID No:304) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 beta" encoded by a nucleic acid that hybridizes to the "S-100 beta" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "Tau" (SEQ ID No:315) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Tau" encoded by a nucleic acid that hybridizes to the "Tau" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, the phosphorylation of tau proteins in vitro or in cells (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the aggregation of tau proteins into filaments or tangles in vitro or in cells (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins

(i) "14-3-3 protein zeta/delta" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "14-3-3 protein zeta/delta" encoded by a nucleic acid that hybridizes to the "14-3-3 protein zeta/delta" nucleic acid or its complement under low stringency conditions,

(ii) "Actin" (SEQ ID No:305) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Actin" encoded by a nucleic acid that hybridizes to the "Actin" nucleic acid or its complement under low stringency conditions,

(iii) "Alpha tubulin" (SEQ ID No:306) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Alpha tubulin" encoded by a nucleic acid that hybridizes to the "Alpha tubulin" nucleic acid or its complement under low stringency conditions,

(iv) "Beta tubulin" (SEQ ID No:307) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Beta tubulin" encoded by a nucleic acid that hybridizes to the "Beta tubulin" nucleic acid or its complement under low stringency conditions,

(v) "Deoxyhypusine synthase" (SEQ ID No:308) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Deoxyhypusine synthase" encoded by a nucleic acid that hybridizes to the "Deoxyhypusine synthase" nucleic acid or its complement under low stringency conditions,

(vi) "Dynactin 2" (SEQ ID No:309) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Dynactin 2" encoded by a nucleic acid that hybridizes to the "Dynactin 2" nucleic acid or its complement under low stringency conditions,

(vii) "MEP50" (SEQ ID No:310) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MEP50" encoded by a

nucleic acid that hybridizes to the "MEP50" nucleic acid or its complement under low stringency conditions,

(viii) "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" (SEQ ID No:311) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" encoded by a nucleic acid that hybridizes to the "Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1" nucleic acid or its complement under low stringency conditions,

(ix) "PPP2CA (PP2A, catalytic subunit, alpha)" (SEQ ID No:312) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2CA (PP2A, catalytic subunit, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2CA (PP2A, catalytic subunit, alpha)" nucleic acid or its complement under low stringency conditions,

(x) "PPP2CB (PP2A, catalytic subunit, beta)" (SEQ ID No:313) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2CB (PP2A, catalytic subunit, beta)" encoded by a nucleic acid that hybridizes to the "PPP2CB (PP2A, catalytic subunit, beta)" nucleic acid or its complement under low stringency conditions,

(xi) "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" (SEQ ID No:314) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)" nucleic acid or its complement under low stringency conditions,

(xii) "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" encoded by a nucleic acid that hybridizes to the "PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)" nucleic acid or its complement under low stringency conditions,

(xiii) "S-100 beta" (SEQ ID No:304) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S-100 beta" encoded by a nucleic acid that hybridizes to the "S-100 beta" nucleic acid or its complement under low stringency conditions, and/or(xiv) "Tau" (SEQ ID No:315) or a functionally active derivative thereof, or a functionally active fragment thereof, or a

homolog thereof, or a variant of "Tau" encoded by a nucleic acid that hybridizes to the "Tau" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

5. PROTOCOLS:

The TAP-technology, which is more fully described in EP 1 105 508 B1 and in Rigaut, et al., 1999, Nature Biotechnol. 17:1030-1032 respectively was used and further adapted as described below for protein purification. Proteins were identified using mass spectrometry as described further below.

5.1 Construction of TAP-tagged bait

The cDNAs encoding the complete ORF were obtained by RT-PCR. Total RNA was prepared from appropriate cell lines using the RNeasy Mini Kit (Qiagen). Both cDNA synthesis and PCR were performed with the SUPERScript One-Step RT-PCR for Long templates Kit (Life Technologies) using gene-specific primers. After 35-40 cycles of amplification PCR-products with the expected size were gel-purified with the MinElute PCR Purification Kit (Qiagen) and, if necessary, used for further amplification. Low-abundant RNAs were amplified by nested PCR before gel-purification. Restriction sites for NotI were attached to PCR primers to allow subcloning of amplified cDNAs into the retroviral vectors pIE94-N/C-TAP thereby generating N- or C-terminal fusions with the TAP-tag (Rigaut et al., 1999, Nature Biotechnol. 17:1030-1032). N-terminal tagging was chosen for the following baits/entry points: Presenilin 2, Aph-1a, Pen-2, APP, Tau, Fe65. C-terminal tagging was chosen for the following baits/entry points: Nicastrin, Aph-1a, Aph-1b, APP695SW, APP-C99, Fe65, X11beta.

Clones were analyzed by restriction digest, DNA sequencing and by in vitro translation using the TNT T7 Quick Coupled Transcription/Translation System (Promega inc.). The presence of the proteins was proven by Western blotting using the protein A

part of the TAP-tag for detection. Briefly, separation of proteins by standard SDS-PAGE was followed by semi-dry transfer onto a nitrocellulose membrane (PROTRAN, Schleicher&Schuell) using the MultiphorII blotting apparatus from Pharmacia Biotech. The transfer buffer consisted of 48 mM Tris, 39 mM glycine, 10% methanol and 0,0375% sodium dodecylsulfate. After blocking in phosphate-buffered saline (PBS) supplemented with 10% dry milk powder and 0,1% Tween 20 transferred proteins were probed with the Peroxidase-Anti-Peroxidase Soluble Complex (Sigma) diluted in blocking solution. After intensive washing immunoreactive proteins were visualized by enhanced chemiluminescence (ECL; Amersham Pharmacia Biotech).

5.2 Preparation of Virus and infection

As a vector, a MoMLV-based recombinant virus was used.

The preparation has been carried out as follows:

5.2.1 Preparation of Virus

293 gp cells were grown to 100% confluency. They were split 1:5 on poly-L-Lysine plates (1:5 diluted poly-L-Lysine [0.01% stock solution, Sigma P-4832] in PBS, left on plates for at least 10 min.). On Day 2, 63 microgram of retroviral Vector DNA together with 13 microgram of DNA of plasmid encoding an appropriate envelope protein were transfected into 293 gp cells (Somia, et al., 1999, Proc. Natl. Acad. Sci. USA 96:12667-12672; Somia, et al. 2000, J. Virol. 74:4420-4424). On Day 3, the medium was replaced with 15 ml DMEM + 10% FBS per 15-cm dish. On Day 4, the medium containing viruses (supernatant) was harvested (at 24 h following medium change after transfection). When a second collection was planned, DMEM 10 % FBS was added to the plates and the plates were incubated for another 24 h. All collections were done as follows: The supernatant was filtered through 0.45 micrometer filter (Corning GmbH, cellulose acetate, 431155). The filter was placed into konical polyallomer centrifuge tubes (Beckman, 358126) that are placed in buckets of a SW 28 rotor (Beckman). The filtered supernatant was ultracentrifuged at 19400 rpm in the SW 28 rotor, for 2 hours at 21 degree Celsius. The supernatant was discarded. The pellet containing viruses was

resuspended in a small volume (for example 300 microliter) of Hank's Balanced Salt Solution [Gibco BRL, 14025-092], by pipetting up and down 100-times, using an aerosol-safe tip. The viruses were used for transfection as described below.

5.2.2 Infection

Cells that were infected were plated one day before into one well of a 6-well plate. 4 hours before infection, the old medium on the cells was replaced with fresh medium. Only a minimal volume was added, so that the cells are completely covered (e.g. 700 microliter). During infection, the cells were actively dividing.

A description of the cells and their growth conditions is given in 5.2.3

To the concentrated virus, polybrene (Hexadimethrine Bromide; Sigma, H 9268) was added to achieve a final concentration of 8 microgram/ml (this is equivalent to 2.4 microliter of the 1 milligram/ml polybrene stock per 300 microliter of concentrated retrovirus). The virus was incubated in polybrene at room temperature for 1 hour. For infection, the virus/polybrene mixture was added to the cells and incubated at 37 degree Celsius at the appropriate CO₂ concentration for several hours (e.g. over-day or over-night). Following infection, the medium on the infected cells was replaced with fresh medium. The cells were passaged as usual after they became confluent. The cells contain the retrovirus integrated into their chromosomes and stably express the gene of interest.

5.2.3 Cell lines

The following Cell-lines were used:

Fe65-complex: HEK-293-cells, SKN-BE2-cells, SH-SY5Y-cells; X11beta-complex: HEK-293-cells, SKN-BE2-cells, SH-SY5Y-cells; Psen-2-complex: SKN-BE2-cells, SH-SY5Y-cells, LAN-cells; Nicastrin-complex: HEK-293-cells, SKN-BE2-cells; Aph-1a-complex: HEK-293-cells, SKN-BE2-cells; Pen-2-complex: HEK-293-cells, SKN-BE2-cells;

APP695SW-complex: HEK-293-cells, SKN-BE2-cells; APP-C99-complex: SKN-BE2-cells; Tau-complex: SKN-BE2-cells, SH-SY5Y-cells

SKN-BE2 cells (American Type Culture Collection-No. CRL-2271) were grown in 95% OptiMEM + 5% iron-supplemented calf serum.

SH-SY5Y-cells were grown in 85% DMEM/F-12, 15% FBS, Non-essential AA

LAN-cells (human neuroblastoma cell line) were grown in 90% RPMI 1640 + 10% FBS

The expression pattern of the TAP-tagged proteins was checked by immunoblot-analysis as described in 5.3.3 and/or by immunofluorescence as described in 5.3.1 or 5.3.2.

5.3 Checking of expression pattern of TAP-tagged proteins

The expression pattern of the TAP-tagged protein was checked by immunoblot analysis and/or by immunofluorescence. Immunofluorescence analysis was either carried out according to section 5.3.1 or to section 5.3.2 depending on the type of the TAP-tagged protein. Immunoblot analysis was carried out according to section 5.3.3.

5.3.1 Protocol for the indirect Immunofluorescence staining of fixed mammalian cells for plasma membrane and ER bound proteins

Cells were grown in FCS media on polylysine coated 8 well chamber slides to 50% confluency. Then fixation of the cells was performed in 4% ParaFormAldehyde diluted in Phosphate Buffer Saline (PBS) solution (0.14M Phosphate, 0.1M NaCl pH 7.4). The cells were incubated for 30 minutes at room temperature in 300 microliters per well. Quenching was performed in 0.1M Glycine in PBS for 2x 20 minutes at room temperature. Blocking was performed with 1% Bovine Serum Albumin (BSA) in 0.3% Saponin + PBS for at least 1 hour at room temperature. Incubation of the primary antibodies was performed in the blocking solution overnight at +4°C. The proper dilution of the antibodies was determined in a case to case basis. Cells were washed in PBS containing 0.3% Saponin for 2x 20 minutes at room temperature. Incubation of the

secondary antibodies is performed in the blocking solution. Alexa 594 coupled goat anti-rabbit is diluted 1:1000 (Molecular Probes). Alexa 488 coupled goat anti-mouse is diluted 1:1000 (Molecular Probes). DAPI was used to label DNA. If Phalloidin was used to label F-actin, the drug is diluted 1:500 and incubated with the secondary antibodies. Cells were then washed again 2x 20 minutes at room temperature in PBS. The excess of buffer was removed and cells were mounted in a media containing an anti-bleaching agent (Vectashield, Vector Laboratories).

5.3.2 Protocol for the indirect Immunofluorescence staining of fixed mammalian cells for non-plasma membrane bound proteins:

Cells were grown in FCS media on Polylysine coated 8 well chamber slides to 50% confluency. Fixation of the cells was performed in 4% ParaFormaldehyde diluted in Phosphate Buffer Saline (PBS) solution (0.14M Phosphate, 0.1M NaCl pH 7.4) for 30 minutes at Room Temperature (RT), 300 microliters per well. Quenching was performed in 0.1M Glycine in PBS for 2x 20 minutes at room temperature. Permeabilization of cells was done with 0.5% Triton X-100 in PBS for 10 minutes at room temperature. Blocking was then done in 1% Bovine Serum Albumin (BSA) in 0.3% Saponin + PBS for at least 1 hour at RT (Blocking solution). Incubation of the primary antibodies was performed in the blocking solution, overnight at +4°C. The proper dilution of the antibodies has to be determined in a case to case basis. Cells were washed in PBS containing 0.3% Saponin, for 2x 20 minutes at RT. Incubation of the secondary antibodies was performed in the blocking solution. Alexa 594 coupled goat anti-rabbit is diluted 1:1000 (Molecular Probes), Alexa 488 coupled goat anti-mouse is diluted 1:1000 (Molecular Probes). DAPI was used to label DNA. If Phalloidin is used to label F-actin, the drug is diluted 1:500 and incubated with the secondary antibodies. Cells were washed 2x 20 minutes at RT in PBS. The excess of buffer was removed and cells were mounted in a media containing an anti-bleaching agent (Vectashield, Vector Laboratories).

5.3.3 Immunoblot analysis

To analyze expression levels of TAP-tagged proteins, a cell pellet (from a 6-well dish) was lysed in 60 μ l DNase I buffer (5% Glycerol, 100 mM NaCl, 0.8 % NP-40 (IGEPAL), 5 mM magnesium sulfate, 100 μ g/ml DNase I (Roche Diagnostics), 50 mM Tris, pH 7.5, protease inhibitor cocktail) for 15 min on ice. Each sample was split into two aliquots. The first half was centrifuged at 13,000 rpm for 5 min. to yield the NP-40-extractable material in the supernatant; the second half (total material) was carefully triturated. 50 μ g each of the NP-40-extractable material and the total material are mixed with DTT-containing sample buffer for 30 min at 50°C on a shaker and separated by SDS polyacrylamide gel electrophoresis on a precast 4-12% Bis-Tris gel (Invitrogen). Proteins were then transferred to nitrocellulose using a semi-dry procedure with a discontinuous buffer system. Briefly, gel and nitrocellulose membrane were stacked between filter papers soaked in either anode buffer (three layers buffer A1 (0.3 M Tris-HCl) and three layers buffer A2 (0.03 M Tris-HCl)) or cathode buffer (three layers of 0.03 M Tris-HCl, pH 9.4, 0.1 % SDS, 40 mM ϵ -aminocaproic acid). Electrotransfer of two gels at once was performed at 600 mA for 25 min. Transferred proteins were visualized with Ponceau S solution for one min to control transfer efficiency and then destained in water. The membrane was blocked in 5% non-fat milk powder in TBST (TBS containing 0.05% Tween-20) for 30 min at room temperature. It was subsequently incubated with HRP-coupled PAP antibody (1:5000 diluted in 5% milk/TBST) for 1 h at room temperature, washed three times for 10 min in TBST. The blot membrane was finally soaked in chemiluminescent substrate (ECL, Roche Diagnostics) for 2 min. and either exposed to X-ray film or analyzed on an imaging station.

5.4 Purification of protein complexes

Protein complex purification was adapted to the sub-cellular localization of the TAP-tagged protein and was performed as described below.

5.4.1 Lysate preparation for cytoplasmic proteins

About 1×10^9 adherent cells (average) were harvested with a cell scraper and washed 3 times in ice-cold PBS (3 min, 550g). Collected cells were frozen in liquid

nitrogen or immediately processed further. For cell lysis, the cell pellet was resuspended in 10 ml of CZ lysis buffer (50 mM Tris-Cl, pH 7.4; 5 % Glycerol; 0,2 % IGEPAL; 1.5 mM $MgCl_2$; 100 mM NaCl; 25 mM NaF; 1 mM Na_3VO_4 ; 1 mM DTT; containing 1 tablet of EDTA-free Protease inhibitor cocktail (Complete™, Roche) per 25 ml of buffer) and homogenized by 10 strokes of a tight-fitted pestle in a dounce homogenizer. The lysate was incubated for 30 min on ice and spun for 10 min at 20,000g. The supernatant was subjected to an additional ultracentrifugation step for 1 h at 100,000g. The supernatant was recovered and rapidly frozen in liquid nitrogen or immediately processed further.

5.4.2 Lysate preparation for membrane proteins

About 1×10^9 adherent cells (average) were harvested with a cell scraper and washed 3 times in ice-cold PBS (3 min, 550g). Collected cells were frozen in liquid nitrogen or immediately processed further. For cell lysis, the cell pellet was resuspended in 10 ml of Membrane-Lysis buffer (50 mM Tris, pH 7.4; 7.5 % Glycerol; 1 mM EDTA; 150 mM NaCl; 25 mM NaF; 1 mM Na_3VO_4 ; 1 mM DTT; containing 1 tablet of EDTA-free Protease inhibitor cocktail (Complete™, Roche) per 25 ml of buffer) and homogenized by 10 strokes of a tight-fitted pestle in a dounce homogenizer. The lysate was spun for 10 min at 750g, the supernatant was recovered and subjected to an ultracentrifugation step for 1 h at 100,000g. The membrane pellet was resuspended in 7,5 ml of Membrane-Lysis buffer containing 0.8% n-Dodecyl- β -D-maltoside and incubated for 1 h at 4°C with constant agitation. The sample was subjected to another ultracentrifugation step for 1h at 100,000g and the solubilized material was quickly frozen in liquid nitrogen or immediately processed further.

5.4.3 Lysate preparation for nuclear proteins

About 1×10^9 adherent cells (average) were harvested with a cell scraper and washed 3 times in ice-cold PBS (3 min, 550g). Collected cells were frozen in liquid nitrogen or immediately processed further. For cell lysis, the cell pellet was resuspended in 10 ml of Hypotonic-Lysis buffer (10 mM Tris, pH 7.4; 1.5 mM $MgCl_2$; 10 mM KCl; 25 mM NaF; 1 mM Na_3VO_4 ; 1 mM DTT; containing 1 tablet of EDTA-free Protease inhibitor

cocktail (Complete™, Roche) per 25 ml of buffer) and homogenized by 10 strokes of a tight-fitted pestle in a dounce homogenizer. The lysate was spun for 10 min at 2,000g and the resulting supernatant (S1) saved on ice. The nuclear pellet (P1) was resuspended in 5 ml Nuclear-Lysis buffer (50 mM Tris, pH 7.4; 1.5 mM MgCl₂; 20 % Glycerol; 420 mM NaCl; 25 mM NaF; 1 mM Na₃VO₄; 1 mM DTT; containing 1 tablet of EDTA-free Protease inhibitor cocktail (Complete™, Roche) per 25 ml of buffer) and incubated for 30 min on ice. The sample was combined with S1, further diluted with 7 ml of Dilution buffer (110 mM Tris, pH 7.4; 0.7 % NP40; 1.5 mM MgCl₂; 25 mM NaF; 1 mM Na₃VO₄; 1 mM DTT), incubated on ice for 10 min and centrifuged at 100,000g for 1h. The final supernatant (S2) was frozen quickly in liquid nitrogen.

5.4.4 Tandem Affinity Purification

The frozen lysate was quickly thawed in a 37°C water bath, and spun for 20 min at 100,000g. The supernatant was recovered and incubated with 0.2 ml of settled rabbit IgG-Agarose beads (Sigma) for 2 h with constant agitation at 4°C. Immobilized protein complexes were washed with 10 ml of CZ lysis buffer (containing 1 Complete™ tablet (Roche) per 50 ml of buffer) and further washed with 5 ml of TEV cleavage buffer (10 mM Tris, pH 7.4; 100 mM NaCl; 0.1 % IGEPAL; 0.5 mM EDTA; 1 mM DTT). Protein-complexes were eluted by incubation with 5 µl of TEV protease (GibcoBRL, Cat.No. 10127-017) for 1 h at 16°C in 150 µl TEV cleavage buffer. The eluate was recovered and combined with 0.2 ml settled Calmodulin affinity beads (Stratagene) in 0.2 ml CBP binding buffer (10 mM Tris, pH 7.4; 100 mM NaCl; 0.1 % IGEPAL; 2mM MgAc; 2mM Imidazole; 1mM DTT; 4 mM CaCl₂) followed by 1 h incubation at 4°C with constant agitation. Immobilized protein complexes were washed with 10 ml of CBP wash buffer (10 mM Tris, pH 7.4; 100 mM NaCl; 0.1 % IGEPAL; 1mM MgAc; 1mM Imidazole; 1mM DTT; 2 mM CaCl₂) and eluted by addition of 600 µl CBP elution buffer (10 mM Tris, pH 8.0; 5 mM EGTA) for 5 min at 37°C. The eluate was recovered in a siliconized tube and lyophilized. The remaining Calmodulin resin was boiled for 5 min in 50 µl 4x Laemmli sample buffer. The sample buffer was isolated, combined with the lyophilised fraction and loaded on a NuPAGE gradient gel (Invitrogen, 4-12%, 1.5 mm, 10 well).

5.4.5 Isolation of the Sambiasin complex of the invention from mouse tissue

Two mouse forebrains (0.6314 g total wet weight) were lysed in 14 mls of 50 mM HEPES pH 7.4; 150 mM NaCl; 1 mM EDTA; 0.5 mM Sodium Vanadate; 10% Glycerol; 1% n-Dodecyl- β -D-maltoside containing standard proteinase inhibitors. The tissue was homogenised in a Waring blender for 30 seconds on ice. Homogenates were incubated on ice for 1 hour and then centrifuged at 13,000 g for 30 min at 4°C. The resulting pellet was stored at -80°C while the supernatant was centrifuged at 50,000 g for 30 min at 4°C and the resulting pellet was also stored at -80°C. 6.5 ml of the supernatant from this second centrifugation step was taken and combined with 25 μ l of anti presenilin-1 antisera (MAB5232, Chemicon). The antibody/lysate mixture was incubated for 1 hour at 4°C with end-over end mixing. Pre-washed protein G sepharose was added and the mixture was incubated overnight at 4°C with end-over mixing. The protein G was recovered by centrifugation at 200 g for 5 min at 4°C. The protein G beads were then washed 5 times in 1ml lysis buffer (containing 0.1% n-Dodecyl- β -D-maltoside rather than 1%). 100 μ l of NuPAGE sample buffer (Invitrogen) was added and the sample incubated at 37°C for 10 min. Samples were separated on 4-12 % NuPAGE bis/tris gels (Invitrogen, 1.5 mm, 10 well). Proteins were visualized by staining with colloidal coomassie (Sigma) and then analysed by LC/MSMS.

5.5 Protein identification by mass spectrometry

5.5.1 Protein digestion prior to mass spectrometric analysis

Gel-separated proteins were reduced, alkylated and digested in gel essentially following the procedure described by Shevchenko et al., 1996, Anal. Chem. 68:850-858. Briefly, gel-separated proteins were excised from the gel using a clean scalpel, reduced using 10 mM DTT (in 5mM ammonium bicarbonate, 54°C, 45 min) and subsequently alkylated with 55 mM iodoacetamid (in 5 mM ammonium bicarbonate) at room temperature in the dark (30 min). Reduced and alkylated proteins were digested in gel with porcine trypsin (Promega) at a protease concentration of 12.5 ng/ μ l in 5mM ammonium bicarbonate. Digestion was allowed to proceed for 4 hours at 37°C and the reaction was subsequently stopped using 5 μ l 5% formic acid.

5.5.2 Sample preparation prior to analysis by mass spectrometry

Gel plugs were extracted twice with 20 μ l 1% TFA and pooled with acidified digest supernatants. Samples were dried in a vacuum centrifuge and resuspended in 13 μ l 1% TFA.

5.5.3 Mass spectrometric data acquisition

Peptide samples were injected into a nano LC system (CapLC, Waters or Ultimate, Dionex) which was directly coupled either to a quadrupole TOF (QTOF2, QTOF Ultima, QTOF Micro, Micromass or QSTAR Pulsar, Sciex) or ion trap (LCQ Deca XP) mass spectrometer. Peptides were separated on the LC system using a gradient of aqueous and organic solvents (see below). Solvent A was 5% acetonitrile in 0.5% formic acid and solvent B was 70% acetonitrile in 0.5% formic acid.

Time (min)	% solvent A	% solvent B
0	95	5
5.33	92	8
35	50	50
36	20	80
40	20	80
41	95	5
50	95	5

Peptides eluting off the LC system were partially sequenced within the mass spectrometer.

5.5.4 Protein identification

The peptide mass and fragmentation data generated in the LC-MS/MS experiments were used to query fasta formatted protein and nucleotide sequence databases maintained and updated regularly at the NCBI (for the NCBI nr, dbEST and the

human and mouse genomes) and European Bioinformatics Institute (EBI, for the human, mouse, *D. melanogaster* and *C. elegans* proteome databases). Proteins were identified by correlating the measured peptide mass and fragmentation data with the same data computed from the entries in the database using the software tool Mascot (Matrix Science; Perkins et al., 1999, *Electrophoresis* 20:3551-3567). Search criteria varied depending on which mass spectrometer was used for the analysis.

TABLE 1

COMPONENTS OF COMPLEXES

Name of complex	Entry Point	All interactors of the complex	Known interactors of the complex	Novel interactors of the complex	Proteins of unknown function
Fe65-complex	Fe65	APP	APP		
		14-3-3 protein epsilon		14-3-3 protein epsilon	
		14-3-3 protein beta/alpha		14-3-3 protein beta/alpha	
		14-3-3 protein eta		14-3-3 protein eta	
		14-3-3 protein gamma		14-3-3 protein gamma	
		14-3-3 protein tau		14-3-3 protein tau	
		14-3-3 protein zeta/delta		14-3-3 protein zeta/delta	
		APLP1	APLP1		
		APLP2	APLP2		
		APP-C99	APP-C99	APP-C99	APP-C99
		ATP-binding cassette, sub-family B, member 7		ATP-binding cassette, sub-family B, member 7	

	ECP-51		ECP-51	
	Fe65	Fe65		
	GAP-associated tyrosine phosphoprotein p62		GAP-associated tyrosine phosphoprotein p62	
	Integral membrane protein 2B (ITM2B)		Integral membrane protein 2B (ITM2B)	
	IP100104084.1		IP100104084.1	IP100104084.1
	Krab box protein ensp000000302970		Krab box protein ensp000000302970	Krab box protein ensp000000302970
	PDZ domain protein MAGI-3		PDZ domain protein MAGI-3	
	PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)		PPP2RBA (PP2A, 55 kDa regulatory subunit B, alpha)	
	Protein similar to probable mitotic centromere associated kinesin		Protein similar to probable mitotic centromere associated kinesin	Protein similar to probable mitotic centromere associated kinesin
	RNB6	RNB6		
	SAP-62		SAP-62	
	Transcription factor CP2	Transcription factor CP2		

		Zinc finger protein 277		Zinc finger protein 277	Zinc finger protein 277
X11b-complex	X11b	ADAMTS-19		ADAMTS-19	ADAMTS-19
		APLP1		APLP1	
		APP	APP		
		Axonemal dynein heavy chain 8		Axonemal dynein heavy chain 8	
		BAT1		BAT1	BAT1
		C20orf11 (sim to a region of RANBPM)		C20orf11 (sim to a region of RANBPM)	C20orf11 (sim to a region of RANBPM)
		Cadherin EGF LAG seven-pass G-type receptor 2		Cadherin EGF LAG seven-pass G-type receptor 2	Cadherin EGF LAG seven-pass G-type receptor 2
		Calsyntenin-1		Calsyntenin-1	
		Calsyntenin-2		Calsyntenin-2	Calsyntenin-2
		Calsyntenin-3		Calsyntenin-3	Calsyntenin-3
		CGB0_HUMAN		CGB0_HUMAN	CGB0_HUMAN
		Chondroitin sulfate proteoglycan 6		Chondroitin sulfate proteoglycan 6	
		Chromatin-specific transcription elongation		Chromatin-specific transcription elongation	

		factor FACT 140 kDa subunit	factor FACT 140 kDa subunit	
		DC6 protein	DC6 protein	
		Dkfp586c1924	Dkfp586c1924	Dkfp586c1924
		Dynein light chain 2A	Dynein light chain 2A	
		Dynein light chain-A	Dynein light chain-A	
		ELAVL3	ELAVL3	
		ENG00000168820 (hypothetical protein with p-loop)	ENG00000168820 (hypothetical protein with p-loop)	ENG00000168820 (hypothetical protein with p-loop)
		Eukaryotic translation initiation factor 4A, isoform	Eukaryotic translation initiation factor 4A, isoform	
		Filamin, gamma	Filamin, gamma	
		FLJ13910	FLJ13910	FLJ13910
		FRAP1	FRAP1	
		GTP-binding protein ERA	GTP-binding protein ERA	
		HADH2/ERAB (mitochondrial enzyme)	HADH2/ERAB (mitochondrial enzyme)	
		HDAC2	HDAC2	
		HERC2 protein	HERC2 protein	HERC2 protein

	HSPC154		HSPC154	HSPC154
	HSPC245		HSPC245	HSPC245
	Hunc18a	Hunc18a		
	HYPOTHETICAL PROTEIN FLJ10618		HYPOTHETICAL PROTEIN FLJ10618	HYPOTHETICAL PROTEIN FLJ10618
	Hypothetical protein FLJ10795		Hypothetical protein FLJ10795	
	HYPOTHETICAL PROTEIN FLJ12599.		HYPOTHETICAL PROTEIN FLJ12599.	HYPOTHETICAL PROTEIN FLJ12599.
	Hypothetical protein FLJ20397		Hypothetical protein FLJ20397	Hypothetical protein FLJ20397
	hypothetical protein MGC13186		hypothetical protein MGC13186	hypothetical protein MGC13186
	IKAP		IKAP	
	Insulinoma-glucagonoma protein 20		Insulinoma- glucagonoma protein 20	
	KIAA0056		KIAA0056	KIAA0056
	KIAA0166		KIAA0166	KIAA0166
	KIAA0325 (FRAGMENT)		KIAA0325 (FRAGMENT)	
	KIAA0564		KIAA0564	KIAA0564

	KIAA0763		KIAA0763	KIAA0763
	Laminin, gamma 1		Laminin, gamma 1	
	LIB (leucine-rich repeat protein)		LIB (leucine-rich repeat protein)	
	MBIP		MBIP	
	MEGF7 (FRAGMENT)		MEGF7 (FRAGMENT)	MEGF7 (FRAGMENT)
	MT-ACT48		MT-ACT48	MT-ACT48
	Myosin IXB		Myosin IXB	
	NEU1		NEU1	
	Neurexin-1	Neurexin-1		
	NIPSNAP1		NIPSNAP1	NIPSNAP1
	NIPSNAP2		NIPSNAP2	
	Paladin		Paladin	Paladin
	PDZ and LIM domain protein 1		PDZ and LIM domain protein 1	PDZ and LIM domain protein 1
	Phosphoenolpyruvate carboxykinase 2 (mitochondrial)		Phosphoenolpyruvate carboxykinase 2 (mitochondrial)	
	PILB		PILB	PILB
	PILT		PILT	PILT
	Procollagen C-		Procollagen C-	

	endopeptidase enhancer		endopeptidase enhancer	
	Programmed cell death 10		Programmed cell death 10	Programmed cell death 10
	Protein similar to AGCP6688		Protein similar to AGCP6688	Protein similar to AGCP6688
	RAB7L1		RAB7L1	RAB7L1
	RANBP1		RANBP1	
	Reelin		Reelin	
	RPGR-interacting protein 1		RPGR-interacting protein 1	
	Serine/threonine phosphatase 6		Serine/threonine phosphatase 6	
	similar to SD27354p [Drosophila melanogaster]		similar to SD27354p [Drosophila melanogaster]	similar to SD27354p [Drosophila melanogaster]
	SNAP-25	SNAP-25		
	Sortilin-related receptor		Sortilin-related receptor	
	STMN3		STMN3	
	STX1A	STX1A		
	SUCLA2		SUCLA2	
	Synaptogyrin 3		Synaptogyrin 3	

		TYK2		TYK2	
		Ubiquitin-protein ligase E3-alpha		Ubiquitin-protein ligase E3-alpha	Ubiquitin-protein ligase E3-alpha
		VEGF nerve growth factor inducible protein		VEGF nerve growth factor inducible protein	
		X11beta	X11beta		
		Zinc finger protein 198		Zinc finger protein 198	
PSEN2-complex	PSEN2	18 kDa microsomal signal peptidase subunit		18 kDa microsomal signal peptidase subunit	
		200 kDa proteasome activator		200 kDa proteasome activator	
		ABCB11		ABCB11	
		Acetolactate synthase homolog		Acetolactate synthase homolog	
		Adrenoleukodystrophy protein		Adrenoleukodystrophy protein	
		Aph-1a	Aph-1a		
		ATM		ATM	
		ATP7A		ATP7A	
		ATP-binding cassette protein, sub-family B,		ATP-binding cassette protein, sub-family B,	

	member 1		member 1	
	ATP-dependent metalloprotease FtsH1 homolog		ATP-dependent metalloprotease FtsH1 homolog	
	BIG1		BIG1	
	BTAF1		BTAF1	
	Calcium-binding protein P22		Calcium-binding protein P22	
	Cation-chloride cotransporter-interacting protein		Cation-chloride cotransporter-interacting protein	
	CD97		CD97	
	CDM_HUMAN		CDM_HUMAN	CDM_HUMAN
	Centromere/kinetochore protein ZW10 homolog		Centromere/kinetochore protein ZW10 homolog	
	Cerebral protein 10		Cerebral protein 10	Cerebral protein 10
	CGI-13		CGI-13	CGI-13
	CGI-51		CGI-51	CGI-51
	cholinergic receptor, nicotinic, alpha polypeptide 3		cholinergic receptor, nicotinic, alpha polypeptide 3	

	CHRNA3		CHRNA3	
	DAAM1		DAAM1	
	DAPK1		DAPK1	
	DKFZp586c1924		DKFZp586c1924	DKFZp586c1924
	DOCK3	DOCK3		
	Down syndrome critical region protein 2		Down syndrome critical region protein 2	
	ECSIT		ECSIT	
	ensp00000297280 (hypothetical protein with p-loop)		ensp00000297280 (hypothetical protein with p-loop)	ensp00000297280 (hypothetical protein with p-loop)
	FACL1		FACL1	
	FLJ20342		FLJ20342	FLJ20342
	FLJ20420		FLJ20420	FLJ20420
	FLJ22555		FLJ22555	FLJ22555
	FLJ22678		FLJ22678	FLJ22678
	Galactosylgalactosylxyloprotein 3-beta-glucuronosyltransferase 3		Galactosylgalactosylxyloprotein 3-beta-glucuronosyltransferase 3	
	HTRA2		HTRA2	
	HU-K4		HU-K4	

	Hypothetical protein FLJ23356		Hypothetical protein FLJ23356	Hypothetical protein FLJ23356
	Hypothetical protein KIAA0455		Hypothetical protein KIAA0455	Hypothetical protein KIAA0455
	Hypothetical protein KIAA0971-I		Hypothetical protein KIAA0971-I	Hypothetical protein KIAA0971-I
	HYPOTHETICAL PROTEIN XP_174405.		HYPOTHETICAL PROTEIN XP_174405.	HYPOTHETICAL PROTEIN XP_174405.
	KIAA0062 (FRAGMENT)		KIAA0062 (FRAGMENT)	KIAA0062 (FRAGMENT)
	KIAA0090		KIAA0090	KIAA0090
	KIAA0103		KIAA0103	KIAA0103
	MGC4248		MGC4248	MGC4248
	MGC5442		MGC5442	MGC5442
	Nicastrin	Nicastrin		
	NICE-3		NICE-3	NICE-3
	NPC1		NPC1	
	NPD002		NPD002	
	NPL4, a component of the nuclear pore complex		NPL4, a component of the nuclear pore complex	NPL4, a component of the nuclear pore complex

		P63 protein		P63 protein	
		Presenilin 2	Presenilin 2		
		Prohibitin		Prohibitin	
		PSMA1		PSMA1	
		PSMA3		PSMA3	
		PSMA4		PSMA4	
		PSMA6		PSMA6	
		PSMB1		PSMB1	
		PSMB2		PSMB2	
		PSMB3		PSMB3	
		PSMB4		PSMB4	
		PSMB5		PSMB5	
		PSMB6		PSMB6	
		PSMC1		PSMC1	
		PSMC2		PSMC2	
		PSMC3		PSMC3	
		PSMC4		PSMC4	
		PSMC5		PSMC5	
		PSMC6		PSMC6	
		PSMD1		PSMD1	
		PSMD11		PSMD11	
		PSMD12		PSMD12	

	PSMD13		PSMD13	
	PSMD2		PSMD2	
	PSMD3		PSMD3	
	PSMD4		PSMD4	
	RPS6KA3		RPS6KA3	
	Serine/threonine phosphatase 6		Serine/threonine protein phosphatase 6	
	SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10.		SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10.	SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10.
	Sortilin 1		Sortilin 1	
	Stearoyl-CoA desaturase		Stearoyl-CoA desaturase	
	STRA6 isoform 1		STRA6 isoform 1	STRA6 isoform 1
	Tparl		Tparl	Tparl
	Ubiquitin-protein ligase EDD		Ubiquitin-protein ligase EDD	
	Voltage-dependent anion channel 2		Voltage-dependent anion channel 2	
	Wolframin		Wolframin	
Nicastrin-	Nicastrin		18 kDa microsomal	

complex	signal peptidase subunit		signal peptidase subunit	
	25 kDa microsomal signal peptidase subunit		25 kDa microsomal signal peptidase subunit	
	Aph-1a	Aph-1a		
	ATP-binding cassette, sub-family A, member 3		ATP-binding cassette, sub-family A, member 3	ATP-binding cassette, sub-family A, member 3
	BACE1	BACE1		
	BSCv protein (FRAGMENT)		BSCv protein (FRAGMENT)	
	CAMK4		CAMK4	
	Casein kinase II beta chain		Casein kinase II beta chain	
	Cathepsin B		Cathepsin B	
	CGI-13		CGI-13	CGI-13
	DCTN1		DCTN1	
	Delta-6 fatty acid desaturase		Delta-6 fatty acid desaturase	
	ENSG00000144840		ENSG00000144840	ENSG00000144840
	FACL3		FACL3	

	FACL4		FACL4	
	FLJ13977		FLJ13977	
	FLJ20342		FLJ20342	FLJ20342
	FLJ20481		FLJ20481	FLJ20481
	FLJ22390		FLJ22390	FLJ22390
	homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)		homolog of yeast golgi membrane protein yip1p (yip1p-interacting factor)	
	ICAM-2		ICAM-2	
	KIAA0095		KIAA0095	KIAA0095
	KIAA0922		KIAA0922	KIAA0922
	KIAA1181 (FRAGMENT)		KIAA1181 (FRAGMENT)	KIAA1181 (FRAGMENT)
	KIAA1533 (FRAGMENT)		KIAA1533 (FRAGMENT)	KIAA1533 (FRAGMENT)
	Mesenchymal stem cell protein DSCD75		Mesenchymal stem cell protein DSCD75	
	Neurotrypsin		Neurotrypsin	
	Nicastrin	Nicastrin		
	NICE-3		NICE-3	
	PAS domain containing		PAS domain containing	

	serine/threonine kinase		serine/threonine kinase	
	Pen-2	Pen-2		
	PP1, regulatory subunit 15B		PP1, regulatory subunit 15B	PP1, regulatory subunit 15B
	Presenilin-1	Presenilin-1		
	Presenilin-2	Presenilin-2		
	Protein amplified in osteosarcoma (OS-9)		Protein amplified in osteosarcoma (OS-9)	
	Protein similar to stromal cell-derived factor 2		Protein similar to stromal cell-derived factor 2	
	Protocadherin beta 8		Protocadherin beta 8	
	REP8 protein		REP8 protein	
	Retinal short-chain dehydrogenase/reductase retSDR2		Retinal short-chain dehydrogenase/reductase retSDR2	
	RING finger protein 5		RING finger protein 5	RING finger protein 5
	Stromal cell-derived factor 2-like 1		Stromal cell-derived factor 2-like 1	
	Thioredoxin domain-containing protein		Thioredoxin domain-containing protein	Thioredoxin domain-containing protein
	tyrosine phosphatase		tyrosine phosphatase	tyrosine phosphatase

Aph-1a-complex	Aph-1a	ensg000000149185		ensg000000149185	ensg000000149185
		18 kDa microsomal signal peptidase subunit		18 kDa microsomal signal peptidase subunit	
		23 kDa microsomal signal peptidase		23 kDa microsomal signal peptidase	
		25 kDa microsomal signal peptidase subunit		25 kDa microsomal signal peptidase subunit	
		ABCC1		ABCC1	ABCC1
		Acetolactate synthase homolog		Acetolactate synthase homolog	Acetolactate synthase homolog
		APLP2		APLP2	
		Aph-1a	Aph-1a		
		APP		APP	
		ATM		ATM	
		ATP1B1		ATP1B1	
		ATP2C1		ATP2C1	
		ATP-binding cassette, sub-family A member 3		ATP-binding cassette, sub-family A member 3	ATP-binding cassette, sub-family A member 3
		Brain-specific GTP-		Brain-specific GTP-	

	binding protein		binding protein	
	CDW92		CDW92	CDW92
	Cerebral protein-10		Cerebral protein-10	Cerebral protein-10
	CGI-13		CGI-13	CGI-13
	CNTNAP1		CNTNAP1	
	Dihydrofolate reductase		Dihydrofolate reductase	
	DNM1		DNM1	
	Endocytic receptor Endo180		Endocytic receptor Endo180	
	ENG		ENG	
	EXT2		EXT2	
	EXTL3		EXTL3	
	FLJ13660		FLJ13660	
	GPR49		GPR49	GPR49
	HK2		HK2	
	HU-K4		HU-K4	
	HUNC18a		HUNC18a	
	HYPOTHETICAL PROTEIN		HYPOTHETICAL PROTEIN	HYPOTHETICAL PROTEIN
	Hypothetical protein (Fragment)		Hypothetical protein (Fragment)	Hypothetical protein (Fragment)

	Hypothetical protein FLJ14562		Hypothetical protein FLJ14562	Hypothetical protein FLJ14562
	Hypothetical protein FLJ23630		Hypothetical protein FLJ23630	Hypothetical protein FLJ23630
	Hypothetical protein KIAA0372		Hypothetical protein KIAA0372	Hypothetical protein KIAA0372
	hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5		hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5	hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5
	hypothetical protein MGC22916		hypothetical protein MGC22916	hypothetical protein MGC22916
	ICAM2		ICAM2	
	IGF2R		IGF2R	
	Insulinoma-glucagonoma protein 20		Insulinoma- glucagonoma protein 20	
	Integral membrane protein 2B (ITM2B)		Integral membrane protein 2B (ITM2B)	
	integral membrane transporter protein		integral membrane transporter protein	integral membrane transporter protein
	ITPR1		ITPR1	

	KIAA0062 (FRAGMENT)		KIAA0062 (FRAGMENT)	KIAA0062 (FRAGMENT)
	KIAA0251 (FRAGMENT)		KIAA0251 (FRAGMENT)	KIAA0251 (FRAGMENT)
	KIAA0363 (FRAGMENT)		KIAA0363 (FRAGMENT)	KIAA0363 (FRAGMENT)
	KIAA0763		KIAA0763	KIAA0763
	KIAA0971		KIAA0971	KIAA0971
	KIAA1250		KIAA1250	KIAA1250
	LRP5		LRP5	
	Mesenchymal stem cell protein DSCD75		Mesenchymal stem cell protein DSCD75	Mesenchymal stem cell protein DSCD75
	MGC4248		MGC4248	MGC4248
	Neurotrypsin		Neurotrypsin	
	Nicastrin	Nicastrin		
	NRP2		NRP2	
	PCDHA10		PCDHA10	PCDHA10
	PCDHB12		PCDHB12	PCDHB12
	PCDHB13: protocadherin beta 13		PCDHB13: protocadherin beta 13	PCDHB13: protocadherin beta 13
	Pcdhb17		Pcdhb17	Pcdhb17

	PCDHB4		PCDHB4	PCDHB4
	PCDHGB1		PCDHGB1	PCDHGB1
	PCDHGB6		PCDHGB6	PCDHGB6
	Pen-2	Pen-2		
	PMPCB		PMPCB	
	PP2C gamma		PP2C gamma	
	Presenilin 1	Presenilin 1		
	Presenilin 2	Presenilin 2		
	Protocadherin 7		Protocadherin 7	Protocadherin 7
	Protocadherin beta 16		Protocadherin beta 16	Protocadherin beta 16
	Protocadherin beta 8		Protocadherin beta 8	Protocadherin beta 8
	RAB-18		RAB-18	
	Rab3 GTPase-activating protein, non-catalytic subunit		Rab3 GTPase-activating protein, non-catalytic subunit	
	Retinal short-chain dehydrogenase/reductase retSDR2		Retinal short-chain dehydrogenase/reductase retSDR2	Retinal short-chain dehydrogenase/reductase retSDR2
	RNASEL		RNASEL	
	Sideroflexin 1		Sideroflexin 1	
	Signal transducer and		Signal transducer and	

	activator of transcription-1	activator of transcription-1	
	Similar to CGI-135 protein	Similar to CGI-135 protein	Similar to CGI-135 protein
	SMAP-1B	SMAP-1B	
	SPTLC2	SPTLC2	
	Sterile alpha and HEAT/Armadillo motif protein	Sterile alpha and HEAT/Armadillo motif protein	Sterile alpha and HEAT/Armadillo motif protein
	Sterol O-acyltransferase 1	Sterol O-acyltransferase 1	
	STMN3	STMN3	
	tegt: testis enhanced gene transcript (bax inhibitor 1)	tegt: testis enhanced gene transcript (bax inhibitor 1)	tegt: testis enhanced gene transcript (bax inhibitor 1)
	Thioredoxin domain-containing protein	Thioredoxin domain-containing protein	Thioredoxin domain-containing protein
	Triple functional domain protein (PTPRF interacting)	Triple functional domain protein (PTPRF interacting)	
	UNC5C	UNC5C	

		Vacuolar ATP synthase membrane sector associated protein m8-9		Vacuolar ATP synthase membrane sector associated protein m8-9	Vacuolar ATP synthase membrane sector associated protein m8-9
		vacuolar protein sorting protein 18		vacuolar protein sorting protein 18	
		Y391_HUMAN		Y391_HUMAN	Y391_HUMAN
Pen-2- complex	Pen-2	Alpha-2 catenin		Alpha-2 catenin	
		Aph-1a	Aph-1a		
		COPINE FAMILY MEMBER.		COPINE FAMILY MEMBER.	COPINE FAMILY MEMBER.
		Copine III		Copine III	
		Dachshund 2		Dachshund 2	
		Delta-1 catenin		Delta-1 catenin	
		KIAA1102 (Fragment)		KIAA1102 (Fragment)	KIAA1102 (Fragment)
		MGC2803		MGC2803	MGC2803
		Nicastrin	Nicastrin		
		Pen-2	Pen-2		
		Presenilin 1	Presenilin 1		
		Presenilin 2		Presenilin 2	

		TNRC15		TNRC15	TNRC15
		TPST1		TPST1	
		ZIP kinase		ZIP kinase	
APP695SW-complex	APP695SW	APP695SW	APP695SW		
		Fe65	Fe65		
		Fe65L1	Fe65L1		
		FLJ10773		FLJ10773	FLJ10773
		GTF2I		GTF2I	
		IL13RA2		IL13RA2	
		Integral membrane protein 2B (ITM2B)		Integral membrane protein 2B (ITM2B)	
		Integral membrane transporter protein		Integral membrane transporter protein	
		JIP-1	JIP-1		
		S-100 alpha		S-100 alpha	
		X11beta	X11beta		
APP-C99-complex	APP-C99	APP		APP	
		APP-C99	APP-C99		
		CAMK2D		CAMK2D	
		Delta-like homolog		Delta-like homolog	

	Fe65	Fe65		
	Fe65L1	Fe65L1		
	Integral membrane transporter protein		Integral membrane transporter protein	
	KIAA1102 (Fragment)		KIAA1102 (Fragment)	KIAA1102 (Fragment)
	KIAA1949		KIAA1949	KIAA1949
	MGC4022		MGC4022	MGC4022
	MGC5442		MGC5442	MGC5442
	NAP-1 related protein		NAP-1 related protein	
	Neurocalcin delta		Neurocalcin delta	
	REST corepressor		REST corepressor	
	S-100 alpha		S-100 alpha	
	S-100 beta		S-100 beta	
	X11beta		X11beta	
Tau-complex	Tau	14-3-3 protein zeta/delta	14-3-3 protein zeta/delta	
		Actin	Actin	
		Alpha tubulin	Alpha tubulin	
		Beta tubulin	Beta tubulin	
	Deoxyhypusine synthase		Deoxyhypusine synthase	
	Dynactin 2		Dynactin 2	

	MEP50		MEP50	MEP50
	Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1		Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1	
	PPP2CA (PP2A, catalytic subunit, alpha)	PPP2CA (PP2A, catalytic subunit, alpha)		
	PPP2CB (PP2A, catalytic subunit, beta)	PPP2CB (PP2A, catalytic subunit, beta)		
	PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)	PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)		
	PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)	PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)		
	S-100 beta		S-100 beta	
	Tau	Tau		

TABLE 2

INDIVIDUAL PROTEINS OF THE COMPLEXES

Protein name	SEQ ID	IPI number	Molecular weight
14-3-3 protein epsilon	1	IPI00000816.1	29174
14-3-3 protein beta/alpha	2	IPI00216318.1	28082
14-3-3 protein eta	3	IPI00216319.1	28219
14-3-3 protein gamma	4	IPI00220642.1	28303
14-3-3 protein tau	5	IPI00018146.1	27764
14-3-3 protein zeta/delta	6	IPI00021263.1	27745
18 kDa microsomal signal peptidase subunit	100	IPI00104128.1	20625
200 kDa proteasome activator	101	IPI00005260.1	206407
23 kDa microsomal signal peptidase	221	IPI00030262.2	20253
25 kDa microsomal signal peptidase subunit	185	IPI00014148.1	25003
ABCB11	102	IPI00030011.1	146393
ABCC1	222	IPI00008338.1	164941
Acetolactate synthase homolog	107	IPI00009963.2	67868
Actin	305	IPI00021439.1	41737
ADAMTS-19	25	IPI00152639.1	134062
Adrenoleukodystrophy protein	108	IPI00017637.1	82909
Alpha tubulin	306	IPI00142632.1	50152

Alpha-2 catenin	280	IP100030907.1	105282
Aph-1a	109	IP100059964.1	28996
APLP1	7	IP100020012.1	72176
APLP2	8	IP100031030.1	86956
APP	9	IP100006608.1	86943
APP695SW	290	CZB000000007.1	78630
APP-C99	10	CZB000000004.1	11277.9
ATM	103	IP100012732.1	350644
ATP1B1	223	IP100006484.1	35061
ATP2C1	224	IP100024344.1	100576
ATP7A	106	IP100028610.1	163335
ATP-binding cassette protein, sub-family B, member 1	104	IP100027481.1	141463
ATP-binding cassette, sub-family A member 3	186	IP100017800.1	191388
ATP-binding cassette, sub-family B, member 7	11	IP100023879.1	82641
ATP-dependent metalloprotease FisH1 homolog	105	IP100045946.1	86503
Axonemal dynein heavy chain 8	26	IP100014845.4	516063
BACE1	187	IP100011518.1	55764
BAT1	27	IP100218291.1	53243
Beta tubulin	307	IP100142634.1	49671

BIG1	110	IPI00002188.1	208709	-
Brain-specific GTP-binding protein	225	IPI00103530.1	63543	
BSCv protein (FRAGMENT)	188	IPI00031131.1	46480	
BTAf1	111	IPI00024802.1	206887	
C20orf11 (sim to a region of RANBPM)	28	IPI00016634.1	26749	
Cadherin EGF LAG seven-pass G-type receptor 2	30	IPI00015346.1	317453	
Calcium-binding protein P22	117	IPI00218924.1	22456	
Calsyntenin-1	31	IPI00007257.1	109793	
Calsyntenin-2	32	IPI00005491.1	107020	
Calsyntenin-3	33	IPI00156997.1	106098	
CAMK2D	297	IPI00013787.1	56297	
CAMK4	189	IPI00002921.1	51926	
Casein kinase II beta chain	190	IPI00010865.1	24942	
Cathepsin B	191	IPI00013478.1	37808	-
Cation-chloride cotransporter-interacting protein	118	IPI00024998.1	96171	
CD97	112	IPI00012052.1	91941	
CDM_HUMAN	113	IPI00019387.1	27860	
CDW92	226	IPI00005068.2	73296	
Centromere/kinetochore protein ZW10 homolog	119	IPI00011631.1	88829	
Cerebral protein 10	120	IPI00018730.1	52118	

CGB0_HUMAN	29	IP100032827.1	14585	-
CGI-13	114	IP100008847.1	52917	
CGI-51	115	IP100215921.1	57429	
cholinergic receptor, nicotinic, alpha polypeptide 3	183	IP100007259.1	55637	
Chondroitin sulfate proteoglycan 6	34	IP100023102.1	141542	
CHRNA3	116	IP100027751.1	57310	
Chromatin-specific transcription elongation factor FACT 140 kDa subunit	35	IP100026970.1	119914	
CNTNAP1	227	IP100219249.1	164756	
COPINE FAMILY MEMBER.	281	IP100173232.1	61891	
Copine III	282	IP100024403.1	60131	
DAAM1	121	IP100000705.1	124245	
Dachshund 2	283	IP100065787.1	65323	
DAPK1	122	IP100021250.1	160018	
DC6 protein	36	IP100024620.1	11529	
DCTN1	192	IP100011446.1	127404	
Delta-1 catenin	284	IP100015202.1	104958	
Delta-6 fatty acid desaturase	193	IP100003544.1	52259	
Delta-like homolog	298	IP100009191.1	41143	
Deoxyhypusine synthase	308	IP100026829.1	40971	
Dihydrofolate reductase	229	IP100030357.1	28844	
Dkfzp586c1924	37	IP100031064.1	21527	

DNM1	228	IP100012033.1	97407
DOCK3	123	IP100217985.1	233103
Down syndrome critical region protein 2	124	IP100030770.1	32854
Dynactin 2	309	IP100013802.2	44231
Dynein light chain 2A	38	IP100023551.1	10922
Dynein light chain-A	39	IP100007675.1	56627
ECP-51	12	IP100009104.1	51157
ECSIT	125	IP100106506.1	49148
ELAVL3	40	IP100031552.2	39547
Endocytic receptor Endo180	233	IP100005707.3	166655
ENG	230	IP100017567.1	70578
ENG00000168820 (hypothetical protein with p-loop)	41	IP100151716.2	30772
ENSG00000144840	194	IP100102897.1	26308
ensp00000297280 (hypothetical protein with p-loop)	184	IP100182852.1	130960
Eukaryotic translation initiation factor 4A, isoform	42	IP100025491.1	46154
EXT2	231	IP100004047.1	82255
EXTL3	232	IP100015135.1	104749
FACL1	126	IP100013161.1	78348
FACL3	195	IP100031397.1	80346
FACL4	196	IP100029737.1	79188

Fe65	13	IP100010843.1	77244	-
Fe65L1	292	IP100023841.1	81080	
Filamin, gamma	45	IP100165017.1	291151	
FLJ10773	291	IP100171198.1	52401	
FLJ13660	234	IP100100927.1	56921	
FLJ13910	43	IP100009707.1	43993	
FLJ13977	197	IP100025520.1	53482	
FLJ20342	127	IP100015713.1	65084	
FLJ20420	128	IP100015833.1	26152	
FLJ20481	198	IP100016418.1	47655	
FLJ22390	199	IP100009343.1	17098	
FLJ22555	129	IP100103303.1	32545	
FLJ22678	130	IP100217885.1	85495	
FRAP1	44	IP100031410.1	288892	
Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3	131	IP100014931.1	37062	
GAP-associated tyrosine phosphoprotein p62	14	IP100008575.1	48227	
GPR49	235	IP100021131.1	99998	
GTF2I	293	IP100054042.1	112416	
GTP-binding protein ERA	46	IP100026512.1	49098	
HADH2/ERAB (mitochondrial enzyme)	47	IP100017726.1	26923	

HDAC2	48	IP100023289.1	55325
HERC2 protein	49	IP100005826.1	527472
HK2	236	IP100005103.1	102368
homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)	219	IP100063544.1	33834
HSPC154	50	IP100107156.1	28202
HSPC245	51	IP100107104.1	26057
HTRA2	132	IP100001663.1	48841
HU-K4	133	IP100163951.1	48771
HU-K4	133	IP100163951.1	48771
Hunc18a	54	IP100046057.1	68736
HYPOTHETICAL PROTEIN	237	IP100164098.1	31105
Hypothetical protein (Fragment)	238	IP100161721.1	94945
HYPOTHETICAL PROTEIN FLJ10618	52	IP100018766.1	34095
Hypothetical protein FLJ10795	55	IP100024779.1	138430
HYPOTHETICAL PROTEIN FLJ12599.	53	IP100182757.1	102917
Hypothetical protein FLJ14562	239	IP100161141.1	67283
Hypothetical protein FLJ20397	56	IP100101654.1	26305
Hypothetical protein FLJ23356	135	IP100031005.1	40050
Hypothetical protein FLJ23630	240	IP100103520.1	73732
Hypothetical protein KIAA0372	241	IP100005634.1	175486

Hypothetical protein KIAA0455	136	IP100160410.1	82983
Hypothetical protein KIAA0971-l	137	IP100013735.1	81463
hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5	275	IP100012235.1	24899
hypothetical protein MGC13186	98	IP100031570.1	20713
hypothetical protein MGC22916	276	IP100172590.1	88020
HYPOTHETICAL PROTEIN XP_174405.	134	IP100159547.1	23035
ICAM-2	200	IP100009477.1	30653
IGF2R	242	IP100007226.1	274309
IKAP	57	IP100028877.1	150191
IL13RA2	294	IP100032199.1	44176
Insulinoma-glucagonoma protein 20	58	IP100103536.1	183267
Integral membrane protein 2B (ITM2B)	16	IP100031821.1	30338
Integral membrane transporter protein	277	IP100020093.1	31735
IP100104084.1	15	IP100104084.1	36759
ITPR1	243	IP100036162.1	313945
JIP-1	295	IP100023133.1	77524
KIAA0056	59	IP100000899.1	169718
KIAA0062 (FRAGMENT)	138	IP100014236.1	58417
KIAA0090	139	IP100160376.1	111759

KIAA0095	201	IP100005680.1	93488
KIAA0103	140	IP100014149.1	34833
KIAA0166	60	IP100001458.1	250749
KIAA0251 (FRAGMENT)	244	IP100010861.1	90027
KIAA0325 (FRAGMENT)	61	IP100141330.2	532367
KIAA0363 (FRAGMENT)	245	IP100004538.1	156999
KIAA0564	62	IP100158296.2	214824
KIAA0763	63	IP100006669.1	94914
KIAA0922	202	IP100021671.1	138688
KIAA0971	246	IP100007231.1	74536
KIAA1102 (Fragment)	285	IP100160387.1	121739
KIAA1181 (FRAGMENT)	203	IP100003635.1	36879
KIAA1250	247	IP100033429.1	197211
KIAA1533 (FRAGMENT)	204	IP100001841.1	72964
KIAA1949	299	IP100150950.1	67959
Krab box protein ensp00000302970	17	IP100154267.1	37912
Laminin, gamma 1	65	IP100003398.1	177607
LIB (leucine-rich repeat protein)	64	IP100057018.2	64414
LRP5	248	IP100024531.1	179173
MBIP	66	IP100009868.1	39236
MEGF7 (FRAGMENT)	67	IP100023954.2	175609
MEP50	310	IP100012202.1	36724

Mesenchymal stem cell protein DSCD75	205	IP100010292.1	23865	-
MGC2803	286	IP100031526.1	18419	
MGC4022	300	IP100010625.1	59797	
MGC4248	141	IP100031582.1	24274	
MGC5442	142	IP100027773.1	26261	
MT-ACT48	68	IP100032410.1	46355	
Myosin IXB	69	IP100003064.1	228624	
NAP-1 related protein	301	IP100155244.1	44159	
NEU1	70	IP100029817.1	45467	
Neurexin-1	73	IP100006314.1	161883	
Neurocalcin delta	302	IP100149712.1	22114	
Neurotrypsin	206	IP100011063.1	97012	
Nicastrin	147	IP100021983.1	78411	
NICE-3	143	IP100032413.1	28779	
NIPSNAP1	71	IP100021086.2	33310	
NIPSNAP2	72	IP100016077.1	33743	
NPC1	144	IP1000005107.1	142149	
NPD002	145	IP100152981.1	68760	
NPL4, a component of the nuclear pore complex	146	IP100001676.1	73788	
NRP2	249	IP100029693.1	104831	

Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1				311	IP100002922.2	55595
P63 protein				148	IP100141318.1	66022
Paladin				77	IP100161782.1	96754
PAS domain containing serine/threonine kinase				207	IP100141040.1	142859
PCDHA10				250	IP100001513.1	102875
PCDHB12				251	IP100001450.1	86770
PCDHB13: protocadherin beta 13				252	IP100001449.1	87552
Pcdhb17				258	IP100045942.1	64852
PCDHB4				253	IP100001429.1	87270
PCDHGB1				254	IP100003890.1	100360
PCDHGB6				255	IP100003897.1	101043
PDZ and LIM domain protein 1				74	IP100010414.2	36072
PDZ domain protein MAGI-3				18	IP100022491.1	111914
Pen-2				209	IP100020516.1	12029
Phosphoenolpyruvate carboxykinase 2 (mitochondrial)				78	IP100004383.1	70637
PILB				75	IP100032871.1	21468
PILT				76	IP100010544.2	60705
PMPCB				256	IP100025726.1	54168
PP1, regulatory subunit 15B				208	IP100045837.1	79125
PP2C gamma				257	IP100006167.1	59272

PPP2CA (PP2A, catalytic subunit, alpha)	312	IP100008380.1	35594
PPP2CB (PP2A, catalytic subunit, beta)	313	IP100003461.1	35575
PPP2R1A (PP2A, 65 KDA regulatory subunit A, alpha)	314	IP100025326.1	65092
PPP2RBA, (PP2A, 55 KDA regulatory subunit B, alpha)	19	IP100220836.1	55642
Presenilin-1	210	IP100026333.1	52163
Presenilin-2	172	IP100028485.1	50140
Procollagen C-endopeptidase enhancer	79	IP100014828.1	47972
Programmed cell death 10	80	IP100026997.1	24658
Prohibitin	173	IP100017334.1	29804
Protein amplified in osteosarcoma (OS-9)	211	IP100013268.1	75562
Protein similar to AGCP6688	81	IP100140709.1	14290
Protein similar to probable mitotic centromere associated kinesin	20	IP100088667.1	18400
Protein similar to stromal cell-derived factor 2	212	IP100034198.1	23026
Protocadherin 7	259	IP100001893.2	116105
Protocadherin beta 16	260	IP100016595.1	84936
Protocadherin beta 8	213	IP100009033.1	87624
PSMA1	149	IP100016832.1	29556
PSMA3	150	IP100016834.1	28302

PSMA4	151	IPI00016836.1	29484
PSMA6	152	IPI00029623.1	27399
PSMB1	153	IPI00025019.1	26489
PSMB2	154	IPI00028006.1	22836
PSMB3	155	IPI00028004.2	22949
PSMB4	156	IPI00000806.1	29192
PSMB5	157	IPI00219629.1	28480
PSMB6	158	IPI00000811.2	25358
PSMC1	159	IPI00011126.2	49185
PSMC2	160	IPI00021435.1	48634
PSMC3	161	IPI00018398.2	49204
PSMC4	162	IPI00020042.2	47366
PSMC5	163	IPI00023919.2	45626
PSMC6	164	IPI00021926.2	44173
PSMD1	165	IPI00015333.1	105866
PSMD11	166	IPI00105598.1	47464
PSMD12	167	IPI00003569.1	52904
PSMD13	168	IPI00003570.1	42945
PSMD2	169	IPI00012268.1	100200
PSMD3	170	IPI00011603.2	60978
PSMD4	171	IPI00022694.1	40737
RAB-18	261	IPI00014577.1	22977

Rab3 GTPase-activating protein, non-catalytic subunit	263	IP100018280.3	155985
RAB7L1	82	IP100024775.1	23155
RANBP1	83	IP100018856.1	23310
Reelin	85	IP100021018.1	388402
REP8 protein	214	IP100010353.1	30541
REST corepressor	303	IP100008531.1	53028
Retinal short-chain dehydrogenase/reductase retSDR2	216	IP100008260.1	32964
RING finger protein 5	215	IP100012608.1	19881
RNASEL	262	IP100015864.1	83533
RNB6	21	IP100008862.1	44792
RPGR-interacting protein 1	84	IP100044777.1	103123
RPS6KA3	174	IP100020898.1	83736
S-100 alpha	296	IP100010824.1	10415
S-100 beta	304	IP100220413.1	10713
SAP-62	22	IP100017341.2	49256
Serine/threonine protein phosphatase 6	90	IP100012970.1	35144
Sideroflexin 1	266	IP100009368.2	35619
Signal transducer and activator of transcription-1	267	IP100030781.1	87335
Similar to CGI-135 protein	268	IP100007052.1	16980

SIMILAR TO GAMMA INTERFERON INDUCIBLE GENE IP10.	175	IP100058185.3	95055
similar to SD27354p [Drosophila melanogaster]	99	IP100103057.1	13291
SMAP-1B	264	IP100072534.1	103077
SNAP-25	86	IP100010470.1	23315
Sortilin 1	177	IP100016022.1	92100
Sortilin-related receptor	91	IP100022608.1	248441
SPTLC2	265	IP100005751.1	62924
Stearoyl-CoA desaturase	178	IP100100476.1	41523
Sterile alpha and HEAT/Armadillo motif protein	269	IP100007919.1	75337
Sterol O-acyltransferase 1	270	IP100019898.1	64763
STMN3	87	IP100021199.2	21017
STRA6 isoform 1	176	IP100154566.1	73533
Stromal cell-derived factor 2-like 1	217	IP100106642.2	23511
STX1A	88	IP100003370.1	33023
SUCLA2	89	IP100021996.2	50331
Synaptogyrin 3	92	IP100013947.1	24555
Tau	315	IP100025499.1	45850
tegt: testis enhanced gene transcript (bax inhibitor 1)	278	IP100022748.2	26538
Thioredoxin domain-containing protein	218	IP100001028.1	32535

TNRC15	287	IP100160501.1	127290
Tpar1	179	IP100102213.1	34906
TPST1	288	IP100030106.1	42188
Transcription factor CP2	23	IP100037599.1	57256
Triple functional domain protein (PTPRF interacting)	271	IP100026676.1	324106
TYK2	93	IP100022353.1	133660
tyrosine phosphatase ensg00000149185	220	IP100102935.1	22844
Ubiquitin-protein ligase E3-alpha	94	IP100156938.1	83595
Ubiquitin-protein ligase EDD	180	IP100026320.1	309352
UNC5C	272	IP100021472.1	103102
Vacuolar ATP synthase membrane sector associated protein m8-9	273	IP100041030.1	39036
vacuolar protein sorting protein 18	279	IP100060946.1	64959
VGF nerve growth factor inducible protein	95	IP100019628.1	67287
Voltage-dependent anion channel 2	181	IP100019625.1	31595
Wolframin	182	IP100008711.1	100306
X11beta	96	IP100017817.1	82512
X11beta	96	IP100017817.1	82512
Y391_HUMAN	274	IP100004584.1	65486
Zinc finger protein 198	97	IP100032608.2	154911
Zinc finger protein 277	24	IP100220069.1	56818

ZIP kinase	289	IPI00015213.1	52536
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TABLE 3

BIOCHEMICAL ACTIVITIES OF THE COMPLEXES

Name of Complex	Biochemical activity
Fe65-complex	Regulator of APP processing and APP function
X11beta-complex	Regulator of APP processing and APP function
PSEN2-complex	Gamma-secretase complex
Nicastrin-complex	Gamma-secretase activity and assembly (trafficking)
Aph-1a-complex	Gamma-secretase activity and assembly (trafficking)
Pen-2-complex	Gamma-secretase activity and assembly (trafficking)
APP695SW-complex	Signalling activity (regulator of transcription)
APP-C99-complex	Signalling activity (regulator of transcription)
Tau-complex	Regulator of microtubules and vesicle transport along microtubules
APP695SW	Signalling activity (regulator of transcription)

TABLE 4

MEDICAL APPLICATIONS OF THE COMPLEXES

Complex	Medical application
Fe65-complex	neurodegenerative disease such as Alzheimer's disease; inflammatory diseases such as chronic inflammatory disorders, rheumatoid arthritis and inflammatory bowel disease; cancer such as prostate cancer and breast cancer and skin cancer
X11b-complex	neurodegenerative disease such as Alzheimer's disease; inflammatory conditions such as ulcerative colitis, Crohn's disease and arterosclerosis
PSEN2-complex	neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders
Nicastrin-complex	neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders
Aph-1a-complex	neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders
Pen-2-complex	neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders
APP695SW-complex	neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders
APP-C99-complex	neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders
Tau-complex	neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders

The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

Various publications are cited herein, the disclosures of which are incorporated by reference in their entireties.

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29. Jan. 2004

CLAIMS

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein, which first protein is selected from the group of proteins in table 1, fourth column of a given complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; and
 - (b) at least one second protein, which second protein is selected from the group of proteins in table 1, fifth column of said given complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said second protein, said variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
2. A protein complex comprising a first protein selected from the proteins listed in table 1, fourth column of a given complex or a homologue or variant thereof, or a functionally active fragment or functionally active derivative of said first protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said first protein under low stringency conditions, and at least one second protein selected from the group of proteins in table 1, fifth column of a given complex, or a variant or homologue thereof, or a functionally active fragment or a functionally active derivative of said second protein, the variant of said second protein being encoded by a nucleic acid that hybridizes to the nucleic acid of said second protein under low-stringency conditions, and wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm

DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

3. A protein complex comprising all proteins selected from the proteins in table 1, third column of a given complex or at least one protein being a homologue thereof, or a variant thereof or functionally active fragment or functionally active derivative of said protein, said variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low stringency conditions;
wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
4. A protein complex that comprises all proteins as listed in table 1, third column for a given complex or at least one protein being a homologue or a variant thereof, or a functionally active fragment or a functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins under low stringency conditions, except at least one protein of the proteins listed in table 5, third column, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C, with the proviso that the complex comprises at least one protein selected from table 1, fifth column of a given complex.

5. The complex of any of Claim 1 - 4 comprising at least one functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein.
6. The complex of Claim 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.
7. The complex of any of Claim 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of Claim 1 - 7 that is involved in at least one biochemical activity as stated in table 3.
9. A process for preparing a complex of any of Claim 1 - 8 and optionally the components thereof comprising the following steps:
expressing a protein of the complex, preferably a tagged protein, in a target cell, or a tissue or an organ, isolating the protein complex which is attached to the protein, preferably the tagged protein, and optionally disassociating the protein complex and isolating the individual complex members.
10. The process according to Claim 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of Claim 9 - 10 wherein the two tags are separated by a cleavage site for a protease.
12. Component of a protein complex obtainable by a process according to any of Claim 9 - 11.
13. Protein selected from the group of proteins in table 1, sixth column of a given complex or a homologue or a variant of thereof, or a functionally active fragment or a

functionally active derivative of said protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

14. Nucleic acid encoding a protein according to Claim 13.
15. Construct, preferably a vector construct, comprising
 - (a) a nucleic acid according to Claim 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or
 - (b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative thereof, or a homologue or a variant thereof, at least one of said proteins being selected from the first group of proteins according to Claim 1 (a) and at least one of said proteins, being selected from the second group of proteins according to Claim 1 (b) or
 - (c) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative thereof, or a homologue or a variant thereof, said proteins being selected from the proteins of complex (II) according to Claim 1.
16. Host cell, containing a vector comprising at least one nucleic acid of Claim 14 and /or a construct of Claim 15 or containing several vectors each comprising at least one nucleic acid encoding at least one protein selected from the first group of proteins according to Claim 1 (a) and at least one nucleic acid encoding at least one protein selected from the second group of proteins according to Claim 1 (b).
17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of

Claim 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody containing the binding domain thereof which binds to any of the proteins of the group of proteins according to Claim 13.

18. A kit comprising in one or more containers:

- (a) the complex of any of Claim 1 – 8 and/or the proteins of Claim 13 and/or
- (b) an antibody according to Claim 17 and/or
- (c) a nucleic acid encoding a protein of the complex of any of Claim 1 – 8 and/or a protein of Claim 13 and/or
- (d) cells expressing the complex of any of Claim 1 – 8 and/or a protein of Claim 13 and, optionally,
- (e) further components such as reagents, buffers and working instructions.

19. The kit according to Claim 18 for processing a substrate of a complex of any one of Claim 1 - 8.

20. The kit according to Claim 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as those as stated in column 2, table 4 of a given complex.

21. Array, preferably a microarray, in which at least a complex according to any of Claim 1 - 8 and/or at least one protein according to Claim 13 and/or at least one antibody according to Claim 17 is attached to a solid carrier.

22. A process for modifying a substrate of a complex of any one of Claim 1 - 8 comprising the step of bringing into contact a complex of any of Claim 1 - 8 with said substrate, such that said substrate is modified.

23. A pharmaceutical composition comprising the protein complex of any of Claim 1 - 8 and/or a protein according to Claim 13.

24. A pharmaceutical composition according to Claim 23 for the treatment of diseases and disorders, preferentially for diseases or disorders such as those as stated in column 2, table 4 of a given complex.
25. A method for screening for a molecule that binds to a complex of any one of Claim 1 - 8 and/or a protein of Claim 13, comprising the following steps:
- (a) exposing said complex or protein, or a cell or organism containing said complex or said protein, to one or more candidate molecules; and
 - (b) determining whether said candidate molecule is bound to the complex or protein.
26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of a complex of any one of Claim 1 - 8 comprising the steps of:
- (a) exposing said complex, or a cell or organism containing said complex to one or more candidate molecules; and
 - (b) determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent upon the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity, or composition of said complex.
27. The method of Claim 26, wherein the amount of said complex is determined.
28. The method of Claim 26, wherein the activity of said complex is determined.

29. The method of Claim 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
30. The method of Claim 26, wherein the amount of the individual protein components of said complex is determined.
31. The method of Claim 30, wherein said determining step comprises determining whether any of the proteins listed in table 1, third column of said complex, or a functionally active fragment or a functionally active derivative thereof, or a variant or a homologue thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low-stringency conditions, is present in the complex.
32. The method of any of Claim 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder, preferentially of a disease or disorder selected from the diseases or disorders such as those as stated in column 2, table 4 of a given complex.
33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of Claim 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as those as stated in column 2, table 4 of a given complex.
34. A method for the production of a pharmaceutical composition comprising carrying out the method of Claim 26 - 31 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, component disposition of, or intracellular localization of the complex of any one of the Claim 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene regulated by the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in a corresponding sample from a subject not having the disease or disorder or predisposition indicated the presence in the subject of the disease or disorder or predisposition in the subject.
36. The method of Claim 35, wherein the amount of said complex is determined.
37. The method of Claim 35, wherein the activity of said complex is determined.
38. The method of Claim 37, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
39. The method of Claim 35, wherein the amount of the individual protein components of said complex is determined.
40. The method of Claim 39, wherein said determining step comprises determining whether any of the proteins according to Claim 13 is present in the complex.
41. The complex of any one of Claim 1 - 8, or a protein of Claim 13 or an antibody or fragment thereof of Claim 17, for use in a method of diagnosing a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as those as stated in column 2, table 4 of a given complex.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity of, component composition of or intracellular localization of, the complex of any one of Claim 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, activity of, or protein composition of, said complex.
43. The method according to Claim 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.
44. The method according to Claim 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.
45. Complex of Claim 1 - 8 and/or a protein as listed in table 1, fifth column of said complex as a target for an active agent of a pharmaceutical, preferably a drug target, in the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as a neurodegenerative disease such as those as stated in column 2, table 4 of a given complex.

29. Jan. 2004

SEQUENCES**SEQID No:1**

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 YKVTQQRDSEMGQQSLLFQIDYPEIAEGIMPRHRFMSAYEQRIEPPDRRWQYLLMAAE
 PYETIAFKVPSREIDKAEGKFWTHWNRETQKFFLQFHFKMEKPPAPPSLPAGPPGVKR
 PPPPLMNGLP RPPLPESLPPPPGGGLPLPMPPTGPAPSGPPGPPQLPPPAPGVHPP
 APVVHPPASGVHPPAPGVHPPAPGVHPPAPGVHPPTSGVHPPAPGVHPPAPGVHPPA
 PGVHPPAPGVHPPAPGVHPPPSAGVHPQAPGVHPAAPAVHPQAPGVHPPAPGMHPQ
 APGVHPQPPGVHPSAPGVHPQPPGVHPSNPGVHPPTPMPPMLRPPLPSEGPGNIPPP
 PPTN

SEQID No:23

MAWALKLPLADEVIESGLVQDFDASLSGIGQELGAGAYSMSDVLALPIFKQEESLPPD
 NENKILPFQYVLCATSPAVKLHDETLTYLNQGQSYEIRMLDNRKLGELPEINGKLVKSIF
 RVVFHDRRLQYTEHQQLEGWRWNRPGDRILDIDIPMSVGIIDPRANPTQLNTVEFLWDP
 AKRTSVFIQVHCISTEFTMRKHGGEKGVFPFRVQIDTFKENENGEYTEHLHSASCQIKVFK
 PKGADRKQKTDREKMEK RTPHEKEKYQPSYETTILTECSPWPEITYVNNSPSPGFNSS
 HSSFSLGEGNGSPNHQPEPPPPVTDNLLPTTTPQEAQQWLHRNRFTFTRLFTNFSGA
 DLLKLTRDDVIQICGPADGIRLFNALKGRMVRPRLTIYVCQESLQLREQQQQQQQQQQK
 HEDGDSNGTFFVYHAIYLEELTAVELTEKIAQLFSISPCQISQIYKQGPTGIHVLISDEMIQ
 NFQEEACFILD TMKAETNDSYHILK

SEQID No:24

VWRKHYYVDGEFASSSVSTGATPPPTRPAALPFLFCRVMAASKTQGAVARMQEDRDGS

CSTVGGVGYGDSKDCILEPLSLPESPGGTTTLEGSPSVPCIFCEEHFPVAEQDKLLKHMI
 IEHKIVIADVCLVADFQRYILYWRKRFT EQPITDFCSVIRINSTAPFEEQENYFLLCDVLP
 DRILREELQKQRLREILEQQQQERNDTNFHGVCMFCNEEFLGNRSVILNHMAREHAFNI
 GLPDNIVNCNEFLCTLQKKLDNLQCLYCEKTFRDKNLTKDHMRKKQHRKINPKNREYDR
 FYVINYLELGKSWEEVQLEDDRELLDHQEDDWSDEEH PASAVCLFCEKQAETIEKLY
 VHMEDAHEFDLLKIKSELGLNFYQQVKLVNFIRRVHQCRCYGVCHVKFKSKADLRTHM
 EETKHTSLLPDRKTWDQLEYFYPTYENDTLLCTLSDESSEDLTAQEQNENVPIISEDTSKL
 YALKQSSILNQLLL

SEQID No:25

MRLTHICCCCLLYQLGFLSNGIVSELQFAPDREEWEVVPALWRREPVD PAGGSGGSA
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 EELESQELPRGSSGAAALSPGAPASWQPPPPPPPPPPPPPAQHAEPDGDEVLLRIPAF
 SRDLYLLLRRDGRFLAPRF AVEQRPNP GPGPTGAASAPQPPAPPDAGCFYTGA VLRHP
 GSLASFSTCGGGLMGFIQLNEDFIFIEPLNDTMAITGHPHRVYRQKRSMEEEKVTEKSAL
 HSHYCGIISDKGRPRSRKIAESGRGKRYSYKLPQEYNIETVVVADPAMVSYHGADAARR
 FILTILNMVFNLFQHKSLGVQVNLRVIKLILLHETPELYIGHHGEKMLESFCKWQHEEFG
 KKNDIHLEMSTNWGEDMTSVDAAILITRKDFCVHKDEPCDTVGIAYLSGMCSEKRKCIIA
 EDNGLNL AFTIAHEMGMHNMGINHDNDHPSCADGLHIMSGEWIKQNLGDVSWSRCSK
 EDLERFLRSKASNCLLQTNPQSVNSVMVPSKLPGMTYTADEQCQILFGPLASFCQEMQ
 HVICTGLWCKVEGEKECRTKLDPPMDGTDCDLGKWCKAGECTSRTSAPEHLAGEWSL
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 AYSVRTSSPKHILQWQAVLDEEKPCALFCSPVGKEQPILLSEKVM DGTSCGYQGLDICA
 NGRQCQKVGCDGLLGLSLAREDHCGVCNNGNGKSKKIKGDFNHTRGAGYVEVLVIPAGAR
 RIKVVEEKPAHSYLALRDAGKQSINSDWKIEHSGAFNLAGTTVHYVRRGLWEKISAKGP
 TTA PLHLLVLLFQDQNYGLHYEYTIPSDPLPENQSSKAPEPLFMWHTSWEDCDATCG
 GGERKTTVSCTKIMSKNISIVDNEKCKYLT KPEPQIRKCNEQPCQTRWMMTEWTPCSR
 TCGKGMQSRQVACTQQLSNGTLIRARERDCIGPKPASAQRCEGQDCMTVWEAGVWS
 EFSVKCGKGIRHRTVRCTNPRKKCVLSTRPREAEDCEDYSKCYVWRMGDWSKCSITC
 GKGMQSRVIQCMHKITGRHGNECFSSSEKPAAYRPCHLQPCNEKINVNTITSPRLAALTF
 KCLGDQWPVYCRVIREKNLCQDMRWYQRCCE TCRDFYAQKLQQKS

SEQID No:26

MMKLYIDNAAPDKLKGLCFFVRCRNDVAINVKTIQEEALFTVLDASKGLLNGIRDMLANI

FLPAVLATNNWGALNQSKQGESEKHIFTETINRYLSFLDGARISIEGTVKLKTIDNVNFSK
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 RMSAKFNYIIEQIKGPSCKAVINVLNVAHSLKLLKNWRDLARITDTANESKDNVRYLYTLE
 KVCQPLYNHDLVSMAGIQNLINAIIRMIHGVSRYNTSERMTSLFIKVTNQMTACKAYI
 TDGGLNHVWDQETPVVLKKIQDCIFLFKEYQASFHKTRKLISESSGEKSFEVSEMYIFGK
 FEAFCRLEKITEMITVVQTYSTLSNSTIEGIDIMAIKFRNIYQGVKKKQYDILDPRRTEFD
 TDFLDFMTKINGLEVQIQAFMNSSFGKILSSQQALQLLQRFQKLNIPCLGLEINHTIERILQ
 YYVAELDATKKASLYHSQKDDPPLARNMPPIAGKILWVRQLYRRISEPINYFFKNSDILSS
 PDGKAVIRQYNKISYVLVEFEVYHTAWIREISQLHYALQATLFVRHPETGKLLVNFDPKI
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 MTPKMKKVESVLRQGLTVLTVSSLTLESFFQEVELVLDMFNQLLKKISDLCMHIDTVLK
 EIAKTVLISLPESGATKVEDMLTLNETYTKEWADILNHKSKHVEEAVRELISIFEQIYEVKY
 TGKVGKQSEQRKHVVFGESETGEGENNDYEANIVNEFDTHDKEDEFKKECKEVFAFFSH
 QLLDSLQKATRLSLDTMKRRIFVARQVENMLIILYGRKQSEDIISFIKSEVHLAIPNVVMIP
 SLDDIQQAINRMIQLTLEVSRGVAHWGQQQIRPIKSVIPSPTTTDVTHQNTGKLLKKEER
 SFEEAIPARKLKNFYPGVAEHKDISKLVLSSSVNSLRKAAHEALQDFQKYKTLWTEDR
 DVKVKEFLANNPSLTEIRSEILHYATFEQEIDELKPIIVGALELHTEPMKLALSIEAKAWK
 MLLCRYLNEEYKKKMSYMAFINEYLKKLRSPIRDLDDVRFAMEALSCIRDNEIQMDMTL
 GPIEEAYAILNRFEVEVTKEESEAVDTLRYSFNKLQSKAVSVQEDLVQVQPKFKSNLLES
 VEVFREDVINFAEAYELEGPMPNIPPQEASNRLQIFQASFDDLWRKFVTYSSGEQLFG
 LPVTDYEVVHKLTRKELNLLQKLYGLYDTVMSSISGYEILWGDVDIEKINAELEFQNR
 RKLPLKGLKDWQAFDLKKRIDDFSESCPLLEMMTNKAMKQRHWDRISELTGTPFDVES
 DSFCLRNIMEAPLLKHKDDIEDICISAIKEKDIEAKLTQVIENWTNQNLISFAAFKKGKELL
 KGTESGEIITLMEDSLMVLGSLLSNRYNAPFKKNIQNWVYKLSTSSDIIEEWLVVQNLWV
 YLEAVFVGGDIKQLPQEAQRFNIDKSWIKIMQRAHENPNVINCCVGDETMGQLLPHL
 HEQLEVCQKSLTGYLEKKRLLFPRFFVSDPVLEILGQASDSHTIQPHLPAVSDNINEVT
 FHKADYDRIMAVISREGEKIVLDNSVMAKGPVEIWLLDLLKMQMSSLHNIIRSAFYQISDS
 GFQLLPFLSHFPAQVGLLGILQMLWTHDSEEALRNAKDDRKIMQVTNQKFLDILNTLISQT
 THDLSKFRVVKFETLITIHVHQRDIFDDLVKMHIKSPTDFEWLKQSRFYFKEDLDQTVVSI
 TDVDFIYQNEFLGCTDRLVITPLTDRCYITLAQALGMNMGGAPAGPAGTGKTETTKDMG
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 VLTARKERKKQFIFSDGDCVDLNPEFGIFLTMPNGYAGRQELPENLKIQFRTVAMMVPD
 RQIIMRVKLASCGFLENVILAQKFYVLYKLCEEQLTKQVHYDFGLRNILSVLRTLGSQKRA
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QIEGLINHPPWNLKLVQLYETSLVRHGLMTLGPSGSGKTTVITILMKAQTECGRPHREM
RMNPKAITAPQMFGRLDTATNDWTDGIFSTLWRKTLKAKKGENIFLILDGPVDAWIENL
NSVLDDNKTTLTANGDRIPMAPSCKLLFEVHNIE NASPATVSRMGMVYISSSALSWRPIL
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YEFYVTDYGDWEHWNKKLQPYYYPTDSIPEYSSILVPNVDNIRTNFLIDTIAKQHKAVLLT
GEQGTAKTVMVKAYLK KYDPEVQLSKSLNFSSATEPMMFQRTIESYVDKRIGSTYGPP
GGRKMTVFIDDINMPVINEWGDQITNEIVRQMMEMEGMYSLDKPGDFTTIVDVQLIAAMI
HPGGGRNDIPQRLKRQFTVFNCTLPSNASIDKIFGIIGCGYFDP CRSFKPQICEMIVNLVS
VGRVLWQWTKVKMLPTPSKFHYIFNLRDLSRIWQGM LTIKAE ECASIPTLLSLFKHECSR
VIADR FITPEDEQWFNAHLTRAVEENIGSDAASCILPEPYFVD FLREMPEPTGDEPEDSV
FEVPKIYELMP SFDFLAEKLQFYQRQFNEIIRGTSLDLVFFKDAMTHLIKISRIIRTSCGNA
LLVGVGSGSKQSL SRLASFIAGYQIFQITLRSYNVTNLTD DLKALYKVAGADGKGITFIF
TDSEIKDEAFLEYLNNLLSSGEISNLFARDEMDEITQGLISVMKRELPRHPPTFDNLYEYF
ISRSRKNLHVVL CFSPVGEKFRARSLKFPG LISGCTMDWFSRWPREALIAVASYFLSDY
NIVCSSEIKRQVVETMGLFHDMVSESCESYFQRYRRRAHVTPKSYLSFINGYKNIYAEK
VKFINEQAERMNIGLDK LMEASESVAKLSQDLAVKEKELAVASIKADEVLAEVTVSAQAS
AKIKNEVQEVKDKAQKIVDEIDSEKVKAESKLEAAKPALEEEAEALNTIKPNDIATVRKLA
KPPHLIMRIMDCV LLLFQKKIDPVTMDPEKSCCKPSWGESLKLMSATGFLWSLQQFPKD
TINEETVELLQPYFNMDDYTFESA KKVCGNVAGLLSWTLAMAIFYGINREVLPLKANLAK
QEGRLAVANAELGKAQALLDEKQAELDKVQAKFDAAMNEKMDLLNDADTCRKKMQAA
STLIDGLSGEKIRWTQQSKEFKAQINRLVGDILLCTGFLSYLGPFNQIFRNYLLKDQWEM
ELRARKIPFTENLNLISMLVDPPTIGEWGLQGLPGDDLSIQNGIIVTKATRYPLLIDPQTQG
KTIKSKEKENDLQVTSLNH KYFRTHLED SLSLGRPLLIEDIHEELDPALDNVLEKNFIKS
GTTFKVKVGDKECDIMDTFKLYITTKLPNPAFTPEINAKTSVIDFTVTMKGLENQLLRRVIL
TEKQELEAERVK LLEDVTFNKRKMKELEDNLLYKLSATKGSLVDDES LIGVLRTTKQTAA
EVSEKLHVA AE TEIKINAAQEEFRPAATRGSILYFLITEMSMVNIMYQTS LAQFLKLF DQS
MARSEKSPLPQKRITNII EYLT YE VFTYSVRGLYENHKFLFVLLMTLKIDLQRGTVKHREF
QALIKGGAALDLKACPPKPYRWILDMTWLNLVELSKLPQFAEIMNQISRNEKGWKS WFD
KDAPEEEIIPDGYNDSLDTCHKLLLIRSWCPDRTVFQARKYIADSLEEKYTEPVILNLEKT
WEESDTRTP LICFLSMGSDPTNQIDALAKKLECRTISMGGGQEVHARKLIQMSMQQ
GGWVLLQNCHLGLEFMEELLETLITTEASDD SFRVWITTEPHDRFPITLLQTS LKFTNEP
PQGVRAGLKRTFAGINQD LLDISNLP MWKPM LYTVAFLHSTVQERRKFGPLGWNIPYEF
NSADFSASVQFIQNH LDECDIKKGVSWNTVRYMIGEVQYGGRVTD DFDKRL LNCFARV

WFSEKMFEPSFCFYTGKIPCKTLDQYFEYIQSLPSLDNPEVFGGLHPNADITYQSNTAS
 AVLETITNIQPKESGGGVGETREAIYRLSEDMLSKLPPDYIPHEVKSRLIKMGLNSMNI
 FLRQEIDRMQRVISILRSSLSDLKLAIEGTIIMSENLRDALDNMYDARIPQLWKRVSWDSS
 TLGFWFTELLERNAQFSTWIFEGRPNVFWMTGFFNPQGFLTAMRQEVTRAHKGWALD
 TVTIHNEVLRQTKEEITSPPGEGVYIYGLYMDGAAWDRRNGKLMESTPKVLFTQLPVLHI
 FAINSTAPKDPKLYVCPIYKKPRRTDLTFITVVYLRTVLSPDHWILRGVALLCDIK

SEQID No:27

YLCFPLLFLNPLLFTPCFHLFCENPSRSPPSPAGPVMAENDVDNELLDYEDDEVETA
 AGGDGAEAPAKKDVKGSYVSIHSSGFRDFLLKPELLRAIVDCGFEHPSEVQHECIPQAIL
 GMDVLCQAKSGMGKTAVFVLATLQQLEPVTGQVSVLVMCHTRELAFAQISKEYERFSKY
 MPNVKVAVFFGGLSIKKDEEVLLKKNCPHIVVGTPGRILALARNKSLNLKHIKHFILDEC DK
 MLEQLDMRRDVQEIFRMTPEHKQVMMFSATLSKEIRPVCRKFMQDPMEIFVDDDETCLT
 LHGLQQYYVKLKDNEKNRKLFDLLDVLEFNQVVIFVKSQRCIALAQLLVEQNFPAAIHR
 GMPQEERLSRYQQFKDFQRRILVATNLFGRGMDIERVNIAFNYPEDSDTYLHRVAR
 AGRFGTKGLAITFVSDENDAKILNDVQDRFEVNISELPDEIDISSYIEQTR

SEQID No:28

MSYAEKPDEITKDEWMEKLNHLHVQRADMNRLIMNYLVTEGFKEAAEKFRMESGIEPS
 VDLETLDERIKIREMILKGQIQEAIALINSLHPELLDTNRYLYFHLQQQHILIRQRETEAA
 LEFAQTQLAEQGEESRECLTEMERTLALLAFDSPEESPFGDLLHTMQRQKVWSEVNQA
 VLDYENRESTPKLAKLLKLLWAQNELDQKKVKYPKMTDLSKGVIEEPK

SEQID No:29

MAMQAAKRANIRLPPEVNRILYIRNLPYKITAEEMYDIFGKYGPIRQIRVGNTPETRGTA
 VVYEDIFDAKNACDHLSGFNVCNRYLVVLYYNANRAFAQKMDTKKKEEQLKLLKEYGIN
 TDPPK

SEQID No:30

MRSPATGVPLPTPPPPLLLLLLLLLPPPLLGDQVGPCRSLSRGRGSSGACAPMGWLC
 PSSASNLWLYTSRCRDAGTELTHGLVPHHDGLRVWCPESEAHPLPPAPEGCPWSCR
 LLGIGGHLSPQGKLTLP EEHPCLKAPRLRCQSCKLAQAPGLRAGERSPEESLGRRKR
 NVNTAPQFQPPSYQATVPENQAPAGTPVASLRAIDPDEGEAGRLEYTMDALFDSRSNQF
 FSLDPVTGAVTTAEELDRETKSTHVFRVTAQDHGMPRRSALATLTILVTDNDHDPVFE

QQEYKESLRENLEVGYEVLTVRATDGDAPPNANILYRLLEGSGGSPSEVFEIDPRSGVI
RTRGPVDREEVESYQLTVEASDQGRDPGPRSTTA AVFLSVEDDNDNAPQFSEKRYVV
QVREDVTPGAPVLRVTASDRDKGSNAV VHY SIMSGNARGQFYLDAQTGALDVVSPLDY
ETTKEYTLRVRAQDGGRPPLSNVSGLVTVQVLDINDNAPIFVSTPFQATVLESVPLGYLV
LHVQAIDADAGDNARLEYRLAGVGHDFPFTINNGTGWISVAAELDREEVDFYSFGVEAR
DHGTPALTASASVSVTVLDVNDNNPTFTQPEYTVRLNEDAAVGTSVVTVSAVDRDAHS
VITYQITSGNTRNRFSITSQSGGGLVSLALPLDYKLERQYVLAVTASDGTRQDTAQIVVN
VTDANTHRPVFQSSHYTVNVNEDRPAGTTVVLISATDEDTGENARITYFMEDSIPQFRID
ADTGAVTTQAELDYEDQVSYTLAITARDNGIPQKSDTTYLEILVNDVNDNAPQFLRDSYQ
GSVYEDVPPFTSVLQISATDRDSGLNGRVFYTFQGGDDGDGDFIVESTSGIVRTLRLRD
RENAQYVLRAYAVDKGMPPARTPMEVTVTVLDVNDNPPVFEQDEFDVFVEENSPIGL
AVARVTATDPDEGTNAQIMYQIVEGNIPEVFQLDIFSGELTALVDLDYEDRPEYVLVIQAT
SAPLVSRATVHVRLDRNDNPPVLGNFEILFN NYVTNRSSSFPGGAIGRVPAHDPDISD
SLTYSFERGNELSLVLLNASTGELKLSRALDNNRPLEAIMSVLVSDGVH SVTAQCALRVT
IITDEMLTHSITLRL EDMSPERFLSP LLGLFIQAVAATLATPPDHVVVFNVQRD TDAPGGH
ILNVSLSVGQPPGPGGGPPFLPSED LQERLYLNRSLT AISAQRVLPFDDNICLREPCEN
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PHGRCRSREGGYTCLCRDGYTGEHCEVSARSGRCTPGVCKNGGTCVNLLVGGFKCD
CPSGDFEKPYPYCVTTRSFP AHSFITFRGLRQRFHFTLALS FATKERDGLLLYNGRFNEK
HDFVALEVIQE QVQLTFSAGESTTTVSPFVPGGVSDGQWHTVQLKYYNKPLLGTGLP
QGPSEQKVAVVTVDGCDTGVALRFGSVLGNYSCAAQGTQGGSKKSLDLTG PLLLGGV
PDLPE SFPVRMRQFVGCMRN LQVDSRHIDMADFIANNGTVPGCPAKKNVCD SNTCHN
GGTCVNQWDAFSC ECPLGFGGKSCAQEMANPQHFLGSSLVAWHGLSLPISQPWYLSL
MFRTRQADGVLLQAITRGRSTITLQLREGHVMLSVEGTGLQASSLRLEPGRANDGDWH
HAQLALGASGGPGHAILSFDY GQQR AEGNLGPRLHGLHLSNITVGGIPGPAGGVARGF
RGCLQGVRVSDTPEGVNSLDPSHGESINVEQGCSLPDPCDSNPCPANSYCSNDWDSY
SCSCDPGY YGDNCTNVCDLNPCEHQSVCTRKPSAPHGYTCECPPNYLGPYCETRIDQ
PCPRGWWGHPTCGPCNCDVSKGFDPCNKTSGECHCKENHYRPPGSPTCLLCD CYP
TGSLSRVCDPEDGQCPCPKPGVIGRQC DRCDNPFAEVT TNGCEVNYDSCPRAIEAGIW
WPRTRFGLPAAAPCPKGSFGTAVRH CDEHRGWLPPNLFNCT SITFSELKGFAERLQRN
ESGLDSGRSQQ LALLLRNATQHTAGYFGSDVKVAYQLATRLLAHESTQRGFGLSATQD
VHFTENLLRVGSALLDTANKRHWELIQQT EGGTAWLLQH YEAYASALAQNMRHTYLS P
FTIVTPNIVISVVR LDKGNFAGAKLPRYEALRGEQPPDLETTVILPESVFRET PPVVRPAG
PGEAQEPEELARRQRRHPELSQGEAVASVIYRTL AGLLPHNYDPDKRSLRVPKRPIINT

PVVSISVHDDEELLPRALDKPVTVQFRLLLETEERTKPICVFWNHSILVSGTGGWSARGC
 EVVFRNESHVSCQCNHMTSFAVLMDVSRRENGEILPLKTLTYVALGVTLAALLTFFFLT
 LLRILRSNQHGIRRNLTAAALGLAQLVFLGGINQADLPFACTVIAILLHFLYLCTFSWALLEAL
 HLYRALTEVRDVNTGPMRFYYMLGWGVPAFITGLAVGLDPEGYGNPDFCWLSIYDTLI
 WSFAGPVAFVSMVFLYILAAARASCAAQRQGFEEKKGPVSGLQPSFAVLLLLSATWLLA
 LLSVNSDTLLFHLYFATCNCIQGPFIFLSYVVLKSKEVRKALKLACSRKPSDPALTTKSTL
 TSSYNCPSPYADGRLYQPYGDSAGSLHSTSRSGKSQPSYIPFLLREESALNPGQGPPG
 LGDPGSLFLEGQDQQHDPDSDSDLSLEDDQSGSYASTHSSDSEEEEEEEEEEEAFAF
 PGEQGWDSLLGPGAERLPLHSTPKDGGPGPGKAPWPGDFGTTAKESSGNGAPEERL
 RENGDALESREGSLGPLPGSSAQPHKGILKKKCLPTISEKSSLLRPLEQCTGSSRGSSA
 SEGSRGGPPPPRPPPRQSLQEQLNGVMPIAMSIKAGTVDEDSSGSEFLFFNFLH

SEQID No:31

MLRRPAPALAPAARLLLGLCGGGVWAARVKNHKPWLEPTYHGIVTENDNTVLLDPP
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 ELQKDYSFTIQAYDCGKGPDTGNVKKSHKATVHIQVNDVNEYAPVFKEKSYKATVIEGK
 QYDSILRVEAVDADCSPQFSQICSYEITPDVPFTVDKDGYYIKNTEKLNKGHEHQYKLTVT
 AYDCGKKRATEDVLVKISIKPTCTPGWQGWNNRIEYEPGTGALAVFPNIHLETCDPVA
 SVQATVELETSHIGKGCDRDTYSEKSLHRLCGAAAGTAELLPSPSGSLNWTMGLPTDN
 GHDSQQVFEEFNGTQAVRIPDGVVSVSPKEPFTISVWMRHGPFGGRKKETILCSSDKTDM
 NRHHYSLYVHGCRLIFLRQDPSEEKKYRPAEFHWKLNQVCDEEWHHYVLNVEFPSVT
 LYVDGTSHEPFSVTEDYPLHPSKIETQLVVGACWQEFSGVENDNETEPVTVASAGGDL
 HMTQFFRGNLAGLTLRSGKLADKKVIDCLYTCKEGLDLQVLEDSGRGVQIQAHPSQLVL
 TLEGEDLGELDKAMQHISYLNRSRQFPTPGIRRLKITSTIKCFNEATCISVPPVDGYVMVLQ
 PEEPKISLSGVHHFARAASEFESSEGVFLFPELRIISTITREVEPEGDGAEDPTVQESLVS
 EEIVHDLDTCEVTVEGEELNHEQESLEVDMARLQKKGIEVSSSELGMTFTGVDTMASY
 EEVLHLLRYRNWHARSLLDRKFKLICSELNGRYSISNEFKVEVNVIHTANPMEHANHMAA
 QPQFVHPEHRSFVDLSGHNLANPHPFVAVPSTATVVIVVCVSFLVFMILGVFRIRAAHR
 RTMRDQDTGKENEMDWDDSAITITVNPMEYEDQHSSEEEEEEEEEEESEDGEEEDD
 ITSAESESSEEEEGEQGDPQNATRQQQLEWDDSTLSY

SEQID No:32

MLPGRLCWVPLLLALGVGSGSGGGGDSRQRRLLAAKVNKHKPWIENTSYHGVITENNDT
 VILDPPPLVALDKDAPVPFAGEICAFKIHGQELPFEAVVLNKTSGEGRRLRAKSPIDCELOKE

YTFIIQAYDCGAGPHETAWKKSHKAVVHIQVKDVNEFAPTFKEPAYKAVVTEGKIYDSIL
 QVEAIDEDCSPQYSQICNYEIVTTDVPFAIDRNGNIRNTEKLSYDKQHQQYEILVTAYDCG
 QKPAAQDTLVQVDVKPVCKPGWQDWTKRIEYQPGSGSMPLFPSIHLETCDGAVSSLQI
 VTELQTNYYIGKGCDRETYSEKSLQKLCGASSGIIDLLPSPSAATNWTAGLLVDSSEMIFK
 FDGRQGAKIPDGIVPKNLTDQFTITMWMKHGSPSPGVRAEKETILCNSDKTEMNRHHYAL
 YVHNCRLVFLLRKDFDQADTFRPAEFHWKLDQICDKEWHYYVINVEFPVVTLYMDGAT
 YEPYLVTDWPIHPSHIAMQLTVGACWQGGGEVTKPQFAQFFHGSLSASLTIRPGKMESQ
 KVISCLQACKEGLDINSLES LGQGIKYHFNPSSQILVMEGDDIGNINRALQKVSYSINSRQF
 PTAGVRRLKVSSKVQCFCGEDVCISIPEVDAYVMVLQAIEPRITLRGTDHFWRPAAQFES
 ARGVTLFPDIKIVSTFAKTEAPGDVKTDDPKSEVLEEMLHNLD FCDILVIGGDLDPRQECL
 ELNHSELHQRHLDATNSTAGYSIYGVGSMSRYEQVLHHIRYRNWRPASLEARRFRIKC
 SELNGRYTSNEFNLEVSILHEDQVSDKEHVNHLIVQPPFLQSVHHPESSRIQHSSVVP
 SIATVVIISVCM LVFV VAMGVYRVRIAHQHFIQETEA AKESEMDWDD SALTITVNPMEKH
 EGP GHGEDETEGEEEEEEAEEEMSSSSSGSDDSEEEEEEEGMGRGRHGQNGARQAQL
 EWDDSTLPY

SEQID No:33

MTLLLLPLLLASLLASCSCNKANKHKPWIEAEYQGIVMENDNTVLLNPPLFALDKDAPLR
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 GANTKKSHKATVHVRVNDVNEFAPVFVERLYRAAVTEGKLYDRILVEAIDGDCSPQYS
 QICYYEILTPNTPFLIDNDGNIENTEKLQYSGERLYKFTVTAYDCGKKRAADDAEVEIQVK
 PTCKPSWQGWNKRIEYAPGAGSLALFP GIRLETCD EPLWNIQATIELQTSHVAKGCDRD
 NYSERALRKLCGAATGEVDLLPMPGPNANWTAGLSVHYSQDSSLIYWFNGTQAVQVP
 LGGPSGLGSGPQDLSLSDHFTLSFWMKHGVT PNKGKKEEETIVCNTVQNE DGF SHYSLT
 VHGCRIAFLYWPLLESARPVKFLWKLEQVCDDEWHHYALNLEFPTVTLYTDGISFDPALI
 HDNGLIHPPRRPALMIGACWTEEKNEKEKEKGDNSTDTTQGDPLSIHHYFHGYLAGFS
 VRSGRLESREVIECLYACREGLDYRDFESLGKGMKVHVNPSQSLLTLEGDDVETFNHA
 LQH VAYMNTLR FATPGVRPLRLTTAVKCFSEESCVSIPEVEGYVVVLQPDAPQILLSGTA
 HFARPAVD FEGTNGVPLFPDLQITCSISHQVEAKKDESWQGTVDTRMSDEIVHNL DG
 CEISLVGDDLDPERESLLLDTTSLQQRGLELTNTSAYLTIAGVESITVYEEILRQARYRLR
 HGAALYTRKFRLSCSEMNGRYSSNEFIVEVNVLHSMNRVAHPSHVLSSQQFLHRGHQP
 PPEMAGHSLASSHRNSMIPSAATLIIVVCVGFLVLMVVLGLVRIHSLHRRVSGAGGPPGA
 SSDPKDPDLFWDD SALTII VNP MESYQNRQSCVTGAVGGQ QEDEDSSDSEVADSPSS
 DERRIETPPHRY

SEQID No:34

MYIKQVIIQGFRSYRDQTIVDPFSSKHNIVVGRNGSGKSNFFYAIQFVLSDEFSHLRPEQ
 RLALLHEGTGPRVISAFVEIIFDNSDNRLPIDKEEVSLRRVIGAKKDQYFLDKKMVTKN DV
 MNLLESAGFSRSNPYYIVKQGKINQMATA PD SQRLKLLREVAGTRVYDERKEESISLMK
 ETEGKREKINELLKYIEERLHTLEEEKEELA QYQKWDKMRRALEYTIYNQELNETRAKLD
 ELSAKRETSGEKSRQLRDAQQDARDK MEDIERQVRELKTKISAMKEEKEQLSAERQEQ
 IKQRTKLELKAKDLQDELAGNSEQRKRLLKERQKLLKIEEKQKELAETEPKFNSVKEKE
 ERGIARLAQATQERTDLYAKQGRGSQFTSKEERDKWIKKELKSLDQAINDKKRQIAAIHK
 DLEDTEANKEKNLEQYNKLDQDLNEVKARVEELDRKYEYEVKNKKDELQSERNYLWREE
 NAEQQALA AKREDLEKKQQLLRAATGKAILNGIDSINKVLDHFRRKGINQHVQNGYHGIV
 MNNFECEPAFYTCVEVTAGNRLFYHIVDSDEVSTKILMEFNKMNLPGEVTFPLNKL DV
 RDTAYPETNDAIPMISKLRYNPRFDKAFKHVFGKTLICRSMEVSTQLARAFTMDCITLEG
 DQVSHRGALTGGYYDTRKSRLELQKDVRKAEELGELEAKLNENLRRNIERINNEIDQL
 MNQMQQIETQQRKFKASRDSILSEM KMLKEKRQQSEKTFMPKQRSLSLEASLHAME
 STRESLKAELGTDLLSQLSLEDQKRVDALNDEIRQLQQENRQLLNERIKLEGIITRVETYL
 NENLRKRLDQVEQELNELRETEGGTVLTATTSELEAINKRVKDTMARSEDLDNSIDKTE
 AGIKELQKSMERWKNMEKEHMDAINHDTKELEKMTNRQQGMLLKKKEECMKKIRELGS L
 PQEAFEKYQTL SLKQLFRKLEQCNT ELKKYSHVNKKALDQFVNFSEQKEKLIK RQEELD
 RGYKSIMELMNVLRLKYEAIQLTFKQVSKNFSEVFQKLVPGGKATLVMKKGDVEGSQS
 QDEGEGSGESERGSQS SVPSVDQFTGVGIRVSFTGKQGEMREMQQLSGGQKSLV
 ALALIFAIQKCDPAPFYLFDEIDQALDAQHRKAVSDMIMELAVHAQFITTTFRP ELLESAD
 KFYGVKFRNKVSHIDVITAEMAKDFVEDDTTHG

SEQID No:35

MAVTLDKDAYYRRVKRLYSNWRKGEDEYANVDAIVSVGVDEEIVYAKSTALQTWLFG
 YELTDTIMVFCDDKIIFMASKKKKVEFLKQIANTKGNENANGAPAITLLIREKNESNKSSFD
 KMIEAIKESKNGKKIGVFSKDKFPGEFMKSWNDCLNKEGFDKIDISAVVAYTIAVKEDGE
 LNLMKKAASITSEVFNKFFKERVMEIVDADEKVRHSLAESVEKAIEEKYLAGADPSTV
 EMCYPPIIQSGGNYNLKFSVVSDKNHMHFGAITCAMGIRFKSYCSNLVRTLMVDPSQEV
 QENYNFLLQLQEELLKELRHGVKICDVYNVMDVVKKQKPELLNKITKNLGF GMGIEFR
 EGSLVINSKNQYKLKKGMVFSINLGFSDLTNKEGKKPEEKTYALFIGDTVLVDEDGPATV
 LTSVKKKVKNVGIFLKNEDEEEEEEEKDEAEDLLGRGSRAALLTERTRNEMTAE EK RRA
 HQKELAAQLNEEAKRRLTEQKGEEQQIQKARKSNVSYKNPSLMPKEPHIR

EMKIYIDKKYETVIMPVFGIATPFHIATIKNISMVEGDYTYLRINFYCPGSALGRNEGNIF
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 DSLVINLNRSNPKLKDLYIRPNIAQKRMQGSLEAHVNGFRFTSVRGDKVDILYNNIKHAL
 FQPCDGEIIVLHFHLKNAIMFGKKRHTDVQFYTEVGEITTDLGKHQHMHDRDDLYAEQ
 MEREMRHKLKTAFKNFIEKVEALTKEELEFEVPFRDLGFNGAPYRSTCLLQPTSSALVN
 ATEWPPFVVTLDLEVELHFERVQFHLKNFDMVIVYKDYSKKVTMINAIPVASLDPIKEWLN
 SCDLKYTEGVQSLNWTKIMKTIVDDPEGFFEQQGWSFLEPEGEGSDAEEGDSESEIED
 ETFNPSEDDYEEEEEDSDEDYSSEAEESDYSKESLGSEESGKDWDELEEEARKADR
 ESRYYYYEEQSRSMSRKRKASVHSSGRGSRNRGSRHSSAPPKKKRK

SEQID No:36

MVVSKMNKDAQMRAAINQKLIETGERERLKELLRAKLIECGWKDQLKAHCKEVIKEKGL
 EHVTVDDLVAEITPKGRALVPDSVKKELLQRIRTFLAQHASL

SEQID No:37

MENHKSNNKENITIVDISRKINQLPEAERNLLENGSVYVGLNAALCGLIANSLFRRILNVT
 KARIAAGLPMAGIPFLTDLTYRCFVSFPLNTGDLDCECTITRSGLTGLVIGGLYPVFLAI
 PVNGGLAARYQSALLPHKGNILSYWIRTSKPVFRKMLFPILLQTMFSAYLGSEQYKLLIK
 ALQLSEPGKEIH

SEQID No:38

MAEVEETLKRLOQSQKGVQGIIVNTEGIPIKSTMDNPTTTQYASLMHSFILKARSTVRDID
 PQNDLTFLRIRSKKNEIMVAPDKDYFLIVIQNPTE

SEQID No:39

MAAVGRVGSFGSSPPGLSSTYTGGPLGNEIASGNNGGAAAGDDEDGQNLWSCILSEVS
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 CNVWILDGDLYHKGLLKFSLDVSLKDTLVMLVVDMSKPWTALDSLQKVASVREHVD
 KLKIPPEEMKQMEQKLIRDFQEYVEPGEDFPASPQRRNTASQEDKDDSVVPLGADTL
 THNLGIPVLVVCTKCDASVLEKEHDYRDEHFDFFQSHIRKFCLRYGAALIYTSVKENKNI
 DLVYKYIVQKLYGFPYKIPAVVVEKDAVFIPAGWDNDKKIGILHENFQTLKAEDNFEDIITK
 PPVRKFVHEKEIMAEDDQVFLMKLQSLAKQPPTAAGRPVDASPRVPGGSPRTPNRSV
 SSNVASVSPIPAGSKKIDPNMKAGATSEGVLANFFNSLLSKKTGSPGGPGVSGGSPAG
 GAGGGSSGLPPSTKKSGQKPVLDVHAELDRITRKPVTVSPTTPTSPTEGEAS

SEQID No:40

MVTQILGAMESQVGGGPAGPALPNGPLLGTNGATDDSKTNLIVNYLPQNMTQDEFKSL
 FGSIGDIESCKLVRDKITGQSLGYGFVNYSDPNDADKAINLNLGLKLTQTKTIKVSYPSS
 ASIRDANLYVSGLPKTMSQKEMEQLFSQYGRITSRILVDQVTGVSRRGVGFIRFDKRIEA
 EEAIKGLNGQKPLGAAEPITVKFANNPSQKTGQALLTHLYQSSARRYAGPLHHQTQRFR
 LDNLLNMAYGVKSPLSLIARFSPIDGMSGLAGVGLSGGAAGAGWCIFVYNLSPEADE
 SVLWQLFGPFGAVTNVKVIRDFTTNKCKGFGFVTMTNYDEAAMAIASLNGYRLGERVL
 QVSFKTSKQHKA

SEQID No:41

MVCTCVEGDNQFIVTEIPHVRQLISGDGVGECRAATEGRTLILEGLEKAERNVLPVLN
 NLENREMQLEDGRFLMSAERYDKLLRDHTKKELDSWKIVRVSENFRVIALGLPVPRYS
 GNPLDPPLRSRFQARDIYYLPFKDQLKLLYSIGANVSAEKVSQLLSFATTLCSQESSTLG
 LPDFPLDSLAAVQILDSFPMMPKHAIQWLYPYSILLGHEGKMAVEGVLRKFELQDSGS
 SLLPKEIVKVEKMMENHVSQASVTIRIADKEVTIK

SEQID No:42

MSASQDSRSRDNGPDGMEPEGVIESNWNEIVDSFDDMNLSESLLRGIYAYGFEEKPSAI
 QQRAILPCIKGYDVIAQAQSGTGKTATFAISILQQIELDLKATQALVLAPTRELAQQIQKV
 MALGDYMGASCHACIGGTNVRAEVQKLQMEAPHIIVGTPGRVFDMLNRRYLSPKYIKM
 FVLDEADEMLSRGFKDQIYDIFQKLNSNTQVVLLSATMPSDVLEVTKKFMRDPIRILVKK
 EELTLEGIRQFYINVEREEWKLDLTLCDLYETLTITQAVIFINTRRKVDWLTEKMHARDFTV
 SAMHGDMDQKERVIMREFRSGSSRVLITDLLARGIDVQQVSLVINYLPTNRENYIH
 RIGRGGFRGRKGVAINMVTEEDKRTLRIETFYNTSIEEMPLNVADLI

SEQID No:43

MDQCVTVERELEKVLHKFSGYGQLCERGLEELIDYTGGLKHEILQSHGQDAELSGTSL
 VLTQCCRIKDTVQKLASDHKDIHSSVSRVGKIDKNFDSDISSVGIDGCWQADSQRLL
 NEVMVEHFFRQGMLDVAEELCQESGLSVDPSQKEPFVELNRILEALKVRVLRPALEWA
 VSNREMLIAQNSSLEFKLHRLYFISLLMGTTNQREALQYAKNFQPFALNHQKDIQVLM
 GSLVYLRQGIENSPYVHLLDANQWADICDIFTRDACALLGLSVESPLSVSFSAGCVALPA
 LINIKAVIEQRQCTGVWNQKDELPIEVDLGKKCWYHSIFACPILRQQTDDNNPPMKLVCG
 HIISRDALNKMFGNSKLCPCPYCPMEQSPGDAKQIFF

SEQID No:44

MLGTGPAAATTAATTSSNVSVLQQFASGLKSRNEETRAKAAKELQHYYVTMELREMSQE
ESTRFYDQLNHHIFELVSSSDANERKGGILAIASLIGVEGGNATRIGRFANYLRNLLPSND
PVVMEMASKAIGRLAMAGDTFTAHEYVEFEVKRALEWLGAADRNEGRRHAAVLVLRELAI
SVPTFFFQQVQPPFDNIFVAVWDPKQAIREGAVAALRACLILTTQREPKEKMPQWYR
HTFEEAEKGFDETLAKEKGMNRDDRIHGALLILNELVRISSMEGERLREEMEEITQQQLV
HDKYCKDLMGFGTKPRHITPFTSFQAVQPQQSNALVGLLGYSSHQGLMGFGTSPSPAK
STLVESRCCRDLMEEKFDQVCQWVLKCRNSKNSLIQMTILNLLPRLAAFRPSAFTDTQY
LQDTMNHVLSVCVKEKERTAAFQALGLLSVAVRSEFKVYLPRVLDIIRAALPPKDFAHKR
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EFEGHSLTQFVRHCADHFLNSEHKEIRMEAARTCSRLLTPSIHLISGHAAHVVSQTAVQV
VADVLSKLLVVGITDPDPDIRYCVLASLDERFDAHLAQAE NLQALFVALNDQVFEIRELAI
CTVGR LSSMNP AFVMP ELRKMLIQILTELEHSGIGRIKEQSARMLGHLVSNAPRLIRPYM
EPILKALILKLKDPDPDPNPGVINNVLATIGELAQVSGLEMRKWVDELFIIMDMLQDSSLL
AKRQVALWTLGQLVASTGYVVEPYRKYPTLLEVLLNFLKTEQNQGTRREAIRVLGLLGA
LDPYKHKVNIGMIDQSRDASAVSLSESKSSQDSSDYSTSEMLVNMGNLPLDEFYPAVS
MVALMRIFRDQSLSHHHTMVVQAIFIFKSLGLKCVQFLPQVMPTFLNVIRVCDGAIREF
LFQQLGMLVSFVKSHIRPYMDEIVTLMREFWVMNTSIQSTIILLIEQIVVALGGEFKLYLPQ
LIPHMLRVFMHDNSPGRIVSIKLLAAIQLFGANLDDYLHLLLPPIVKLFDAPEAPLPSRCAA
LETVDRLTESLDFTDYASRIHPIVRTL DQSP ELRSTAMDTLSSLVFQLGKKYQIFIPMVNK
VLVRHRINHQR YDVLICRIVKGYTLADEEEDPLIYQHRMLRSGQG DALASGPVETGPMK
KLHVSTINLQKAWGAARRVSKDDWLEWLRRLSLELLKDSSSPSLRSCWALAQAYNPMA
RDLFNAAFVSCWSELNEDQQDELIRSIELALTSQDIAEVTQTLLNLAEFMEHSDKGPLPL
RDDNGIVLLGERAAKCRAYAKALHYKELEFQKGPTPAILESLISINNKLQQPEAAAGVLE
YAMKHFGELEIQATWYEKLHEWEDALVAYDKKMDTNKDDPELMLGRMRCLEALGEWG
QLHQQCCEKWTLVND ETQAKMARMAAAA WGLGQWDSMEEYTCMIPRDTHDGAFY
RAVLALHQDLFSLAQQCIDKARDLLDAELTAMAGESYSRAYGAMV SCHMLSELEEVIQY
KLVPERREIIRQIWWERLQGCQRIVEDWQKILMVRSLVSPHEDMRTWLKYASLCGKS
GRLALAHKTLVLLLGVDP SRQLDHPLPTVHPQVTYAYMKNMWKSARKIDAFQHMQH FV
QTMQQQAQHAIATEDQQHKQELHKLMARCFLKLGEWQLNLQGINESTIPKVLQYYSA
TEHDRSWYKAWHAWAVMNFEAVLHYKHQ NQARDEKKLRHASGANITNATTAATTA
TATTASTEGSNSESEAESTENSPTPSPLQKKVTE DLSKTLLMYT VPAVQGFFRSISLSR

GNNLQDTRLRVLTWFDYGHWPDVNEALVEGVKAIQIDTWLQVIPQLIARIDTPRPLVGRL
 IHQLLTDIGRYHPQALIYPLTVASKSTTTARHNAANKILKNMCEHSNTLVQQAMMVSEELI
 RVAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAY
 GRDLMEAEWCRKYMKSGNVKDLTQAWDLYYHVFRISKQLPQLTSLELQYVSPKLL
 MCRDLELAVPGTYDPNQPIIRIQSIAPSLQVITSKQRPRKLTLMGSNGHEFVLLKGHED
 LRQDERVMQLFGLVNTLLANDPTSLRKNLSIQRYAVIPLSTNSGLIGWVPHCDTLHALIR
 DYREKKKILLNIEHRIMLRMAPDYDHLTLMQKVEVFEHAVNNTAGDDLAKLLWLKSPSS
 EVWFDRRTNYTRSLAVMSMVGILGLGDRHPSNLMLDRLSGKILHIDFGDCFEVAMTR
 EKFPKIPFRLTRMLTNAMEVTGLDGNRYRITCHTVMVLEHREHKDSVMAVLEAFVYDPLL
 NWRLMDTNTKGNKRSRTRTDSYSAGQSVEILDGVELGEPAHKKTGTTVPESIHSGFIGD
 GLVKPEALNKKAIQIINRVRDKLTGRDFSHDDTLDVPTQVELLIKQATSHENLCQCYIGW
 CPFW

SEQID No:45

MMNNSGYSDAGLGLGDETDEMPSTEKDLAEDAPWKKIQQNTFTRWCNEHLKCVGKRL
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 DSKAIVDGNLKLILGLIWTILHYSISMPMWEDEDEDARKQTPKQRLLGWIQNKVPQLPI
 TNFNRDWQDGKALGALVDNCAPGLCPDWEAWDPNQPVENAREAMQQADDWLGVPO
 VIAPEEIVDPNVDEHSVMTYLSQFPKAKLKPGAPVRSKQLNPKKAIAYGPGIEPQGNTVL
 QPAHFTVQTVDAAGVGEVLVYIEDPEGHTEEAKVVPNNDKDRTYAVSYVPKVAGLHKVT
 VLFAGQNIERSPFENVGMALGDANKVSARGPGLEPVGNVANKPTYFDIYTAGAGTGD
 VAVVIVDPQGRRTVEVALEDKGDSTFRCTYRPAMEGPHTVHVAFAGAPITRSPFPVH
 VSEACNPACRASGRGLQPKGVRVKEVADFKVFTKGAGSGELKVTVKGPKGTEEPVK
 VREAGDGVFECEYYPVVPGKYVVTITWGGYAIPRSPFEVQVSPEAGVQKVRWGPGL
 ETGQVGKSADFVVEAIGTEVGTLGFSIEGPSQAKIECDDKGDGSCDVRYWPTEPGEYA
 VHVICDDEDIRDSPFIAHILPAPPDCFPDKVKAFGPGLEPTGCIVDKPAEFTIDARAAGKG
 DLKLYAQDADGCPIDIKVIPNGDGTFRCSYVPTKPIKHTIIISWGGVNVPKSPFRVNVGEG
 SHPERVKVYGPGVEKTGLKANETYFTVDCSEAGQGDVSGIKCAPGVVGPAAEADIDFD
 IIKNDNDTFTVKYTPPGAGRYTIMVLFANQEIPASPFHIKVDPSHDASKVKAEGPGLNRT
 GVEVGKPTHFTVLTGAGKAKLDVQFAGTAKGEVVRDFEIIDNHDYSYTVKYTAVQQG
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 QGQLDVRMTSPSRRPIPCKLEPGGGAEAAVRYMPPEEGPYKVDITYDGHPVPGSPF
 AVEGVLPPDPSKVCAYGPGLKGGLVGTPAPFSIDTKGAGTGGLGLTVEGPCAEKIECQ
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GEAATFTVDCSEAGEAELTIEILSDAGVKAEVLIHNNADGTYHITYSPAFFPGTYTITIKYGG
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 RVLNPSGAKTDTYVTDNGDGTYRVQYTAYEEGVHLVEVLYDEVAVPKSPFRVGVTEGC
 DPTRVRAFGPGLEGGLVNKANRFTVETRGAGTGGLGLAIEGPSEAKMSCKDNKDGSC
 TVEYIPFTPGDYDVNITFGGRPIPGSPFRVPVKDVDPGKVKCSGPGLGAGVRARVPQT
 FTVDCSQAGRAPLQVAVLGPTGVAEPVEVRDNGDGTHTVHYTPATDGPYTVAVKYAD
 QEVPRSPFKIKVLPAMDASKVRASGPGLNASGIPASLPVEFTIDARDAGEGLLTVQILED
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 VTVSIGGHGLGACLGPRIGQETVITVDAKAAGEGKVTCTVSTPDGAELDVDVVENHD
 GTFDIYYTAPEPGKYVITIRFGGEHIPNSPFHVLACDPLPHEEEPSEVPQLRQPYAPPRP
 GARPTHWATEEPVVPVEPMESMLRPFNLVIPFAVQKGELTGEVRMPSGKTARPNITDN
 KDGTITVRYAPTEKGLHQMGIKYDGNHIPSPLQFYVDAINSRRHVSAYGPGLSHGMVNK
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 PGSPFTAKITGDDSMRTSQLNVGTSTDVSLKITESDLSQLTASIRAPSGNEEPCLLKRLP
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 HVPGPSFTVKVTGEGRMKESITRRRQAPSIATIGSTCDLNLKIPGNWFQMVSQAERLTR
 TFTRSSHTYTRTERTEISKTRGGETKREVRVEESTQVGGDPFPAVFGDFLGRERLGSF
 GSITRQQEGEASSQDMTAQVTSPSGKVEAAEIVEGEDSAYSVRFPQEMGPHTVAVKY
 RGQHVPGSPFQFTVGPLGEGGAHKVRAGGTGLERGVAGVPAEFSIW TREAGAGGLSI
 AVEGPSKAEIAFEDRKDGSCGVSYVVQEPGDYEVSIFNDEHIPDSPFVVPVASLSDDA
 RRLTVTSLQETGLKVNQPASFAVQLNGARGVIDARVHTPSGAVEECYVSELDSDKHTIR
 FIPHENGVSIDVKFNGAHIPGSPFKIRVGEQSQAGDPGLVSAYGPGLEG GTTGVSSEFI
 VNTLNAGSGALSVTIDGPSKVQLDCRECPEGHVVYTPMAPGNYLIAIKYGGPQHIVGS
 PFKAKVTGPRLSGGHSLHETSTVLVETVTKSSSSRGSSSYSSIPKFSSDASKVVTRGPGL
 SQAFVGQKNSFTVDCSKAGTNMMMVGVHGPKTPCEEVYVKHMGNRVYNVYTVKEK
 GDYILIVKWGDESVPGPSPFKVKVP

SEQID No:46

RQAWHEVAAPSWRGARLVQSALRVWQVGPHVARERVIPFSSLLGFQRRCVSCVAGS
 AFSGPRLASASRSNGQGSALDHFLGFSQPDSSVTPCVPAVSMNRDEQDVLLVHHPDM
 PENSRLRVVLLGAPNAGKSTLSNQLLGRKVFPVSRKVHTTRCQALGVITEKETQVILLD
 TPGIISPGKQKRHHLELSLLEDPWKSMESADLVVVLVDVSDKWTRNQLSPQLLRCLTKY
 SQIPSVLVMNKVDCLKQKSVLLELTAALTEGVVNGKKLKMQRQAFHSHPGTHCPSPAVK

DPNTQSVGNPQRIGWPHFKEIFMLSALSQEDVKTLKQYLLTQAQPGPWEYHSAVLTSQ
TPEEICANIIREKLLLEHLPQEVYPYNVQOKTAVWEEGPGGELVIQOKLLVPKESYVKLLIGP
KGHVISQIAQEAGHDLMDIFLCDVDIRLSVKLLK

SEQID No:47

MAAACRSVKGLVAVITGGASGLGLATAERLVGQGASAVLLDLPNSGGEAQAKKLGNNC
VFAPADVTSEKDVQTALALAKGKFRVDVAVNCAGIAVASKTYNLKKGQTHLTLEDFORV
LDVNLMGTFNVIRLVAGEMGQNEPDQGGQRGVIINTASVAAFEGQVGOAAYSASKGGI
VGMTLPIARDLAPIGIRVMTIAPGLFGTPLLTSLPEKVCNFLASQVPFPSRLGDPAEY AHL
VQAIENPFLNGEVIRLDGAIRMQP

SEQID No:48

MAYSQGGGKKKVCYYYDGDIGNYYYGQGHMPKPHRIRMTHNLLLNYGLYRKMEIYRP
HKATAEEMTKYHSDEYIKFLRSIRPDNMSEYSKQMHIFNVGEDCPAFDGLFEFCQLSTG
GSVAGAVKLNRRQQTDMAVNWAGGLHHAKKYEASGFCYVNDIVLAILELLKYHQRVLYID
IDIHHGDGVVEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNFP MCDGID
DESYGQIFKPIISKVMEMYQPSAVVLQCGADSLSGDRLGCFNLTVKGHAKCVEVVKTFN
LPLLMLGGGGYTIRNVARCWTYETAVALDCEIPNELPYNDYFEYFGPDFKLHISPSNMT
NQNTPEYMEKIKQRLFENLRMLPHAPGVQMQAIPEDAVHEDSGDEDEDGEDPDKRISIRA
SDKRIACDEEFSDSEDEGE GRRNVADHKKGAKKARIEEDKKETEDKKTDVKEEDKSK
DNSGEKTDTKGTKSEQLSNP

SEQID No:49

MPSESFCLAAQARLDSKWLKTDIQLAFTRDGLCGLWNEMVKDGEIVYTGTTESTQNGEL
PPRKDDSVESGTTKKEDLNDKEKKDEEETPAPIYRAKSILDSWVWGKQPDVNELKECL
SVLVKEQQALAVQSATTTLSALRLKQRLVILERYFIALNRTVFQENVKVKWKSSGISLPP
VDKKSSRPAGKGVEGLARVGSRAALSFAFAFLRRWRSGEDADLCSELLQESLDALRA
LPEASLFDESTVSSVWLEVVERATRFLRSVVTGDVHGT PATKGP GSIP LQDQHLALAILL
ELAVQRGTL SQMLSAILLLLQLWDSGAQETDNERSAQGTSAPLLPLLQRFQSIICRKDAP
HSEGDMHLLSGPLSPNESFLRYLTLPQDNEL AIDL RQTAVVVM AHLDR LATPCMPPLCS
SPTSHKGS LQEVIGWGLIGWKYYANVIGPIQCEGLANLGV TQIACA EKRF LILSRNGRVY
TQAYNSDTLAPQLVQGLASRNIVKIAAHS DGHY LALAATGEVYSWGCGDGGRLGHGD
TVPLEEPKVISAFSGKQAGKHVVHIACGSTYSAAITAEGELYTWGRGNYGRLGHGSSSED
EAIPMLVAGLKGLKVIDVACGSGDAQTLAVTENGQVWSWGDGDY GKLGRGGSDGCKT

PKLIEKLQDL DVVKVRCGSQFSIALTKDGQVYSWGKGDNQRLGHGTEEHVRYPKLLEG
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 GIACGPAQSFAWSSCSEWSIGLRVPFVVDICSMTFEQLDLLLLRQVSEGMDGSADWPPP
 QEKECVAVATLNLRLQLHAAISHQVDPEFLGLGLGSILLNSLKQTVVTLASSAGVLSTV
 QSAAQAVLQSGWSVLLPTAEERARALSALLPCAVSGNEVNISPGRRFMIDLLVGSLMAD
 GGLESALHAAITAEIQDIEAKKEAQKEKEIDEQEANASTFHRSRTPLDKDLINTGICESSG
 KQCLPLVQLIQQLLRNIASQTVARLKDVARRISSCLDFEQHSRERSASLDWLLRFQRLLI
 SKLYPGESIGQTS DISSPELMGVGSLLKKYTALLCTHIGDILPVAASIASTSWRHFAEVAYI
 VEGDFTGVLLPELVVSIVLLLSKNADLMQEAGAVPLLGGLEHLDRFNHLAPGKERDDH
 EELAWPGIMESFFTQGNCRNNEEVT LIRKADLENHNKDGGFWTVIDGKVYDIKDFQTQS
 LTGNSILAQFAGEDPVVALEAALQFEDTRESMHAFVCVGYLEPDQEIVTIPDLGSLSSPLI
 DTERNLGLLLGLHASYLAMSTPLSPVEIECAKWLQSSIFSGGLQTSQIHYRYNEEKDED
 HCSSPGGTPASKSRLCSHRRALGDHSQAFLQAIADNNIQDHNVKDFLCQIERYCRQCH
 LTPIMFPPEHPVEEVGRLLLCCLLKHEDLGHVALSLVHAGALGIEQVKHRTLPKSVVDV
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 PRWRRIAQKIIRERRRKKRVPKKPESMDDEEKIGNEESDLEEACILPHSPINVDKRPIAICS
 PKDKWQPLLSTVTGVHKKYKWLKQNVQGLYPQSPLLSTIAEFALKEEPVDVEKMRKCLL
 KQLERA EVRLEGIDTILKLASKNFFLPSVQYAMFCGWQRLIPEGIDIGEPLTDCLKDVDLI
 PPFNRMLLEVTFGKLYAWAVQNIRNVLMDASATFKELGIQPVPLQTITNENPSGPSLGTI
 PQARFLLVMLSMLTLQHGANNDLLLLNSGMLALTQTALRLIGPSCDNVEEDMNASAQG
 ASATVLEETRKETAPVQLPVSGPELAAMMKIGTRVMRGVDWKWGDQDGPPLGLGRVI
 GELGEDGWIRVQWDTGSTNSYRMGKEGKYDLKLAELPAAQPSAEDSDTEDDSEAEQ
 TERNIHPTAMMFTSTINLLQTLCLSAGVHAEIMQSEATKTLCGLLRMLVESGTTDKTSSP
 NRLVYREQHRSWCTLG FVRSIALTPQVCGALSSPQWITLLMKVVEGHAPFTATSLQRQI
 LAVHLLQAVLP SWDKTERARDMKCLVEKLFDFLGSLLTTCSSDVPLLRESTLRRRRVRP
 QASLTATHSSTLAEV VALLRTLHSLTQWNGLINKYINSQLRSITHSFVGRPSEGAQLED
 YFPDSENPEVGGLMAVLAVIGGIDGRLRLGGQVMHDEFGEGETVTRITPKGKITVQFSDM
 RTCRV CPLNQLKPLPAVAFNVNLPFTEPMLS VWAQLVNLAGSKLEKHKIKKSTKQAF
 GQVDLDLLRCQQLKLYILKAGRALLSHQDKLRQILSQPAVQETGTVHTDDGAVVSPDLG
 DMSPEGPQPPMILLQQLLASATQPSPVKAIFDKQELEAAALAVCQCLAVESTHPSSPGF
 EDCSSSEATTPVAVQHIHPARVKRRKQSPVPALPIVVQLMEMGFSRRNIEFALKSLTGA
 SGNASSLP GVEALVGWLLDHSDIQVTELSADTVSDEYSDEEVVEDVDDAAYSMSTGA
 VVTESQTYKKRADFLSNDDYAVYVRENIQVGMVMVRCCRAYEEVCEGDVGKVIKLD RDG
 LHDLNVQCDWQQKGGTYWVRYIHVELIGYPPPSSSSHIKIGDKVRVKASVTT PKYKWG

SVTHQSVGVVKAFSANGKDIIVDFPQQSHWTGLLSEMELVPSIHPGVTCDCGCMFPING
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GMLLDSWSRMVKSLNVSSSVNQASRLIDGSEPCWQSSGSQGKHWIRLEIFPDVLVHRL
KMIVDPADSSYMPSLVVVSGGNSLNNLIELKTININPSDTTVPLLNDYTEYHRYIEIAIKQC
RSSGIDCKIHGLILLGRIRAEEDLAAVPFLASDNEEEDEKGNSSGLIRKKAAGLESAAT
IRTKVFWGLNDKDQLGGLKGSKIKVPSFSETLSALNVVQVAGGSKSLFAVTVEGKVYA
CGEATNGRLGLGISSGTVPIPRQITALSSYVVKVAVHSGGRHATALTVDGKVFWSWEGG
DDGKLGHFSRMNCDKPRLEALKTKRIRDIACGSSHSAALTSSGELYTWGLGEYGRGLGH
GDNTTQLKPKMKVLLGHRVIQVACGSRDAQTLALTDEGLVFSWGDGDFGKLGRGGS
EGCNIPQNIERLNGQGVQCIECGAQFSLALTKSGVWWTWGKGDYFRLGHGSDVHVRK
PQVVEGLRGKKIVHVAVGALHCLAVTDSGQVYAWGDNDHGQQGNGTTTNNRKPRTLQV
GLEGQKITRVACGSSHSVAWTTVDVATPSVHEPVLFQTARDPLGASYLGVPDADSSA
ASNKISGASNSKPNRPSLAKILLSLDGNLAKQQALSHILTALQIMYARDAVVGALMPAAMI
APVECPSFSSAAPSDASAMASPMNGEECMLAVDIEDRLSPNPWQEKREIVSSEDAVTP
SAVTPSAPSASARPFIPVTDDLGAASIIAETMTKTEDVESQNKAAAGPEPQALDEFTSLLI
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DGVNRIVSVRSGREWSDWSSELRI PGDELKWK FIDSGSVNGWGW RFTVYPIMPAAGP
KELLSDRCVLSCPSMDLVTCLLDFRLNLASNRSIVPRLAASLAACAQLSALAASHRMWA
LQRLRKLTTTEFGQSININRLLGENDGETRALSFTGSALAALVKGLPEALQRQFEYEDPI
VRGGKQLLHSPFFKVLVALACDLELDTLPCCAETHKWAWFRRYCMASRVAVALDKRTP
LPRLFLDEVAKKIRELMADSENMDVLHESHDIKFREQDEQLVQWMNRRPDWTL SAG
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TGYGAGGRLGIGGTESVSTPTLLESIQHVFIKKVAVNSGGKHCLALSSEGEVYSWGEAE
DGKLGHGHNRSPCRPRVIESLRGIEVVDVAAGGAHSACVTAAGDLYTWGKGGRYGRLG
HSDSEDQLKPKLVEALQGHRVVDIACGSGDAQTLCLTDDDTVWSWGDGDYGKLGRG
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HLSELFPCPCIPMFDLEGS LDETGLGPSVGFDTLRGILISQGKEAAFRKV VQATMVRDRQ
HGPVVELNRIQVKRSRSKGLAGPDGTSVFGQMCAKMSSFGPDSLLLPHRVWKVKF
VGESVDDCGGGYSESIAEICEELQNGLTPLLIVTPNGRDESGANRDCYLLSPAARAPVH
SSMFRFLGVLLGIAIRTGSPLSLNLAEPVWKQLAGMSLTIALDSEVDKDFIPGLMYIRDNE
ATSEEF EAMSLPFTVPSASGQDIQLSSKH THITLDNRAEYVRLAINYRLHEFDEQVA AVR

EGMARVVPVPLLSLFTGYELETMVCGSPDIPLHLLKSVATYKGIEPSASLIQWFWWEVME
SFSNTERSLFLRFVWGRTRLPRTIADFRGRDFVIQVLDKYNPPDHFLPESYTCFFLLKLP
RYSCKQVLEEKLKYAIHFCKSIDTDDYARIALTGEPAAADDSSDDSDNEDVDSFASDSTQ
DYLTGH

SEQID No:50

MICTFLRAVQYTEKLHRSSAKRLLLPYIVLNKACLKTEPSLRGGLQYQKKTLRPRCILGVT
QKTIWTQGPSRPAKEDGSKQVSVHRSQRGGTAVPTSQKVKEAGRDFTYLIVVLFGISI
TGGLFYTIFKELFSSSSPSKIYGRALEKCRSHPEVIGVFGESVKGYGEVTRRGRRQHV
FTEYVKDGLKHTCVKFYIEGSEPGKQGTVYAQVKENPGSGEYDFRYIFVEIESYPRRTIII
EDNRSQDD

SEQID No:51

MAATSGTDEPVSGELVSVAHALSIPAESYGNDPDIEMAWAMRAMQHAEVYYKLISVD
PQFLKLTKVDDQIYSEFRKNFETLRIDVLDPEELKSESACEKWRPFCLKFNGIVEDFNYG
TLLRLDCSQGYTEENTIFAPRIQFFAIEIARNREGYNKAVYISVQDKEGEKGVNNGGEKR
ADSGEEENTKNGGEKGADSGEEKEEGINREDKTDKGGEKGKEADKEINKSGEKAM

SEQID No:52

MSQRDTLVHLFAGGCGGTVGAILTCPLEVVKTRLQSSSVTLYISEVQLNTMAGASVNRV
VSPGPLHCLKVILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFDPDST
QVHMISAAMAGFTAITATNPWLKTRLQLDARNRGERRMGAFECVRKVYQTDGLKGFY
RGMSASYAGISETVIHFVIYESIKQKLLEYKTASTMENGEESVKEASDFVGMMLAAATSK
TCATTIAYPHVVRTLRREEGTKYRSFFQTLSSLVQEEGYGSLYRGLTTHLVRQIPNTAIM
MATYELVVYLLNG

SEQID No:53

MSQFKRQRINPLPGGRNFSGTASTSLLGPPPGLLTPPVATELSQNARHLQGGEKQRVF
TGIVTSLHDYFGVVDEEVFFQLSVVKGRLPQLGEKVLVKAAYNPGQAVPWNNAVKVQTL
SNQPLLKSPAPPLLHVAALGQKQGILGAQPQLIFQPHRIPPLFPQKPLSLFQTSHTLHLS
HLNRFPARGPHGRLDQGRSDDYDSKKRKQRAGGEPWGAKKPRHDLPPYRVHLTPYT
VDSPICDFLELQRRYRSLLVPSDFLSVHLSWLSAFPLSQPFSLHHPRIQVSSEKEAAPD
AGAEPITADSDPAYSSKVLILLSSPGLEELYRCCMLFVDDMAEPRETPEHPLKQIKFLLGR
KEEEAVLVGGEWSPSLDGLDPQADPQVLVRTAIRCAQAQTGIDLSGCTKWWRFAEFQ

YLQPGPPRRLQTVVVYLPDVWTIMPTLEEWELCQQKAAEAAPPTQEAQGETEPTTEQA
 PDALEQAADTSRRNAETPEATTQQETDLDPEAPPPLEPAVIARPGCVNLSLHGIVED
 RRPKERISFEAGVMVLAELFLEMLQRDFGYRVYKMLLSLPEKVVSPPEPEKEEAAKEEA
 TKEEEAIKEEVVKEPKDEAQNEGPATESEAPLKEDGLLPKPLSSGGEEEEKPRGEASED
 LCEMALDPELLLLRRDDGEEEFAGAKLEDSEVRSVASNQSEMEFSSLQDMPKELDPSAV
 LPLDCLLAFVFFDANWCGYLHRRDLERILLTLGIRLSAEQAKQLVSRVVTQNICQYRSLQ
 YSRQEGLDGGLPEEVLFGNLDLLPPPGKSTKPGAAPTEHKALVSHNGSLINVGSLLQRA
 EQQDSGRLYLENKIHTLELKLEESHNRFSATEVTNKTLLAEMQELRVRLAEAEETARTA
 ERQKSQQLRLLQELRRRLTPQLEIQRVVEKADSWVEKEEPAPSN

SEQID No:54

MAPIGLKAVVGEKIMHDVIKKVKKKGWVKVLVVDQLSMRMLSSCCKMTDIMTEGITIVED
 INKRREPLPSLEAVYLITPSEKSVHSLISDFKDPPTAKYRAAHVFFTDSCPDAFNLVKS
 RAAKVIKTLTEINIAFLPYESQVYSLDSADSFQSFYSPHKAQMKNPILERLAEQIATLCATL
 KEYPAVRYRGEYKDNALLAQLIQDKLDAYKADDPTMGEGPDKARSQLLILDRGFDPSPP
 VLHELTFQAMSYDLLPIENDVYKYETSGIGEARVKEVLLDEDDDLWIALRHKHIAEVSQE
 VTRSLKDFSSSKRMNTGEKTTMRDLSQMLKKMPQYQKELSKYSTHLHLAEDCMKHYYQ
 GTVDKLCRVEQDLAMGTDAEGEKIKDPMRAIVPILLDANVSTYDKIRIILLYIFLKNGITEE
 NLNKLQHAQIPPEDSEIITNMAHLGVPIVTDSTLRRRSKPERKERISEQTYQLSRWTPPIK
 DIMEDTIEDKLDTKHYPYISTRSSASFSTTAVSARYGHHKNKAPGEYRSGPRLIIFILGG
 VSLNEMRCAYEVTQANGKWEVLIGSTHILTPTKFLMDLRHPDFRESSRVSFEDQAPTM
 E

SEQID No:55

VAGVRPSSPHGLVGAVSVGGAGVMAVETLSPDWEFDRVDDGSQKIHAEVQLKNYGKF
 LEEYTSQLRRIEDALDDSIGDVWDFNLDPIALKLLPYEQSSLLELIK TENKVLNKVITVYAA
 LCCEIKKLKYEATKIFYNGLLFYGEGATDASMVEGDCQIQMGRFISFLQELSCFVTRCY
 EVVMNVVHQLAALYISNKIAPKIIETTGVHFQTMYEHLGELLTVLLTLDEIIDNHITLKDHW
 TMYKRLKSVHHNPSKFGIQEEKLPFEKFLKLEGQLLDGMIFQACIEQQFDSLNGGVS
 VSKNSTFAEEFAHSIRSIFANVEAKLGEPSEIDQRDKYVGICGLFVLHFQIFRTIDKKFYKS
 LLDICKKVPAILTANIIWFPDNFLIQIPAAAKLLDRKSLQAIIHRDFTLQQKAQSLTKDV
 QSYVVFVSSWMMKMESILSKEQRMDKFAEDLTNRCNVFIQGFLYAYSISTIIKTMTNLYM
 SMQKPMTKTSVKALCRLVELLKAIEHMFYRRSMVVADSVSHITQHLQHQAHSISVAKK
 RVISDKKYSEQRLDVLSALVLAENTLNGPSTKQRRILVSLALSVGTQMKTFKDEELFPLQ

VVMKKLDLISELRERVQTQCDCFLYWHRVFPYLDVYENAVDAARLHYMFSA LRDC
 VPAMMHARHLESYEILLDCYDKEIMEILNEHLLDKLCKEIEKDLRLSVHHLKLD DRNPFK
 VGMKDLALFFSLNPIRFFNRFIDIRAYVTHYLDKTFYNLTVALHDWATYSEMRNLATQR
 YGLVMTEAHLPSQTLEQGLDVLEIMRNIHIFVSRYLNLNNQIFIERTSNNKHLNTINIRHI
 ANSIRTHGTGIMNTTVNFTYQFLKKKFYIFSQFMYDEHIKSRLIKDIRFFREIKDQNDHKY
 PFDRAEFNRGIRKLGITPEGQSYLDQFRQLISQIGNAMGYVRMIRSGGLHCSSNAIRFV
 PDLEDIVNFEELVKEEGLAEETLKAARHLDSVLSDHTRNSAEGTEYFKMLVDVFAPEFR
 RPKNIHLRNFYIIVPPLTLNFVEHSISCKEKLNKKNKIGAAFTDDGFAMGVAYILKLLDQYR
 EFDSLHWFSVREKYLKEIRAVAKQQNVQSASQDEKLLQTMNLTQKRLDVYLQEFELL
 YFSLSSARIFFRADKTAAEENQEKKKEEETKTSNGDLSDSTVSADPVVK

SEQID No:56

MRLKLSILSTALLRATDTINSQGQFPSYLETVTKDILAPNLQWHAGRTAAAIRTA AVSCL
 WALTSSSEVLSAEQIRDVQETLMPQVLTLEEDSKMTRLISCRINTFLKTSGGMTDPEKLI
 KIYPELLKRLDDVSNDVRMAAASTLVTWLQCVKGANAKSYYQSSVQYLYRELLVHLDDP
 ERAIQDAILEVLKEGSGLPDLLVRETEAVIHKHRSATYCEQLLQHVQAVPATQ

SEQID No:57

MRNLKLFRTLEFRDIQGPGNPQCFSLRTEQGTVLIGSEHGLIEVDPVSREVKNESVSLVA
 EGFLPEDGSGRIVGVQDLLDQESVCVATASGDVILCSLSTQQLECVGSGVASGISVMSW
 SPDQELVLLATGQQTLIMMTKDFEPILEQQIHQDDFGESKFITVGWGRKETQFHGSEGR
 QAAFQMQMHESALPWDDHRPQVTWRGDGQFFAVSVVCPETGARKVRVWNREFALQ
 STSEPVAGLGPALAWKPSGSLIASTQDKPNQQDIVFFEKNGLLHGHFTLPFLKDEVKVN
 DLLWNADSSVLAVRLEDLQREKSSIPKTCVQLWTVGNYPHWYLYKQSLSFSTCGKSKIVSL
 MWDPVTPYRLHVLCCQGWHLAYDWHWTDRSVGDNSSDLSNVAIDGNRVLVTVFR
 QTVVPPPMCTYQLLFPHPVNQVTFLAHPQKSNDLAVLDASNQISVYKCGDCPSADPTV
 KLGAVGGSGFKVCLRTPHLEKRYKIQFENNEDQDVNPLKLGLLTWIEEDVFLAVSHSEF
 SPRSVIHHLTAASSEMDEEHGQLNVSSSAAVDGVIIISLCCNSKTKSVVLQLADGQIFKYL
 WESPSLAIKPWKNSSGGFPVRFYPCTQTELAMIGEEECVLGLTDRCRFFINDIEVASNIT
 SFAVYDEFLLLTTHSHTCQCFCRLDASFCTLQAGLSSNHVSHGEVLRKVERGSRIVTVV
 PQDTKLVLQMPRGNLEVHHRALVLAQIRKWLDKLMFKEAFECMRKLRLNLPYDHN
 KVFLGNVETFIKQIDSVNHINLFFTELKEEDVTKTMY PAPVTSSVYLSRDPDGNKIDLVCD
 AMRAVMESINPHKYCLSILTSHVKKTTPELEIVLQKVHELQGNAPSDPDVSAEEALKYL
 LHLVDVNELYDHSLGTYDFDLVLMVAEKSQKDPKEYLPFLNTLKKMETNYQRFTIDKYL

KRYEKAIGHLSKCGPEYFPECLNLIKDKNLYNEALKLYSPSSQQYQDISIAYGEHLMQEH
 MYEPAGLMFARCGAHEKALS AFLTCGNWKQALCVAAQLNFTKDQLVGLGRTLAKLV
 EQRKHIDAAMVLEESAQDYEEAVLLLLLEGAAWEEALRLVYKYNRLDIIETNVKPSILEAQ
 KNYMAFLDSQTATFSRHKKRLLVVRELKEQAQQAGLDDEVPHGQESDLFSETSSVVS
 SEMSGKYSHSNSRISARSSKNRRKAERKKHSLKEGSPLEDLALLEALSEVVQNTENLKD
 EVYHILKVLFLFEFDEQGRELQKAFEDTLQLMERSLPEIWTLTYYQQNSATPVLGPNSTAN
 SIMASYQQQKTSVPVLD AELFIPPKINRRTQWKLSLLD

SEQID No:58

MVQKKKFCPRLLDYLIVGARHPSSDSVAQTPELLRRYPLEDHTEFPLPPDVVFFCQPE
 GCLSVRQRRMSLRDDTSFVFTLTDKDTGVTRYGICVNFYRSFQKRISKGKGEGGAGSR
 GKEGTHATCASEEGGTESSESGSSLQPF SADSTPDVNQSPRGKRRAKAGSRSRNSTL
 TSLCVLSHYPFFSTFRECLYTLKRLVDCCSERLLGKKLGIPRGVQRDTMWRIFTGSLLE
 EKSSALLHDLREIEAWIYRLLRSPVPVSGQKRVDIEVLPQELQPALTFALPDPSRFTLVDF
 PLHLPLELLGVDACLQLLT CILLEHKVVLQSRDYNALSMSVMAFVAMIYPLEYMFVPIPL
 PTCMASAEQLLLAPTPYIIGVPASF FLYKLDFKMPDDVWLVDLDSNRVIAPTNAEVLPILP
 EPESLELKKHLKQALASMSLNTQPILNLEKFHEGQEIPLLLGRPSNDLQSTPSTEFNPLIY
 GNDADSVDVATRVAMVRRFFNSANVLQGFQMHTRTLRLFP RPVVAFAQGSFLASRPRQ
 TPFAEKLARTQAVEYFGEWILNPTNYAFQRIHNNMFDPALIGDKPKWYAHQLQPIHYRV
 YDSNSQLAEALSVPPERDSDSEPTDDSGSDSMDYDDSSSSYSSLGDFVSEMMKCDIN
 GDTPNVDPLTHAALGDASEVEIDELQNQKEAE EPGPDSENSQENPPLRSSSSTTASSS
 PSTVIHGANSEPADSTEMDDKAAVGVS KPLPSVPPSIGKSNVDRRQAEIGEGSVRRRIY
 DNPYFEPQYGFPP EDEDEQGESYTPRFSQHVS GNRAQKLLRPNSLRLASDSDAESD
 SRASSPNSTVSNTSTEGFGGIMSFASSLYRNHSTSFSLSNLTLPTKGAREKATPFPSLK
 VFGLNTLMEIVTEAGPGSGEGNRRALVDQKSSVIKHSPTVKREPPSPQGRSSNSSENQ
 QFLKEVVHSLVDGQGVGWLNMKKVRRLL ESEQLRVFVLSKLNRMVQSEDDARQDIIPD
 VEISRKVYKGMLDLLKCTVLSLEQSYAHAGLGGMASIFGLLEIAQTHYYSKEPDKRKRSP
 TESVNTPVGKDPGLAGRGDPKAMAQLRVPQLGPRAPSATGKGPKELDTRSLKEENFIA
 SIELWNKHQEVKKQKALEKQRPEVIKPVFDLGETEEKKSQISADSGVSLTSSSQRTDQD
 SVIGVSPAVMIRSSSQDSEVSTVVSNS SGETLGADSDLSSNAGDGP GGEGSVHLASSR
 GTLSDSEIETNSATSTIFGKAHSLKPCIKEKLAGSPIRTSEDVSQRVYLYEGLLGRDKGS
 MWDQLEDAAMETFSISKERSTLWDQM QFWEDAFLDAVMLEREGMGMDQGPQEMIDR
 YLSLGEHDRKRLEDDERLLATLLHNLISYMLLMKVNKNDIRKKVRRRLMGKSHIGLVYSQ
 QINEVLDQLANLNGRDLSIWSSGSRHMKKQTFVVHAGTDTNGDIFFMEVCDDCVVLR

NIGTVYERWWYEKLINMTYCPKTKVLCLWRRNGSETQLNKFYTKKCRELYYCVKDSME
 RAAARQQSIKPGPELGGEFPVQDLKTGEGGLLQVTLEGINLKFMHNQVFIELNHIKKCNT
 VRGVFVLEEFVPEIKEVVSHKYKTPMAHEICYSVLCLFSYVAAVHSSEEDLRTPPRPVSS

SEQID No:59

AAASRCPGIMVALRGLGSGLQPWCPDLRLLEWVDTVWELDFTETEPDPSIEAEIETGL
 AAFTKLYESLLPFATGEHGSMESIWTFFIENNVSHSTLVALFYHFVQIVHKKNVSVQYRE
 YGLHAAGLYFLLLEVPGSVANQVFHPVMFDKCIQTLKKSWPQESNLNRKRKKEQPKSS
 QANPGRHRKRKGKPPRRREDIEMDEIIIEQEEDENICFSARDLSQIRNAIFHLLKNFLRLLPKF
 SLKEKPQCVQNCIEVFVSLTNFEPVLHECHVTQARALNQAKYIPELAYYGLYLLCSPHIG
 EGDKVISCVFHQMLSVILMLEVGEGSHRAPLAVTSQVINCRNQAVQFISALVDELKESIF
 PVVRILLQHICAKVVDKSEYRTFAAQSLVQLLSKLPCEYAMFIAWLYKYSRSSKIPHRV
 FTLDVVLALLELPEREVDNTLSLEHQKFLKHKFLVQEIMFDRCLDKAPTVRSKALSSFAH
 CLELTVTSASESILELLINSPTFSVIESHPGTLLRNSSAFSYQRQTSNRSEPSGEINIDSSG
 ETVGSGGERCVMAMLRRRIRDEKTNVRKSALQVLVSILKHCDVSGMKEDLWILQDQCRD
 PAVSVRKQALQSLTELLMAQPRCVQIQKAWLRGVVPVMDCESTVQEKALEFLDQLLL
 QNIRHHSHFHSGDDSQVLAWALLTLTTESQELSRYLNKAFHWSKKEKFSPTFINNVIS
 HTGTEHSAPAWMLLSKIAGSSPRLDYSRIIQSWEKISSQQNPNSNTLGHILCVIGHIAKHL
 PKSTRDKVTDVAVKCKLNGFQWSLEVISSAVDALQRLCRASAETPAEEQELLTQVCGDV
 LSTCEHRLSNIVLKENG TGNMDEDLLVKYIFTLGDIACLCPARVEKRIFLLIQSVLASSAD
 ADHSPSSQGSSEAPASQPPPQVRGSMPSVIRAHAITLGKLCLQHEDLAKKSIPALVRE
 LEVCEDVAVRNNVIIVMCDLCIRYTIMVDKYIPNISMCLKDSDPFIRKQTLILLTNLLQEEFV
 KWKGSLFFRFVSTLIDSHPDIA SFGEFCLAHLLLKRNPVMFFQHFIECIFHFNNYEKHEKY
 NKFPQSEREKRLFSLKGKSNKERRMKIYKFLLEHFTDEQRFNITSKICLSILACFADGILPL
 DLDASELLSDTFEVLSSKEIKLLAMRSKPKDLLMEEDDMALANVVMQEAQKKLISQVQ
 KRNFIENIPIIISLKTVLEKNKIPALRELMHYLREVMQDYRDELKDFFAVDKQLASELEYD
 MKKYQEQLVQEQLAKHADVAGTAGGAEVAPVAQVALCLETVPVPAGQENPAMSPAV
 SQPCTPRASAGHVAVSSPTPETGPLQRLLPKARPMSTIAILNSVKKAVESKSRHRSR
 SLGVLPFTLNSGSPEKTCSQVSSYSLEQESNGEIEHVTKRAISTPEKSISDVTFGAGVSYI
 GTPRTPSSAKEKIEGRSQGNDILCLSLPDKPPPQPPQWNVRSPARNKDTPACSRRLR
 KTPLKTAN

SEQID No:60

MWNDIELLTNDDTGSGYLSVGSRKHEGTALYQVDLLVKISSEKASLNPKIQACSLSDGFI

IVADQSVILLDSICRSLQLHLVFDTEVDVVGLCQEGKFLLVGERSGNLHLIHVTSKQTLLT
 NAFVQKANDENRRTYQNLVIEKDGSNEGTYMMLLTYSGFFCITNLQLLKIQQAIENVDF
 STAKKLQGQIKSSFISTENYHTLGCLSLVAGDLASEVPVIIGGTGNCAFSKWEPDSSKKG
 MTVKNLIDAEIIGAKKFQLIDNLLFVLDTDNVLSLWDIYTLTPVWNWPSLHVVEEFLLTTE
 ADSPSSVTWQGITNLKLIALTASANKKMKNLMVYSLPTMEILYSLEVSSVSSLVQTGISTD
 TIYLLEGVCKNDPKLSEDSVSVLVLRCLTEALPENRLSRLLHKHRFAEAESEFAIQFGLDV
 ELVYKVKS NHILEKLALSSVDASEQTEWQQLVDDAKENLHKIQDDEFV VNYCLKAQWIT
 YETTQEMLNYAKTRLLKKEDKTALIYSDGLKEVLRAHAKLTTFYGAFGPEKFSGSSWIEF
 LNNEDDLKDIFLQLKEGNLVCAQYLWLRHRANFESRFDVKMLESLLNSMSASVSLQKLC
 PWFKNDVIPFVRRTVPEGQIILAKWLEQAARNLELTDKANWPENGLQLAEIFFTAECTDE
 LGLASSWHWISLKDYQNTTEVCQLRTLNNLRELITLHRKY NCKLALSDFEKENTTTIVF
 RMFDKVLAPELIPSILEKFIRVYMREHDLQEEELLLLYIEDLLNRCSSKSTSLFETAWEAK
 AMAVIACLSDTDLIFDAVLKIMYAAVVPWSAAVEQLVKQHLEMDHPKV KLLQESYKLME
 MKKLLRGYGIREVNLLNKEIMRVVRYILKQDVPSSLEDALKVAQAFMLSDDEIYSLRIIDLI
 DREQGEDCLLLLKSLPPAEAEKTAERVIIWARLALQEEP DHSKEGKAWRMSVAKTSVDI
 LKILCDIQKDNLQKKDECEEMKLKFKEVASLQENFEVFLSFEDYSNSSLVADLREQHIKA
 HEVAQAKHKPGSTPEPIAAEVRSPSMESKLHRQALALQMSKQELEAELTLRALKDGNIK
 TALKKCSDLFKYHCNADTGKLLFLT CQKLCQMLADNVPVTPVGLNLPSMIHDLASQAA
 TICSPDFLLDALELCKHTLMAVELSRQCQMDDCGILMKASFGTHKDPYEEWSYS DFFSE
 DGIVLESQMVLPIYELISSLVPLAESKRYPLESTSLPYCSLNEG DGLVLPVINSISALLQN
 LQESSQWELALRFVVGSGTGCLQHSVSNFMNATLSEKLFGETTLVKSRHVVMELKEKA
 VIFIRENATTLHKVFNCRLVDLDLALGYCTLLPQKDV FENLWKLIDKAWQNYDKILAISLV
 GSELASLYQEIEMGLKFRELSTDAQWGIRLGKLGISFQPVFRQHFLTKKDLIKALVENID
 MDTSLILEYCSTFQLDCDAVLQLFIETLLHNTNAGQGQGDASMD SAKRRHPKLLAKALE
 MVPLLTSTKDLVISLSGILHKLDPYDYEMIEVVLKVIERADEKITNININQALSILKHLKSYR
 RISPPVDLEYQYMLEHVITLPSAAQTRLPPHLIFFGTAQNF WKILSTELSEESFPTLLLISK
 LMKFSLDTLYVSTAKHVFEKKLKP KLLKLTQAKSSTLINKEITKITQTIESCLLSIVNPEWAV
 AIAISLAQDIPEG SFKISALKFCLYLAERWLQNIPSQDEKREKAEALLKKLHIQYRRSGTEA
 VLIAHKLNTEEYLRVIGKPAHLIVSLYEHPSINQRIQNSSGTDYPDIHAAA KEIAEVNEINLE
 KVWDMLEKWLCPSTKPGKEKPSSELFQEDEALRRVQYLLLSRPIDYSSRMLFVFATST
 TTTLGMHQLTFAHRTRALQCLFY LADKETIESLFFKKPIEEVKSYLRCITFLASFETLNIPITY
 ELFCSSPKEGMIKGLWKNHSHESMAVRLVTELCLEYKIYDLQLWNGLLQKLLGFNMIPY
 LRKVLKAISSIHSLWQVPYFSKAWQRV IQIPLLSASCPLSPDQLSDCSES LIAVLECPVSG
 DLDLIGVARQYIQLELPAFALACLMLMPHSEKRHHQIKNFLGSCDPQVILKQLEEHMNTG

QLAGFSHQIRSLILNNIINKKEFGILAKTKYFQMLKMHAMNTNNITELVNYLANDLSLDEA
SVLITEYSKHCGKPVPPDTAPCEILKMFLSGLS

SEQID No:61

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FLNQLQSGVNRWIREIQKVTKLDRDPASGTALQEISFWNLERALYRIQEKRESPEVLLT
LDILKHGKRFHATVSFDTDTGLKQALETVNDYNPLMKDFPLNDLLSATELTKIRQALVAIF
THLRKIRNTKYPIQRALRLVEAISRDLSQLLKVLGTRKLMHVAYEEFEKVMVACFEVFQ
TWDDEYEKLQVLLRDIVKRKREENLKMVWRINPAHRKLQARLDQMRKFRRQHEQLRA
VIVRVLRPQVTAVAQQNQGEVPEPQDMKVAEVLFDAADANAIEEVNLAYENVKEVDGL
DVSKEGTEAWEAAMKRYDERIDRVETRITARLRDQLGTAKNANEMFRIFSRFNALFVRP
HIRGAIREYQTQLIQRVKDDIESLHDKFKVQYPQSQACKMSHVRDLPPVSGSIIWAKQID
RQLTAYMKRVEDVLGKGWENHVEGQKLKQDGDSFRMKNLTQEIFDDWARKVQQRNL
GVSGRIFTIESTRVRGRTGNVLKLVNLFPEITLSKEVRNLKWLGFVRPLAIVNKAHQAN
QLYPFAISLIESVRTYERTCEKVEERTISLLVAGLKKEVQALIAEGIALVWESYKLDPPYV
QRLAETVFNFQEKVDDLLIIEEKIDLEVRSLCTMYDHKTFSEILNRVQKAVDDLNLHSYS
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TEEEKFYRNALTRMPDGPVALEESYSAVMGIVSEVEQYVKVWLQYQCLWDMQAENIY
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VELYRNGQRILLEKQRFQFPPSWLYIDNIEGEWGAFNDIMRRKDSAIQQQVANLQMKIV
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 EVEQMIRDLEASIARYKEEYAVLISEAQAIKADLAAVEAKVNRSTALLKSLSAERERWEK
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 EYLSNADERLRWQASSLPADDLCTENAIMLKR FNRYPLIIDPSGQATEFIMNEYKDRKIT
 RTSFLDDAFRKNLESALRFGNPLLVDVESYDPVLNPVLNREVRRTGGRVLITLGDQDI
 DLSPSFVIFLSTRDPTVEFPDLC SRVTFVNFTVTRSSLQSQCLNEVLKAERP DVDEKRS
 DLLKLQGEFQLRLRQLEKSL LQALNEVKGRILDDDTIITTLENLKREAAEVTRKVEETDIV

MQEETVSQQYLPLSTACSSYFTMESLKQIHFLYQYSLQFFLDIYHNVLYENPNLKGVT
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 PPGVKANMLRTFSSIPVSRICKSPNERARLYFLLAWFHAIQERLRYAPLGWSKKYEFGE
 SDLRSACD TVDTWLDDTAKASGRQNISPDKIPWSALKTLMAQSIYGGRVDNEFDQRLL
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 LPLNNAERVLLTTQGVDMISKMLKMQMLEDDEDDLAYAETEKTRTDSTSDGRPAWMRTLH
 TTASNWLHLIPQTLSHLKRTVENIKDPLFRFFEREVKMGAKLLQDVRQDLADVQVCEG
 KKKQTNYLRTLINELVKGILPRSWSHYTVPAGMTVIQWVSDFSERIKQLQNISLAAASGG
 AKELKNIHVCLGGLFVPEAYITATRQYVAQANSWSLEELCLEVNVTTSSQGATLDACSF
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 RADLIFTVD FEIATKEDPRSFYERGVAVLCTE

SEQID No:62

MQSRLLLLGAPGGHGGPASRRMRLLLRQVVQRRPGGDRQRPEVRLLHAGSGADTGD
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 LEKAERNVLPVLNNLLENREMQL EDGRFLMSAERYDKLLRDHTKKELDSWKIVRVSENF
 RVIALGLPVPRYSGNPLDPPLRSRFQARDIYYLPFKDQLKLLYSIGANVSAEKVSQLLSF
 ATTLCSESSTLGLPDFPLDSLAAAVQILDSFPMPIKHAIQWLYPYSILLGHEGKMAVE
 GVLKRFELQDSGSSLLPKEIVKVEKMMENHVSQASVTIRIADKEVTIKVPAGTRLLSQPC
 ASDRFIQTLSHKQLQAEMMQSHMVKDICLIGGKGCGKT VIAKNFADTLGYNIEPIMLYQD
 MTARDLLQQRYTLPNGDTAWRSSPLVNAALEGKLVLLDGIHRVNAGTLAVLQRLIHDRE
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 PEFLTMFFFHYMKPLVKSEEIQVIKEKVPNPVQEALDKLLSFTHKLRETQDPTAQSLAAS
 LSTRQLLRISRRLSQYPNENLHSAVTKACLSRFLPSLARSAL EKNLADATIEINTDDNLEP
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 LLVGNQGVGKNKIVDRFLHLLNRPREYIQLHRD TT VQTLTLQPSVKDGLIVYEDSPLVKA
 VKLGHILVVDEADKAPTNVTCILKTLVENGEMILADGRRIVANSANVNGRENVVVIHPDF
 RMIVLANRPGFPFLGNDFFGT LGDIFSCHAVDNPKPHSELEMLRQYGP NVPEPILQKLV
 AAFGELRSLADQGIINYPYSTREVVNIVKHLQKFPT EGLSSVVRNVFDFDSYNNDMREILI

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 VVTVDMGGHIRLWETGLERLQSRSLMEWRNMIGQDDRNMQITINRDSGEDVSSPKHGK
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 VKRAAREMGQRAFQQRLEIQMSEYDAATYERFSGAVRRQVHSLRIILDNLQAKGKER
 QWLRHQATGELDDAKIIDGLTGEKAIYKRRGELEPQLGSPQQKPKRLRLVVDVSGSMY
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 QRLEILKTMHAHSQFCMSGDHTLEGTEHAIKEIVKEEADEYFVIVLSDANLSRYGIHPAKF
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SEQID No:63

MLERKYGGRLVTRHAARTIQTAFRQYQMKNKNERLRSSMSSENRMSSRRIVLSNMRMQF
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 DTSCRSTPSLERQEQRRLRVEHLPLLTIEPPSDSSVDLSDRSERGSLKRQSAYERSLGG
 QQGSPKHGPHSGAPKSLPREPELRPRPPRPLDSHLAINGSANRQSKSESDYSDGDN
 DSINSTSNSNDTINCSSSESSSRDSLREQTLQTYHKEARNSWDSPAFAFNDVIRKRHYR
 IGLNLFNKKPEKGVQYLIERGFPDTPVGVAHFLLQRKGLSRQMIGEFLGNRQKQFN
 VLDVDEMDFSTMEALRKFQAHIRVQGEAQKVERLIEAFSQRYSICNPGVVRQFR
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 RELKTNEDHVSQVQKVEKLIVGKKPIGSLHPGLGCVLSLPHRRLVCYCRLFEVPDPNKP
 QKLGLHQREIFLNDLLVVTKIFQKKKNSVTYSFRQSFSLYGMQVLLFENQYYPNGIRLT
 SSVPGADIKVLINFNAPNPQDRKKFTDDLRESIAEVQEMEKHRIESELEKQKGVVRPSM
 SQCSSLKKESGNGTLRACLDDSYASGEGLKRSALSSSLRDLSEAGKRGRSSAGSLE
 SNVEFQPFEPQLQPSVLCS

SEQID No:64

MPLKHYYLLLLVGCQAWGAGLAYHGCPSSECTCSRASQVECTGARIVAVPTPLPWNAMS
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 KNSLTHISPRVFQHLGNLQVLRLYENRLTDIPMGTFDGLVNLQELALQQNQIGLLSPGLF
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 DNHISSLPDNVFSNLRQLQVLILSRNQISFISPGAFNGLTELSLHTNALQDLDGNVFR
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SEQID No:65

MRGSHRAAPALRPRGRLWPVLAVLAAAAAAGCAQAAMDECTDEGGRPQRCMPEFVN
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 DTTWWQSQTMLAGVQYPSSINLTLLHLGKAFDITYVRLKFHTSRPESFAIYKRTREDGPW
 IPYQYYSGSCENTYSKANRGFIRTGGDEQQALCTDEFSDFSPLTGGNVAFASTLEGRPS
 AYNFDNSPVLQEWVTATDIRVTLNRLNTFGDEVFNDPKVLKSYYYAISDFAVGGRCCKN
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 RSQECYFDPELYRSTGHGGHCTNCQDNTDGAHCERCENFFRLGNNEACSSCHCSP
 VGSLSTQCDSYGRCSCKPGVMGDKCDRCQPGFHSLTEAGCRPCSCDPSGSDIECNV
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 WRPALTPFEFQKLLNNLTSLKIRGTYSERSAGYLDDVTLASARPGPGVPATWVESCTCP
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 CDDGYFGDPLGRNGPVRLCRLCQCSDNIDPNAVGNCRNLTGECLKCIYNTAGFYCDR
 CKDGGFFGNPLAPNPADKCKACNCNPYGTMKQQSSCNPVTGQCECLPHVTGQDCGAC
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 GPEGCKPCDCHPEGSLSLQCKDDGRCECREGFVGNRCDQCEENYFYNRSWPGCQE
 CPACYRLVKDKVADHRVKLQELESILANLGTGDEMVTDAQAFEDRLKEAEREVMDLLRE
 AQDVKDQDQNLMDRLQRVNNTLSSQISRLQNIRNTIEETGNLAEQARAHVENTERLIEIA
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TSTEAYNLLLRTLAGEHQTAFEIEELNRKYEQAKNISQDLEKQAARVHEEAKRAGDKAV
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 EKGKTEQQTADQLLARADA¹¹AKALAE¹¹EAAKGRDTLQEANDILNNLKDFDRRVNDNKTA
 AEEALRKIPAINQTITEANEKTR¹¹EAQQALGSAAADATEAKNKAHEAERIASAVQKNATST
 KAEAERTFAEVTDLNEVNNMLKQLQEAEKELKRKQDDADQDMM¹¹MAGMASQAAQEA
 EINARKAKNSVTSLLSIINDLLEQLGQLDTV¹¹DLNKLNEIEGTLNKA¹¹KDEM¹¹KVSD¹¹LDRK¹¹VSD
 LENEAKKQEA¹¹AIMDYN¹¹RDIEEIMKDIRNLEDIRKTLPSGCFNTPSIEKP

SEQID No:66

MAAATEHNRPSSGDRNLERRCSPNLSREVL¹¹YEIFRSLHTLVGQLDLRDDVVKITIDWNK
 LQSLSAFQPALLFSALEQHILYLQPF¹¹LAKLQSPIKEENTTAVEEIGRTEMGNKNEVNDKF
 SIGDLQEEEEKH¹¹KESDLRDVKK¹¹TQIHFDPEVVQIKAGKAEIDRRISAFIERKQAEINENNVR
 EFCNVIDCNQENSCARTDAIFTPYPGFKSHVKVSRVVNTYGPQTRPEGIPGSGHKPNS
 MLRDCGNQAVEERLQ¹¹NIEAHLRLQTGGPVPRDIYQRIKKLEDKILELEGISPEYFQSVSF
 SGKRRKVQPPQQNYSLAELDEKISALKQALLRKSREAESMATHHLP

SEQID No:67

LCNGVND¹¹CGDNSDESPQQNCRPRTGEENCNVNNGGCAQKCQMVRGAVQCTCHTGY
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 VLLFANRIDIRQVLPHRSEY¹¹TLLLNNLENAIALDFHHRREL¹¹VFWSDVTLD¹¹RILRANLNGSN
 VEEVSTGLESPGGLAVDWVHDKLYWTD¹¹SGTSRIEVANLDGAHRKVLLWQNLEKPRAI
 ALHPMEGTIYWTDWGNTPRIEASSMDGSGRRRIADTHLFWPNGLTIDYAGRRMYWVDA
 KHHVIERANLDGSHRKAVISQGLPH¹¹PF¹¹AITVFEDSLYWTDWHTKSINSANKFTGKNQEII
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 ACAQSLDKFLLFARRMDIR¹¹RISFDTE¹¹DLSD¹¹VIPLAD¹¹VRSAVALDWDSRDDHVYWTDVS
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CSHLCLPRPSGFSCACPTGIQLKGDGKTCDPSPETYLLFSSRGSIRRIISLDTSDHTDVHV
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 ARNLYWTDGTGRNTIEASRLDGSCRKVLINNSLDEPRAIAVFPRKGYLFWTDWGHIAKIER
 ANLDGSEKVLINTDLGWPNGLTLDYDTRRIYWVDAHLDRIESADLNGKLRQVLVGHVS
 HPFALTQQDRWIYWTDWQTKSIQRVDKYSGRNKETVLANVEGLMDIIVVSPQRQTGTN
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 LSILLILVVIAALMLYRHKKSFTDPGMGNLTYSNPSYRTSTQEVKIEAIPKPA MYNQLCY
 KKEGGPDHNYTKEKIKIVEGICLLSGDDAEWDDLKQLRSSRGGLLRDHVCMKTDTVSIQ
 ASSGSLDDTEMEQLLQEEQSECSSVHTAATPERRGSLPDTGWKHERKLSSESQV

SEQID No:68

MRRAPCVRDKLREIVGASTNWRDHVKAMEERKLLHSFLAKSQDGLPPRRMKDSYIEVL
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 DMCKKSLSPEQDIKFSGHVSWSVGKTSMEVKMQMFQLHGDEFQVLDATFVMVARDSE
 NKGPAFVNPLIPESPEEEELFRQGELNKGRRIAFSSTSLKMAPSAEERTTIHEMFLSTL
 DPKTISFRSRVLPNAVWMENSKLKSLEICHQPQERNIFNRIFGGFLMRKAYELAWATAC
 SFGGSRPFVAVDDIMFQKPVEVGSLLFLSSQVCFTQNNYIQVRVHSEVASLQEKQHTT
 TNVFHFTFMSEKEVPLVFPKTYGESMLYLDGQRHFNSMSGPATLRKDYLVEP

SEQID No:69

MSVKEAGSSGRREQAAYHLHIYPQLSTTESQASCRVTATKDSTTSDDVIKDAIASRLDGL
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 TIKYVHMLVAQATATRRLVERGLLPRQQADFDLCLNLPTELTEGNLLKNLKHRFLQQKI
 YTYAGSILVAINPFKFLPIYNPKYVKMYENQQLGKLEPHVFALADVAYYTMLRKRVNQCI
 VYPGESGSGKTQSTNFLIHCLTALSQKGYASGVERTILGACPVLEAFGNAKTAHNNNSS
 RFGKFIQVSYLESGIVRGAVVEKYLLEKSRLVSQEKDERNYHVFFYLLLVSEEEERQEF
 QLKQPEDYFYLNQHNLIKIEDGEDLKHDFERLKQAMEMVGFLPATKKQIFAVLSAILYLG
 VTYKKRATGREGGLEVGPPPEVLDLTSQLLKVKREILVEVLTKRKTVTVNDKLILPYSLSEA
 ITARDSMAKSLYSALFDWIVLRINHALLNKKDVEEAVSCLSIGVLDIFGFEDFERNSEFQF
 CINYANEQLQYYFNQHIFKLEQEEYQGEGITWHNIGYTDNVGCIHLISKKPTGLFYLLDEE
 SNFPHATSQTLLAKFKQQHEDNKYFLGTPVMEPAFIIQHFAGKVYQIKDFREKNMDYM
 RPDIVALLRGSDSSYVRELIGMDPVAVFRWAVLRAAIRAMAVLREAGRLRAERA EKAAG
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PRAFILKSKGIKQKQIIPKNLLDSKSLKLIISMTLHDRTTKSLLHLHKKKKPPSISAQFQTSL
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 VVRKILLQSWFRMVLERRHFLQMKRAAVTIQACWRSYRVRRALERTQAAYVLQAAWR
 GYWQRKLYRHQKQSIIRLQSLCRGHLQRKSFSSQMISEKQKAEKEREALAAAGAE
 GGQQAAGGQQVAEQGPEPAEDGGHLASEPEVQPSDRSPLEHSSPEKEAPSPEKTL
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 DAERLASAVELWRGKKLVAAASPSAMLSQSLDLSDRHRATGAALTPTEERRTSFSTSD
 VSKLLPSLAKAQPAEETDGERSAKKPAVQKKKPGDASSLPDAGLSPGSQVDSKSTFK
 RLFLHKTCDKKYSLEGAEELNAVSGHVLEATTMKGLEAPSGQQHRHAAGEKRTKE
 PGGKGKKNRNVKIGKITVSEKWRESVFRQITNANELKYLDEFLLNKINDLRSQKTPIESLF
 IEATEKFRSNIKTMYSPNGKIHVGKDLMENYQIVVSNLATERGQKDTNLVLNLFQSL
 DEFTRGYTKNDFEPVKQSKAQKKKKRQKQERAVQEHNGHVFAVSYQVSIQVQSCQCLSYIW
 LMDKALLCSVCKMTCHKKCVHKIQSHCSYTYGRKGEPGAEPGHFGVCVDSLTSKASV
 PIVLEKLLHEVEMHGLYTEGLYRKSGAANRTRELRLQALQTDPAAVKLENFPIHAITGVK
 QWLRELPEPLMTFAQYGDFLRAVELPEKQEQLAAIYAVLEHLPEANHNSLERLIFHLVKV
 ALLEDVNRMSPGALAIIFAPCLLRCPDNSDPLTSMKDVLCITTCVEMLIKEQMRKYKVKM
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SEQID No:70

MTGERPSTALPDRRWGPRILGFWGGCRVWVFAAIFLLLSLAASWSKAENDFGLVQPLV
 TMEQLLWVSGRQIGSVDTFRITLITATPRGTLLAFEAARKMSSSDEGAKFIALRRSMDQ
 GSTWSPTAFIVNDGDVPDGLNLGAVVSDVETGVVFLFYSLCAHKAGCQVASTMLVWSK
 DDGVSWSTPRNLSLDIGTEVFAPGPGSGIQKQREPRKGRILVCGHGTLELDGVFCLLS
 DDHGASWRYGSGVSGIPYGGPKQENDFNPDECQPYELPDGSSVINARNQNNYHCHC
 RIVLRSYDACDTRLRPRDVTDFPELVDPVVAAGAVVTSSGIVFFSNPAHPEFRVNLTLRW
 SFSNGTSWRKETVQLWPGPSGYSSLATLEGSMDEEQAPQLYVLYEKGRNHYESIS
 VAKISVYGTL

SEQID No:71

MAPRLCSISVTARRLLGGPGPRAGDVASAAAARFYSKDNEGSWFRSLFVHKVDPRKDA
 HSTLLSKKETS NLYKIQFHNVKPEYLDAYNSLTEAVLPKLHLDEDYPCSLVGNWNTWYG
 EQDQAVHLWRFSGGYPALMDCMNKLKNNKEYLEFRRERSQMLLSRRNQLLLEFSFWN
 EPQPRMGPNIELRTYKLKPGTMIEWGNNWARAIKYRQENQEAVGGFFSQIGELYVVH
 HLWAYKDLQSREETR NAAWRKRGWDENVYYTVPLVRHMESRIMIPLKISPLQ

SEQID No:72

MAARVLRARGAAWAGG LLQRAAPCSLLPRLRTWTSSSNRSREDSWLKSLFVRKVDPR
 KDAHSNLLAKKETS NLYKLQFHNVKPECLEAYNKICQEVLPKIHEDKHYPCTLVGTWNT
 WYGEQDQAVHLWRYEGGYPALTEVMNKLRENKEFLEFRKARSDMLLSRKNQLLLEFS
 FWNEPVRSGPNIELRSYQLRPGTMIEWGNYWARAIRFRQDGNEAVGGFFSQIGQLY
 MVHHLWAYRDLQTREDIR NAAWHKHGWEELVYYTVPLIQEMESRIMIPLKTSPLQ

SEQID No:73

MGTALLQRGGCFLLCLSLLLLGCWAELGSGLEFPGAEGQWTRFPKWNACCSEMSFQ
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 RIRRQFRNTTLFIDQVEAKWVEVKSKRRDMTVFSGLFVGGLPPELRAAALKLTASVRE
 REPFGKWIRDVRVNSSQVLPVDSGEVKLDDEPPNSGGGSPCEAGEEGEGGVCLNGG
 VCSVDDQAVCDCSRTGFRGKDCSQEDNNVEGLAHLMMGDQGKSKGKEEYIATFKG
 SEYFCYDLSQNPIQSSSDEITLSFKTLQRNGLMLHTGKSADYVNLALKNGAVSLVINLGS
 GAFEALVEPVNGKFNDNAWHDKVTRNLRQHSGIGHAMVTISVDGILTTTGYTQEDYT
 MLGSDDFFYVGGSPSTADLPGSPVSNFMGCLKEVVYKNNDVRLELSRLAKQGDPKM
 KIHGVVAFKCNVATLDPITFETPESFISLPKWNAKKTGSISFDFRTTEPNGLILFSHGKP
 RHQKDAKHPQMIKVDFFAIEMLDGHLYLLLDMGSGTIKIKALLKKVNDGEWYHVD FQRD
 GRS GTISVNTLRTPYTAPGESEILDLDDELYLGGLPENKAGLVFPTEVWTALLNYGYVG
 CIRDLFIDGQSKDIRQMAEVQSTAGVKPSCSKETAKPCLSNPCKNNGMCRDGWNRYV
 CDCSGTGYLGRSCEREATVLSYDGSMFMKIQLPVVMHTEAEDVSLRFRSQRAYGILMA
 TTSRDSADTLRLELDAGR VKLTVNLDCIRINCNSSKGPETLFAGYNLNDNEWHTVRVVR
 RGKSLKLTVD DQQAMTGQMAGDHTRLEFHNIETGIITERRYLSSVPSNFIGHLQSLTFN
 GMAYIDLCKNGDIDYCELNARFGFRNIIADPVTFTKSSYVALATLQAYTSMHLFFQFKT
 TSLDGLILYNSGDGND FIVVELVKGYLHYVFDLGNGANLIKSSNKPLNDNQWHNVMIS
 RDTSNLHTVKIDTKITTQITAGARNLDLKS DLYIGGVAKETYKSLPKLVHAKEGFQGCLAS
 VDLNGRLPDLISDALFCNGQIERGCEGPSTTCQEDSCSNQGVCLQQWDGFSCDCSMT

SFSGPLCNDPGTTYIFSKGGGQITYKWPPNDRPSTRADRLAIGFSTVQKEAVLVRVDSS
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 PVIERYPAGRQLTIFNSQATIIIGGKEQGQPFQGGQLSGLYYNGLKVLNMAAENDANIAIVG
 NVRLVGEVPSSMTTESTATAMQSEMSTSIMETTTTTLATSTARRGKPPTKEPISQTTDDIL
 VASAECPSSDDEDIDPCEPSSGGLANPTRAGGREPYPGSAEVIRESSSTTGMVVGIVAAA
 ALCILILLYAMYKYRNRDEGSYHVDESRNYISNSAQSN GAVVKEKQPSSAKSSNKNKKN
 KDKEYVV

SEQID No:74

MTTQQIDLQGGPGPWGFRLVGGKDFEQPLAISRVTPGSKAALANLCIGDVITAIDGENTS
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 SAHNRSAMPFTASPASSTTARVITNQYNNPAGLYSSENISNFNNALESKTAASGVEANS
 RPLDHAQPPSSLVIDKESEVYKMLQEKEQELNEPPKQSTSFLVLQEILESEEKGDPNKPS
 GFRSVKAPVTKVAASIGNAQKLPMCDKCGTGIVGVFVKLRDRHRHPECYVCTDCGTNL
 KQKGHFFVEDQIYCEKHARERVTPPEGYEVVTVFPK

SEQID No:75

MGAGAETGRGQRAAAPERRHGRLLWLLRGLTLGTAPRRAVRGQAGGGGPGTAGIVG
 EAGSLATCELPLAKSEWQKKLTPEQFYVTREKGTPEPPFSGIYLNNEAGMYHCVCCDS
 PLFSSEKKYCSGTGWPSFSEAHGTSGSDESHTGILRRLDTSLGSARTEVVCKQCEAHL
 GHVFPDGPNGQRF CINSVALKFKPRKH

SEQID No:76

MTSAAPAKKPYRKAPPEHRELRL EIPGSRLEQEEPLTDAERMKLLQEENEELRRRLASA
 TRRTEALERELEIGQDCLELELGQSREELDKFKDKFRRLQNSYASQRTNQELEDKLHT
 LIKKAEMDRKTL DWEIVELTNKLLDAKNTINKLEELNERYRLDCNPAVQLLKCNKSHFRN
 HKFADLPCELQDMVRKHLHSGQEAAASPGPAPSLAPGAVVPTSVIARVLEKPE SLLLNSA
 QSGSAGRPLAEDVFVHVD MSEGVP GDPASPPAPGSPTPQPNGECHSLGTARGSP EEE
 LPLPAFEKLN PYPTPSPPHPLYPGRRVIEFSEDKVRIPRNSPLPNCTYATRQAISLSLVEE
 GSERARPSVPSTPASAQASPHHQPSAPLTL SAPASSASSEEDLLVSWQRAFVD RTP
 PPAAVAQRTAFGRDALPELQRHFAHSPADRDEVVQAPSARPEESE LLLPTEPD SGFPR
 EEEELNLPISPEEERQSLLPINRGTEEGPGTSHTEGRAWPLPSSSRPQRSPKRMGVHH
 LHRKDSL TQAQEQGNLLN

SEQID No:77

MGTTASTAQQTVSAGTPFEGLOGSGTMDSRHSVSIHSFQSTSLHNSKAKSIIPNKVAPV
 VITYNCKEEFQIHDELLKAHYTLGRLSDNTPEHYLVQGRYFLVRDVTEKMDVLGTVGSC
 GAPNFRQVQGGGLTVFGMGQPSSLGFRRLVQKLQKDGHRECVIFCVREEPVLFLRADE
 DFVSYTPRDKQNLHENLQGLGPGVRVESLELAIRKEIHDFQAQLSENTYHVYHNTEDLWG
 EPHAVAIHGEDDLHVTEEVYKRPLFLQPTYRYHRLPLPEQGSPLEAQLDAFVSVLRETP
 SLLQLRDAHGPPPALVFSCQMGVGRTNLGMVLGTLILLHRSGTTSQPEAAPTQAKPLP
 MEQFQVIQSFLRMVPQGRRMVEEVDRAITACAEHLHDLKEVVLENQKKLEGIRPESPAQ
 GSGSRHSVWQRALWSLERYFYLLFNYYLHEQYPLAFALSFSRWLCAHPELYRLPVTLS
 SAGPVAPRDLIARGSLREDDLVSPDALSTVREMDVANFRRVPRMPIYGTAQPSAKALG
 SILAYLTDAKRRLRKVVWVSLREEAVLECDGHTYSLRWPGPPVAPDQLETLEAQLKAHL
 SEPPPGKEGPLTYRFQTCLTMQEVFSQHRRACPLTYHRIPMPDFCAPREEDFDQILLE
 ALRAALSKDPGTGFVFSCLSGQGRTTAMVVAVLAFWHIQGFPEVGEEELVSVDAKF
 TKGEFQVVMKVQLLPDGHRVKKEVDAALDTVSETMTMPMHYHLREIIICTYRQAKAAKE
 AQEMRRLQLRSLQYLERIVCLILFNAYLHLEKADSWQRPFFSTWMQEVASKAGIYEILNE
 LGFPELESGEDQPFSLRYRWQEQSCSLEPSAPEDLL

SEQID No:78

MAALYRPLRLNWHGLSPLGWPSCRSIQTLRVLSGDLGQLPTGIRDFVEHSARLCQPE
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 TVPLPPGGARGQLGNWMSPADFORAVDERFPGCMQGRMTMYVLPFSMGPVGSPLSRI
 GVQLTDSAYVVASMRIMTRLGTPVLQALGDGDFVKCLHSGVQPLTGQGEPPVSQWPCN
 PEKTLIGHVPDQREIISFGSGYGGNSLLGKKCFALRIASRLARDEGWLAEHMLILGITSPA
 GKKALCAAFFPSACGKTNLAMMRPALPGWKVECVGDDIAWMRFDSEGRRLRAINPENG
 FFGVAPGTSATTNPNAMATIQSNTIFTNVAETSDGGVYWEGIDQPLPPGVTVTSWLGKP
 WKPGDKEPCAHNPNSRFCAPARQCPIMDPAWEAPEGVPIDAIIFGRRPKGVPLVYEF
 NWRHGVFVGRAMRSESTAAAEHKGKIIMHDPFAMRPFFGYNFGHYLEHWLSMEGRKG
 AQLPRIFHVNWFRRDEAGHFLWPGFGENARVLDWICRRLEGEDSARETPIGLVPKEGA
 LDLSGLRAIDTTQLFSLPKDFWEQEVDIRSYLTEQVNQDLPKEVLAELEALERRVHKM

SEQID No:79

MLPAATASLLGPLLTACALLPFAQQQTPNYTRPVFLCGGDVKGESGYVASEGFPNLYP
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 APLVAPGNQVTLRMTTDEGTGGRGFLWYSGRATSGTEHQFCGGRLEKAQGTLTTPN

WPESDYPPGISCSWHIIAPPDQVIALTFEKFDLEPDTYCRYDSVSVFNGAVSDD\$RRLG
 KFCGDAVPGSISSEGNELLVQFVSDLSVTADGFSASYKTLPRGTAKEGQGPGPKRGTE
 PKVKLPPKSQPPEKTEESPSAPDAPTCPKQCRRTGTLQSNFCASSLVVTATVKSMVRE
 PGEGLAVTVSLIGAYKTGGLDLPSPTGASLKFYVPCKQCPPMKKGVSYLLMGQVEEN
 RGPVLPPESFVVLHRPNQDQILTNLSKRKCPSQPVRAAASQD

SEQID No:80

MRMTMEEMKNEAETTSMVSMPLYAVMYPVFNELERVNLSAAQTLRAAFIKAOKENPGL
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 EINDRVRFLQTIKDIASAIKELLDTVNNVFKKYQYQNRRALEHQKKEFVKYSKSFSDTLKT
 YFKDGKAINVFVSANRLIHQTNLILQTFKTVA

SEQID No:81

MTSALTQGLERIPDQLGYLVLSEGAVLASSGDLENDEQAASAISELVSTACGFRLHRGM
 NVPFKRLSGEPLPLPLVVVLGAGGYFQGLLGFSSSSLLPSPGVSGLATFLPLGLPGIRIV
 NEKARERRSSRGHSSSNL

SEQID No:82

MGSRDHLFKVLVVGDAAVGKTSLVQRYSQDSFSKHYKSTVGVDFAKVLQWSDYEIVR
 LQLWDIAGQERFTSMTRLYYRDASACVIMFDVTNATTFSNSQRWKQDLDSKLTLPNGE
 PVPCLLLANKCDLSPWAVSRDQIDRFSKENGFTGWTETSVKENKNINEAMRVLIEKMM
 RNSTEDIMSLSTQGDIYNLQTKSSSWSCC

SEQID No:83

MAAAKDTHEDHDTSTENTDESNHDPQFEPIVSLPEQEIKTLEEDEEEELFKMRAKLFRFA
 SENDLPEWKERGTGDVKLLKHKEKGAIRLLMRRDKTLKICANHITPMMEKPNAGSDR
 AWWWNTHADFADEC PKPELLAIRFLNAENAQKFKTKFEECRKEIEEREKKAGSGKNDH
 AEKVAEKLEALSVKEETKEDAEKQ

SEQID No:84

MLDSSDSSSQPHWSNELIAEQLQQQVSQLQDQLDAELEDKRKVLELSREKAQNEDLK
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 QVLNELQVSHAETTLELEKTRDMLILQRKINV CYQEELEAMMTKADNDNRDHKEKLERL
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QGENLFELHIHQAFLTSAALAQAGDTQPTTFCTYSFYDFETHCTPLSVGPQPLYDFTSQ
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 SIQVQLDWKFPYIPPESEFLKPEAQTKGKDTKDSSKISSEEEKASFPSQDQMASPEVPIEA
 GQYRSKRKPPHGGGERKEKEHQVVSYSRRKHGKRIGVQGKNRMEYLSLNILNGNTPQQ
 VNYTEWKFSETNSFIGDGFKNQHEEEEMTLSSHALKQKEPLHPVNDKESSEQGGSEVSE
 AQTTDSDDVIVPPMSQKYPKADSEKMCIEIVSLAFYPEAEVMSDENIKQVYVEYKFYDLP
 LSETETPVSLRKPRAGEEIHFFHSKVIDLDPQEQQGRRRFLFDMLNGQDPDQGHCLKFTV
 VSDPLDEEKKECEEVGYAYLQLWQILESGRDILEQELDIVSPEDLATPIGRLKVSLQAAA
 VLHAIYKEMTEDLFS

SEQID No:85

MERSGWAROTELLALLGATLRARAAAGYYPRFSPFFFLCTHHGELEGDGEQGEVLISL
 HIAGNPTYYPVPGQEYHVTISTSTFFDGLLVTLGLYTSTSVQASQSIGGSSAFGFGIMSDHQ
 FGNQFMCSVVASHVSHLPTTNLSFIWIAPPAGTGCVNFMATATHRGQVIFKDALAQQLC
 EQGAPTDVTVHPLAEIHSDSIILRDDFDSYHQLQLNPNIWVECNNCETGEQCGAIMHG
 NAVTFCEPYGPRELITTGLNTTTASVLQFSIGSGSCRFSYS DPSIIVLYAKNNSADWIQLE
 KIRAPSNVSTIIHILYPEDAKGENVQFQWKQENLRVGEVYEACWALDNILIINSAHRQVV
 LEDSLDPVDGTGNWLFFPGATVKHSCQSDGNSIYFHGNEGSEFNFATTRDVDLSTEDIQ
 EQWSEEFESQPTGWDVLGAVIGTECGTIESGLSMVFLKDGGERKLCTPSMDTTGYGNLR
 FYFVMGGICDPGN SHENDIILYAKIEGRKEHITLDTLSYSSYKVPSLVSVVINPELQTPATK
 FCLRQKNHQGHNRNVWAVDFFHVLPVLPSTMSHMIQFSINLGCETHQPGNSVSLEFST
 NHGRSWSLLHTECLPEICAGPHLPHSTVYSSENYSGWNRITIPNAALTRNTRIRWRQ
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 ESFGSSRLSSYHNFYSIRGAEVSFSGCVLASGKALVFNKEGRRQLITSFLDSSQSRFLQ
 FTLRLGSKSVLSTCRAPDQPGEGVLLHYSYDNGITWKLLEHYSYLSYHEPRIISVELPGD
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SKPRFVYLELPAAAKTPCTRFRWWQPVFSGEDYDQWAVDDIILSEKQKQIIPVINPTLP
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 RELSEPTMYHTGDFEEWTRITIVIPRSLASSKTRFRWQIQUSSSQKNVPPFGLDGVYISEP
 CPSYCSGHGDCISGVCFCDLGYTAAQGTCVSNVPHNEMFDRFEGKLSPLWYKITGA
 QVGTGCGTLNDGKSLYFNGPGKREARTVPLDTRNIRLVQFYIQIGSKTSGITCIKPRTRN
 EGLIVQYSNDNGILWHLLRELD FMSFLEPQIISIDL PQDAKTPATAFRWWQPPHGHKHA
 QWALDDVLIGMNDSSQTGFQDKFDGSIDLQANWYRIQGGQVDIDCLSM TALIFTENIG
 KPRYAETWDFHVSASTFLQFEMSMGCSKPFSSNSHVSQQLQYSLNNGKDWHLVTEECVP
 PTIGCLHYTESSITSERFQNWKRITVYLPLSTISPRTRFRWQIQUANYTVGADSWAIDNVVL
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 QFSISGGITWHLMDIFYFPQTNNILFINVPLPYTAQTNATRFRLWQPYNNGKKEEIVWD
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 NEVGEHSITTRDLNVNENTI IQFEINVG CSTDSSSADPVRLEFSRDFGATWHLLLPLCYH
 SSSHVSSLCSTEHHPSSTYYAGTMQGWRRREVVFHFGKLHLGSGVRFRWYQGFYPAGS
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 QLESDRFLLMSSGGKPSRKCGILSSGNNLFFNEDGLRMLMTRDLDSLHARFVQFFMRLG
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 GDALVFIEKASTRYVVSTDVAVNEDSFLQIDFAASCSVTDSCYAIELEYSVDLGLSWHPL
 VRDCLPTNVECSRYHLQRILVSDTFNKWTRITLPLPPYTRSQATRFRWHQPAFPDKQQ
 TW AIDNVYIGDGCIDMCSGHGRCIQGNCVCDEQWGGLYCDDPETS LPTQLKDNFNRA
 PSSQNWLT VNGGKLSTVCGAVASGMALHFSGGCSRLLVTVDLNL TNAEFIQFYFMYGC
 LITPNNRNQGV LLEYSVNGGITWNLLMEIFYDQYSKPGFVNILLPPDAKEIATRFRWWQP
 RHDGLDQNDWAIDNV LISGSADQRTVMLDTFSSAPVPQHERSPADAGPVGRIAFDMFM
 EDKTSVNEHWLFHDDCTVERFCDSPDGVMLCGSHDGREVYAVTHDLTPTEGWIMQFK
 ISVGCKVSEKIAQNQIHVQYSTDFGVSWNYLVPQCLPADPKCSGVSQPSVFFPTKGW
 KRITYPLPESLVGNPVFRFRFYQKYS DMQWAIDNFYLGPGCLDNCRGHGDCLREQCICD
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 VRQAVTQDLDLRGAKFLQYWGRIGSENNMTSCHRPICRKEGVLLDYSTDGGITWTLLH
 EMDYQKYISVRHDYILLPEDALTNTTRLRWWQPFVISNGIVVSGVERAQWALDNILIGGA
 EINPSQLVDTFDDEGTSHEENWSFY PNAVRTAGFCGNPSFHL YWPNNKKDKTHNALSS
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CSPFQFHEATIYNSVNSSSWKRITIQLPDHVSSSATQFRWIKGGEETEKQSWAIDHVIYIG
 EACPKLCSGHGYCTTGAICICDESFQGDDCSVFSHDLPSYIKDNFESARVTEANWETIQ
 GGVIGSGCGQLAPYAHGDSLYFNCGCQIRQAATKPLDLTRASKIMFVLQIGSMSQTDSCN
 SDLSGPHAVDKAVLLQYSVNNGITWHVIAQHQPDKFTQAQRVSYNVPLEARMKGVLLR
 WWQPRHNGTGHDQWALDHVEVVLVSTRKQNYMMNFSRQHGLRHFYNRRRRSLRRY
 P

SEQID No:86

MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQL
 ERIEEMDQINKDMKEAEKNLTDLGKFCGLCVPCPNKLKSSDAYKKAWGNNQDGVVA
 SQPARVVDEREQMAISGGFIRRVTDARENEMDENLEQVSGIIGNLRHMAIDMGNEIDT
 QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG

SEQID No:87

MASTISAYKEKMKELSVLSLICSCFYTQPHPNTVYQYGDMEVKQLDKRASGQSFEVILK
 SPDDLSPESPMLSSPPKKKDTSLLELQKRLEAAEERRKTQEAQVLKQLAERREHEREV
 LHKALEENNNFSRQAEKLNKYMELSKEREHLAALRERLREKELHAAEVRNKEQRE
 MSG

SEQID No:88

MKDRTQELRTAKDSDDDDDAVTVDRDRFMDEFFEQVEEIRGFIDKIAENVEEVKRKHS
 AILASPNPDEKTKEELEELMSDIKKTANKVRSKLKSIEQSIEQEEGLNRSSADLRIRKTQH
 STLSRKFFVEVMSEYNATQSDYRERCKGRIQRQLEITGRITTTSEELEDMLESGNPAIFAS
 GIIMDSSISKQALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAV
 DYVERAVSDTKKAVKYQSKARRKKIMIIICCVILGIVIASTVGGIFA

SEQID No:89

MAASMFYGRVLVAVATLRNHRPRTAQRAAAQVLGSSGLFNNHGLQVQQQQQRNLSLHE
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 KGGVKIVFSPEEAKAVSSQMIGKKLFTKQTGEKGRICNQVLVCERKYPRREYYFAITME
 RSFQGPVLIGSSHGGVNIEDVAAETPEAIKEPIDIEEGIKKEQALQLAQKMGFPPNIVESA
 AENMVKLYSLFLKYDATMIEINPMVEDSDGAVLCMDAKINFDSNSAYRQKKIFDLQDWT
 QEDERDKDAAKANLNYIGLDGNIGCLVNGAGLAMATMDIIKLHGGTPANFLDVGGGATV

HQVTEAFKLITSDKKVLAILVNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVRLQGTRVDDA
KALIADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKFQLPI

SEQID No:90

MAPLDLDKYVEIARLCKYLPENDLKRLCDYVCDLLEESNVQPVSTPVTVCEDIHQFY
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ITQVYGFYDECQTKYGNANAWRYCTKVFDMLTVAALIDEQILCVHGGGLSPDIKTLDQIRTI
ERNQEIPHKGAFCDLVWSDPEDVDTWASPRGAGWLFgakVTNEFVHINNKLICRAH
QLVHEGYKFMFDEKLVTVWSAPNYCYRCGNIASIMVFKDVNTREPKLFRAVPDSERVIP
PRTTTPYFL

SEQID No:91

MATRSSRRESRLPFLFTLVALLPPGALCEVWTQRLHGGSAPLPQDRGFLVVQGDPREL
RLWARGDARGASRADEKPLRRKRSAALQPEPIKVYGGVSLNDSHNQMVVHWAGEKS
NVIVALARDSLALARPKSSDVVYSYDYGKSFKKISDKLNFGLGNRSEAVIAQFYHSPADN
KRYIFADAYAQYLWITFDFCNTLQGFSIPFRAADLLLHASKASNLLLGFDRSHPNKQLWKS
DDFGQTWIMIQEHVKSFSWGIDPYDKPNTIYIERHEPSGYSTVFRSTDFQSSRENQEVIL
EEVRDFQLRDKYMFATKVHLLGSEQQSSVQLWVSFGRKPMRAAQFVTRHPINEYYIA
DASEDQVFVVCVSHSNRNTNLYISEAEGLKFSLSLENVLYYSPGGAGSDTLVRYFANEPF
ADFHRVEGLQGVIATLINGSMNEENMRSVITFDKGGTWEFLQAPAFTGYGEKINCELS
QGCSLHLAQRLSQLLNQLRRMPILSKESAPGLIATGSVGKNLASKTNVYISSSAGARW
REALPGPHYWTWGDHGGIITAIAQGMETNELKYSTNEGETWKTFFSEKPVFVYGLLTP
GEKSTVFTIFGSNKENVHSLILQVNATDALGVPCTENDYKLWSPSDERGNECLLGHK
TVFKRRTPHATCFNGEDFDRPVVVSNCSTREDYECDFGFKMSEDLSEVCVPDPFEFS
GKSYSPPVPCPVGSTYRRTRGYRKISGDTCSGGDVEARLEGELVPCPLAEENEFILYAV
RKSIYRYDLASGATEQLPLTGLRAAVALDFDYEHNCLYWSDLALDVIQRLCLNGSTGQE
VIINSGLETVEALAFEPLSQLLYWVDAGFKKIEVANPDGDFRLTIVNSSVLDRPRALVLVP
QEGVMFWTDWGDLPKGIYRSNMDGSAAYHLVSEDVKWPNGISVDDQWIYWTDAYLE
CIERITFSGQQRSVILDNLPHPYAIAVFKNEIYWDDWSQLSIFRASKYSGSQMEILANQLT
GLMDMKIFYKGKNTGSNACVPRPCSLCLPKANNRSRSCRCPEDVSSSVLPSGDLMCD
CPQGYQLKNNTCVKEENTCLRNQYRCSNGNCINSIWWCDFDNDCGDMSDERNCPTTI
CDLDTQFRCQESGTCIPLSYKCDLEDDCGDNSDESHCEMHQCRSDEYNCSSGMCIRS
SWVCDGDNDRCRDWSDEANCTAIYHTCEASNFCRNGHCIPQRWACDGDGTDCCQDGS
DEDPVNCEKKCNCFRCPNGTCIPSSKHCDGLRDCSDGSDEQHCEPLCTHFMDFVCKN

RQQCLFHSMVCDGIIQCRDGSDEDAAFAGCSQDPEFHKVCDEFGFQCQNGVCISLIWK
 CDGMDDCGDYSDEANCENPTEAPNCSRYFQFRCENGHCIPNRWKCDRENDCGDWS
 DEKDCGDSHILPFSTPGPSTCLPNYYRCSSGTCVMDTWVCDGYRDCADGSDEEACPL
 LANVTAASTPTQLGRCDRFEFECHQPKTCIPNWKRCDCGHQDCQDGRDEANCPTHSTL
 TCMSREFQCEDGEACIVLSERCDGFLDCSDESDEKACSDELTVYKVQNLQWTADFSG
 DVTLTWMRPKKMPSASCYVNVYYRVVGESIWKTLETHSNKTNTVLKVLKPDTTYQVKV
 QVQCLSKAHNTNDFVTLRTPEGLPDAPRNLQLSLPREAEGVIVGHWAPPIHTHGLIREYI
 VEYSRSGSKMWASQRAASNFEIKNLLVNTLYTVRVA AVTSRGIGNWSDSKSITTIGK
 VIPPPDIHIDSYGENYLSFTLTMESDIKVNNGYVVNLFWAFDTHKQERRTLNFRGSILSHKV
 GNLTHTSYEISAWAKTDLGDSPLAFEHVMTRGVRPPAPSLKAKAINQTAVECTWTGP
 RNVVYGIFYATSFLDLYRNPKSLTTS LHNKTVIVSKDEQYLFLVRVVVPYQGPSSDYVVV
 KMIPDSRLPPRHLHVHTGKTSVVIKWESPYDSPDQDLLYAI AVKDLIRKTDRSYKVKS
 NSTVEYTLNKLEPGGKYHII VQLGNMSKDSSIKITTVSLAPDALKIITENDHVLLFWKSLA
 LKEKHFNESRGYEIHMFD SAMNITAYLGNTTDNFFKISNLKMGHNYTFTVQARCLFGNQI
 CGEPAILLYDELGSGADASATQAARSTDVA AVVPILFLILLSLGVGFAILYTKHRRQLQSS
 FTA FANSHYSSRLGSAIFSSGDDLGEDDEDAPMITGFSDDVPMVIA

SEQID No:92

MEGASFGAGRAGAALDPVSFARRPQTLLRVASWVFSIAVFGPIVNEGYVNTDSGP ELR
 CVFNGNAGACRFGVALGLGAFLACAAFLLLDVRFQQISSVRDRRRAVLLDLGFSGLWS
 FLWFVGFCFLT NQWQRTAPGPATTQAGDAARAAIAFSFFSILSWVALTVKALQRFRLGT
 DMSLFATEQLSTGASQAYPGYPVGSGVEGTETYQSPPTETLDTSPKGYQVPAY

SEQID No:93

MPLRHWGMARGSKPVGDGAQPMAAMGGLKVLLHWAGPGGGEPWVTFSESSLTAE
 VCIHIAHKVGITPPCFNL FALFDAQAQVWLPPNHILEIPRDASLMLYFRIRFYFRNWHGM
 NPREPAVYRCGPPGTEASSDQTAQGMQLLDPASFEYLF EQGKHEFVNDVASLWELST
 EEEIHHFKNESLGM AFLHLCHLALRHGIPLEEVAKKTSFKDCIPRSFRRHIRQHSALTRLR
 LRNVFRRFLRDFQPGRLSQQMMVMVKYLATLERLAPRFGTERVPVCHLRLLAQAEGEPC
 YIRDSGVAPTDPGPESAAGPPTHEVLVTGTGGIQWWPV EEEVNKEEGSSGSSGRNPQ
 ASLFGKKAKAHKAFGQPADRPREPLWAYFCDFRDITHVVLKEHCVSIHRQDNKCLELSL
 PSRAAALS FVSLVDGYFRLTADSSHYLCHEVAPPRLVMSIRDGIHGPLEPFVQAKLRPE
 DGLYLIHWSTSHPYRLILTVAQRSQAPDGMQSLRLRKFP IEQQDGAFVLEGWGRSFP
 VRELGAALQGCLLRAGDDCFSLRRCCLPQPGETSNLIIMRGARASPRTLNLSQLSFHRV

DQKEITQLSHLGQGTRTNVYEGRLRVEGSGDPEEGKMDDDEDPLVPGRDRGQELRVVL
 KVLDP SHHDIALAFYETASLMSQVSHTHLAFVHGVCVRGPENSMVTEYVEHGPLDVWL
 RRERGHVPMWKMVVAQQLASALSYLENKNLVHGNVCGRNILLARLGLAEGTSPFIKL
 SDPGVGLGALSREERVERIPWLAPECLPGGANSLSSTAMDKWGFATLLEICFDGEAPL
 QSRSPSEKEHFYQRQHRLEPEPSCPQLATLTSQCLTYEPTQRPSFRILRDLTRVQPHNL
 ADVLTVNRDSPAVGPTTFHKRYLKKIRDLGEGHFGKVS LYCYDPTNDGTGEMVAVKAL
 KADCGPQHRS GWKQEIDILRTLYHEHIIKYKGCCEDQGEKSLQLVMEYVPLGSLRDYLP
 RHSIGLAQLLLFAQQICEGMAYLHAHDYIHRDLAARNVLLDNDRLVKIGDFGLAKAVPEG
 HEYYRVREDGDS PVFWYAPECLKEYKFYYASDVWSFGVTLYELLTHCDSSQSPPTKFL
 ELIGIAQQQMTVLRLTELLERGERLPRPDKCPCVYHLMKNCWETEASFRPTFENLIPIL
 KTVHEKYQQQAPS VFSVC

SEQID No:94

MVLIWRRSRYLLREIEAQWSISALWEGFQKWRDNFLQIVQLIQHVYSVWTASRTVFIKII
 VTRHTSTGGGFCDCGDTEAWKTGPFVCVNHPEGRAGTIKENSRCPLNEEVIVQARKIFP
 SVIKYVVENTIWEEEEKELPPELQIREKNERYCYVLFNDEHHSYDHVIYSLQRALDCELA
 AQLHTTAIDKEGRRAVKAGAYAACQEAKEDIKSHSENVSQHPLHVEVLHSEIMAHQKFA
 LRLGSWMNKIMSYS SDFRQIFCQACLREEPDSENPC LISRLMLWD AKLYKGARKILHELI
 FSSFFMEMEYKKLFAMEFVKYYKQLQKEYISDDHDRSISITALSVQMFTVPTLARHLIEE
 QNVISVITETLLEVLPEYLD RNNKFNFQGYSDKLG RYVAVICDLKYILISKPTIWTERLR
 MQFLEGFRSFLKILTCMQGMEEIRRQVGQHIEVDPDWEAAIAIQMQLKNILLMFQEWCA
 CDEELLVAYKECHKAVMRCSTSFSSSKTVVQSCGHSLET KSYRVSEDLVSIHLPLSRT
 LAGLHVRLSRLGAVSRLHEFVSFEDFQVEVLVEYPLRCLVLVAQVVAEMWRRNGLSLIS
 QVFYYQDVKCREEMYDKDIIMLQIGASLMDPNKFLLLVLQRYELAEAFNKTISTKDQDLIK
 QYNTLIEEMLQVLIYIVGERYVPGVGNVTKEEVTMREIHL LCIEMPHSAIAKNLPEN

SEQID No:95

MKALRLSASALFCLLLINGLGAAPPGRPEAQPPPLSSEHKEPVAGDAVP GPKDGSAPEV
 RGARNSEPQDEGELFQGVDPRALAAVLLQALDRPASPPAPSGSQQGPEEEEEAEALLTE
 TVRSQTHSLPAAGEPEPAAPPRPQTPENGPEASDPSEELEALASLLQELRDFSPSSAK
 RQQETAAAETETRTHTLTRVNLESPGPERVWRASWGEFQARVPERAPLPPPAPSQFQ
 ARMPDSGPLPETHKFGEGVSSPKTHLGEALAPLSKAYQGVAAPFPKARRAESALLGGS
 EAGERLLQQGLAQVEAGRRQAEATRQAAAQEERLADLASDLLLQYLLQGGARQRGLG
 GRGLQEAAEERESAREEEEEAEQERRGGEERVGEEDEEAAEAAEAEADEAERARQNAL

LFAEEEDGEAGAEDKRSQEETPGHRRKEAEGTEEGGEEEDDEEMDPQTIDSLIELSTK
 LHLPADDDVVSIIIEVEEKRNRRKKKAPPEPVPPPRAAPATHVRSPQPPPPPPSARDELP
 DWNEVLPPWDREDEVEYPPGPYHPFPNYIRPRTLQPPSALRRRRHYHHALPPSRHYPG
 REAQARHAQQEEAEAEERRLQEQEELENYIEHVLLRRP

SEQID No:96

MAHRKLESVSGSMLDHRVRPGPVPHSQEPESEDMELPLEGYVPEGLELAALRPESPA
 PEEQECHNHSPDGDSSSDYVNNTSEEEDYDEGLPEEEEGITYYIRYCPEDDSYLEGMD
 CNGEEYLAHSAHPVDTDECQEAVEEWTDGAGPHPHGHEAEGSQDYDPDGQLPIPEDEP
 SVLEAHDQEEDGHYCASKEGYQDYYPEEANGNTGASPYRLRRGDGDLEDQEEDIDQI
 VAEIKMSLSMTSITSASEASPEHGPEPGPEDSVEACPPIKASCSPSRHEARPKSLNLLPE
 AKHPGDPQRGFKPKTRTPEERLKWPHQVCNGLEQPRKQQRSDLNGPVDNNIPETK
 KVASFPSFVAVPGPCEPEDLIDGIIFAANYLGSTQLLSERNPSKNIRMMQAEAVSRVKR
 MQKAAKIKKKANSEGDAQTLTEVDLFISTQRIKVLNADTQETMMDHALRTISYIADIGNIV
 VLMARRRMPPRSASQDCIETTPGAQEGKKQYKMICHVFESDAQLIAQSIGQAQFSVAYQ
 EFLRANGINPEDLSQKEYSDIINTQEMYNDLIHFSNSENCKELQLEKHKGEILGVVVVE
 SGWGSILPTVILANMMNGGPAARSGKLSIGDQIMSINGTSLVGLPLATCQGIKGLKNQT
 QVKLNIVSCPPVTTVLIKRPDLKYQLGFSVQNGIICSLMRGGIAERGGVRVGHRIIEINGQ
 SVVATAHEKIVQALSNSVGEIHMKTMPAAMFRLLTGQETPLYI

SEQID No:97

MDTSSVGGLELTDQTPVLLGSTAMATSLTNVGNFSFGPANPLVSRSNKFQNSSVEDDD
 DVVFIIEPVQPPPPSVPVVADQRTITFTSSKNEELQGNDKITPSSKELASQKGSVSETIVI
 DDEEDMETNQGQEKNSSNFIERRPPETKNRTNDVDFSTSSFSRSKVNAGMGNSGITTE
 PDSEIQIANVTTLETGVSSVNDGQLENTDGRDMNLMITHVTSLQNTNLGDVSNGLQSSN
 FGVNIQTYTPSLTSQTKTGVPFPNPGRMNVAGDVFNQGESATHHNPDSWISQSASFPR
 NQKQPGVDSLSPVASLPKQIFQPSVQQQPTKPVKVTANCKKPLQKGQTAYQRKGSA
 HLFCTTCLSSFSHKPAPKKLCVMCKKDITTMKGTIVAQVDSSESFQEFCTSCSLSLYED
 KQNPTKGALNKSRTCICGKLTEIRHEVSFKNMTHKLCSDHCFNRMYRMANGLIMNCCEQ
 CGEYLPSKGAGNNVLVIDGQQKRFFCCQSCVSEYKQVGSHPSFLKEVRDHMQDSFLMQ
 PEKYGKLTCTGCRTOCRFFDMTQCIGPNGYMEPYCSTACMNSHKTKYAKSQSLGIIC
 HFCKRNSLPQYQATMPDGKLYNFCNSSCVAKFQALSMQSSPNGQFVAPSDIQLKCN
 CKNSFCCKPEILEWENKVHQFCKTCSDDYKKLHCIVTYCEYCQEEKTLHETVNFSGVK
 RPFCEGCKLLYKQDFARRLGLRCVTCNYCSQLCKKGATKELDGVVRDFCSEDCKKF

QDWYYKAARCDCCCKSQGTLKERVQWRGEMKHFCQDQHCLLRFYCQQNEPNMTTQKG
 PENLHYDQGCQTSRTKMTGSAPPPSPTPNKEMKNKAVLCKPLTMTKATYCKPHMQTK
 SCQTDDTWRTEYVPVPIPVVYIPVPMHMYSQNIPVPTTVPVVPVVPVFLPAPLDSSEKI
 PAAIEELKSKVSSDALDTELLTMTDMMSEDEGKTETTNINSVIIETDIIGSDLLKNSDPETQ
 SSMPDVPYEPDLIDIEIDFPRAAEELDMENEFLLPPVFGEEYEEQPRPRSKKKGAKRKAV
 SGYQSHDDSSDNSECSFPFKYTYGVNAWKHWVKTRQLDEDLLVLDELKSSKSVKLKE
 DLLSHTTAELNYGLAHFVNEIRRPNGENYAPDSIYYLCLGIQEYLCGSNRKDNIFIDPGY
 QTFEQELNKILRSWQPSILPDGSIFSRVEEDYLWRIKQLGSHSPVALLNTLFYFNTKYFG
 LKTVEQHLRLSFGTVFRHWKKNPLTMENKACLRYQVSSLCGTDNEDKITTKGRKHEDD
 EPVFEQIENTANPSRCPVKMFECYLSKSPQNLNQRMDVFYQLQPECSSSTDSPVWYTST
 SLDRNTLENMLVRVLLVKDIYDKDNYELDEDTD

SEQID No:98

MARHVFLTGPVGKTTLIHKASEVLKSSGVPVDGFYTEEVRQGGRRIGFDVVTLSGTR
 GPLSRVGLEPPPGKRECRVGQYVVDLTSFEQLALPVLARNADCSSGPGQRVCVIDEIGK
 MELFSQLFIQAVRQTLSTPGTIILGTIPVPGKPLALVEEIRNRKDVKFVNTKENRNHLL
 PDIVTCVQSSRK

SEQID No:99

MAAPPEPGEPEERKSLKLLGFLDVENTPCARHSILYGLSGSVVAGFGHFLTSRIRRS
 DVGVGGFILVTLGCWFHCRYNYAKQRIQERIAREEIKKILYEGTHLDPERKHNGSSSN

SEQID No:100

MLSLDFLDDVRRMNKRQLYYQVLNFGMIVSSALMIWKGLMVITGSESPIVVVLSGSMEP
 AFHRGDLLFLTNRVEDPIRVGEIVVFRIEGREIPVHRVLKIHEKQNGHIKFLTKGDNNAVD
 DRGLYKQGQHWLEKKDVVGRARGFVPYIGIVTILMNDYPKFYAVLFLLGLFVLVHRE

SEQID

No:101AESDLQLAQIKCNLGRAVQLQELWPGGLFWTRKLSTYIRLYGRKFSKEDHVLFIK
 LLYELVSIPKLEISMMQG FARLLINLLKKKELLSRADLELPWRPLYDMVERILYSKTEHLG
 LNWFPNSVENILKTLVKSCRPFYFADATAEMLEEWRLMCPFDVTMOKAITYFEIFLPTS
 LPPELHHKGFKLWFDELIGLWVSVQNLPOWEGQLVNLFARLATDNIGYIDWDPYVPKIF
 TRILRSLNLPVGSSQVLVPRFLTAYDIGHAVIWITAMMGPSKLVQKHLAGLFNSITSFY
 HPSNNGRWLNKLMKLLQRLPNSVVRRLHRERYKKPSWLTPVPDSHKLTDQDVTDFVQ

CIIQPVLLAMFSKTGSLEAAQALQNLALMRPELVIPPVLERTYPALETLTEPHQLTATLSC
VIGVARSLVSGGRWFPEGPTHMLPLLMRALPGVDPNDFSKCMITFQFIATFSTLVPLVD
CSSVLQERNDLTEVERELCSATAEFEDFVLQFMDRCFGLIESSTLEQTREETETEKMT
LESLVELGLSSTFSTILTQCSKEIFMVALQKVFNSTSHIFETRVAGRMVADMCRAAVKC
CPEESLKLFPVPHCCSVITQLTMNDDVLNDEELDKELLWNLQLLSEITRVDGRKLLLYREQ
LVKILQRTLHLTCKQGYTLSCNLLHHLLRSTTLIYPTEYCSVPGGFDKPPSEYFPIKDWG
KPGDLWNLGIQWHVPSSEEVSAFYLLDSFLQPELVKLQHC GDGKLEMSRDDILQSLTI
VHNCLIGSGNLLPPLKGEPVTNLVPSMVSLEETKLYTGLEYDLSRENHREVIATVIRKLLN
HILDNSED DTKSLFLIIKIIGDLLQFQGSHKHEFDSRWKSFNLVKKSMENRLHGKKQHIRA
LLIDRVMLQHELRTLVEGCEYKKIHQDMIRDLLRLSTSSYSQVRNKAQQTFFAALGAYN
FCCRDIIPLVLEFLRPDRQGVTQQQFKGALYCLLGNHSGVCLANLHDWDCIVQTWPAIV
SSGLSQAMSLEKPSIVRLFDDLAEKIHRQYETIGLDFTIPKSCVEIAELLQQSKNPSINQIL
LSPEKIKEGIKRQQEK NADALRNYENLVDTL LDGVEQRNLPWKFEHIGIGLLSLLLRDDR
VLPLRAIRFFVENLNHDAIVVRKMAISAVAGILKQLKRTHKKLTINPCEISGCPKPTQIIAGD
RPDNHWLHYDSKTIPRTKKEWESSCFVEKTHWGYTWPKNMVVYAGVVEEQPKLGRS
REDMTEAEQIIFDHFSDPKFVEQLITFLSLED RKGKDKFNPRRFCLFKGIFRNFD DAFLPV
LKPHLEHLVADSHESTQRCVAEIIAGLIRGSKHWTFEKVEKLWELLCP LLRTALS NITVET
YNDWGACIATSCESRDPRKLHWFELLLESPLSGEGGSFVDACRLYVLQGGGLAQQEW
RVPELLHRLKYLEPKLTQVYKNVRERIGSVLTYIFMIDVSLPNTTPTISPHVPEFTARILE
KLKPLMDVDEEIQNHVMEENGIGEEDE RTQGIKLLKTILKWLMASAGRSFSTAVTEQLQL
LPLFFKIAPVENDNSYDELKRDAKLCLSLMSQGLLYPHQVPLVLQVLKQTARSSSWHAR
YTVLTYLQTMVFYNLFIFLNNEDAVKDIRWLVISLLEDEQLEVREMAATTLSGLLQCNFLT
MDSPMQIHFEQLCKTKLPKKRKRDPGSGVGTIPSAELVKRHAGVLGLGACVLSSPYDV
PTWMPQLLMNLSAHLNDPQPIEMTVKKTL SNFRRTHHDNWQEHKQQFTDDQLLVLTDL
LVSPCYA

SEQID No:102

MSDSVILRSIKKFGEENDGFESDKSYNNDDKKSRLQDEKKGDGVRVGFFQLFRFSSTDI
WLMFVGS LCAFLHGIAQPGVLLIFGTMTDVFIDYDVELQELQIPGKACVNNTIVWTNSSL
NQNM TNGTRCGLLNIESEMIKFASY YAGIAVAVLITGYIQICFWVIAAARQIQKMRKFYFR
RIMRMEIGWFDCNSVGELNTRFSDDINKINDAIADQMALFIQRMTSTICGFL LGFFRGWK
LTLVIISVSPLIGIGAATIGLSVSKFTDYELKAYAKAGVVADEVISSMRTVA AFGGEKREVE
RYEKNLVFAQRWGIRKGIVMGFFTGFVWCLIFLCYAVAFWYGSTLV LDEGEYTPGTLVQ
IFLSVIVGALNLGNASPCLEAFATGRAAATSIFETIDRKPIIDCMSEDGYKLDRIKGEIEFHN

VTFHYPSRPEVKILNDLNMVIKPGEMTALVGPSGAGKSTALQLIQRFYDPCEGMVTVDG
 HDIRSLNIQWLRDQIGIVEQEPVLFSTTIAENIRYGREDATMEDIVQAAKEANAYNFIMDL
 PQQFDTLVGEQGGQMSGGQKQRVAIARALIRNPKILLDMATSALDNESEAMVQEVLS
 KIQHGHTIISVAHRLSTVRAADTIIGFEHGTAVERGTHEELLERKGVYFTLVTLQSQGNQA
 LNEEDIKDATEDDMLARTFSRGSYQDSLRSIRQRSKSQLSYLVHEPPLAVVDHKSTYE
 EDRKDKDIPVQEEVEPAPVRRILKFSAPWPYMLVGSVGA AVNGTVTPLYAFLFSQILG
 TFSIPDKEEQRSQINGVCLLFVAMGCVSLFTQFLQGYAFAKSGELLTKRLRKFGFRAML
 GQDIAWFDDLNRNSPGALTTRLATDASQVQGAAGSQIGMIVNSFTNTVTAMIIAFSFSWK
 LSLVILCFFPFLALSGATQTRMLTGFA SRDKQALEMVGQITNEALSNI RTVAGIGKERRFI
 EALETELEKPFKTAIQKANIYGFCFAFAQCIMFIANSASYRYGGYLISNEGLHFSYVFRVIS
 AVVLSATALGRAFSYTPSYAKAKISAARFFQLLDRQPPISVYNTAGEKWDNFQGGKIDFVD
 CKFTYPSRPDSQVLNGLSVSISPGQTLAFVGSSGCGKSTSIQLLERFYDPDQGKVMIDG
 HDSKKVNVQFLRSNIGIVSQEPVLFACSIMDNIKYGDNTKEIPMERVIAAAKQAQLHDFV
 MSLPEKYETNVGSQGSQSLSRGEKQRIAIARAIVRDPKILLDEATSALDTESEKTVQVAL
 DKAREGRTCIVIAHRLSTIQNADIIVMAQGVVIEKGTHEELMAQKGAYYKLVTTGSPIS

SEQID No:103

MSLVLNDLLICCRQLEHDRATERKKEVEKFKRLIRDPETIKHLDRHSDSKQGKYLNWDA
 VFRFLQKYIQKETECLELRIAKPNVSASTQASRQKKMQEISSLVKYFIKCANRRAPRLKCQE
 LLNYIMDTVKDSSNGAIYGADCSNILLKDILSVRKYWCEISQQQWLELFSVYFRLYLKPS
 QDVHRVLVARIIHAVTKGCCSQT DGLNSKFLDFFSKAIQCARQEKSSSGLNHILAALTIFL
 KTLAVNFRIRVCELGDEILPTLLYIWTQHRLNDSLKEVIIELFQLQIYIHPKGAKTQEKGA
 YESTKWR SILYNLYDLLVNEISHIGSRGKYSSGFRNIAVKENLIELMADICHQVFNEDTRS
 LEISQSYTTTQRESSDYSVPCKRKKIELGWEVIKDH LQKSQNDFDLVPWLQIATQLISKY
 PASLPNCELSPLLMLSQLLPQQRHGERTPYVLRCLTEVALCQDKRSNLESSQKSDLLK
 LWNKIWCITFRGISSEQIQAENFGLLGAI IQGSLVEVDREFWKLFTGSACRPSCPAVCC
 TLALTTSIVPGAVKMGIEQNMCEVNRSFSLKESIMKWLLFYQLEGDLENSTEVPPIHLSN
 FPHLVLEKILVSLTMKNCKAAMNFFQSVPECEHHQKDKEELSFSEVEELFLQTTFDKMD
 FLTIVRECGIEKHQSSIGFSVHQNLKESLDRCLLGLSEQLLNNYSSEITNSETLVRC SRLL
 VGVLGCCYCYMGVIAEEEEAYKSELFQKANS LMQCAGESITLFKNKTNEEFRIGSLRNMMQ
 LCTRCLSNCTKKSPNKIASGFFLRLLTSKLMNDIADICKSLASF IKKPFDRGEVESMEDDT
 NGNLMEVEDQSSMNL FNDYPDSSVSDANEPGESQSTIGAINPLAEEYLSKQDLLFLDML
 KFLCLCVTTAQTNTVSFRAADIRRKLLMLIDSSTLEPTKSLHLHMYLMLLKELPGEEYPLP
 MEDVLELLKPLSNVCSLYRRDQDVCKTILNHVLHVVKNLGQSNMDSENTRDAQQGFLT

VIGAFWHLTKERKYIFSVRMALVNCLKTLLEADPYSKWAILNVMGKDFPVNEVFTQFLAD
NHHQVRMLAAESINRLFQDTKGDSSRLLKALPLKLQQTAFENAYLKAQEGMREMSHSA
ENPETLDEIYNRKSULLTIAVVLSCSPICEKQALFALCKSVKENGLEPHLVKKVLEKVSE
TFGYRRLEDFMASHLDYLVLEWLNLDQTEYNLSSFPFILLNYTNIEDFYRSCYKVLIPHLV
IRSHFDEVKSIANQIQEDWKSLLTDCFPKILVNILPYFAYEGTRDSGMAQQRETATKVYD
MLKSENLLGKQIDHLFISNLPEIVVELLMTLHEPANSSASQSTDLCDFSGDLDPAPNPPH
FPSHVIKATFAYISNCHKTKLKSILEILSKSPDSYQKILLAICEQAAETNNVYKKHRILKIYHL
FVSLLLKDIKSGLGGAFAFVLRDVIYTLIHYINQRPSCIMDVSLRSFSLCCDLLSQVCQTA
VTYCKDALENHLHVIVGTLIPLVYEQVEVQKQVLDLLKYLVIDNKDNENLYITIKLLDPFPD
HVVFKDLRITQQKIKYSRGPFSLLIEINHFLSVSVYDALPLTRLEGLKDLRRQLELHKDQ
MVDIMRASQDNPDGIMVKLVVNLLQLSKMAINHTGEKEVLEAVGSCLEVGPIDFSTIA
IQHSDKASYTKALKLFEDKELQWTFIMLTYNNTLVEDCVKVRSAAVTCLKNILATKTGH
SFWEIYKMTTDPMLAYLQPFRTSRKKFLEVPRFDKENPFEGLDINLWIPLSENHDIWIK
TLTCAFLDSGGTKCEILQLLKPMCEVKTDFCQTVLPYLIHDILLQDTNESWRNLLSTHVQ
GFFTSLRHFSTSRSTTPANLDSESEHFFRCCLDKKSQRTMLAVVDYMRQKRPSS
GTIFNDAFWLDLNYLEVAKVAQSCAAHFTALLYAEIYADKKSMDDQEKRSALAFEEGSQS
TTISLSEKSKEETGISLQDLLLEIYRSIGEPDSLYGCGGGKMLQPITRLRTEHEAMWG
KALVTYDLETAIPSSTRQAGIIQALQNLGLCHILSVYLGKLDYENKDWCPPELEELHYQAA
WRNMQWDHCTSVSKEVEGTSYHESLYNALQSLRDREFSTFYESLKYARVKEVEEMCK
RSLESVYSLYPTLSRLQAIGELESIGELFSRSVTHRQLSEVYIKWQKHSQLLKDSDFSQ
EPIMALRTVILEILMEKEMDNSQRECIKDILTKHLVELSILARTFKNTQLPERAIFQIKQYNS
VSCGVSEWQLEEAQVFWAKKEQSLALSILKQMIKKLDASCAANNPSLKLTYTECLRVCG
NWLAECLNPAVIMQTYLEKAVEVAGNYDGESSDELNRNGKMKAFSLARFSDTQYQR
IENYMKSSSEFENKQALLKRAKEEVGLLREHKIQTNRYTVKVQRELELDELALRALKEDRK
RFLCKAVENYINCLLSGEEHDMWVFRLCSLWLENSGVSEVNGMMKRDGMKIPTYKFLP
LMYQLAARMGTKMMGGLGFHEVLNNLISRISMDHPHHTLFILALANANRDEFLTKEVA
RRSRITKNVPKQSSQLDEDRTEAANRIICTIRSRRPQMVRSEALCDAYIILANLDATQW
KTQRKGINIPADQPITKLKNLEDVVVPTMEIKVDHTGEYGNLVTIQSFKAEFRLAGGVNLP
KIIDCVGSDGKERRQLVKGRDDLQDAVMQQVFQMCNTLLQRNTETRKRKLTICTYKV
VPLSQRSGVLEWCTGTVPIGEFLVNNEGGAHKRYRPNDFAFQCQKKMMEVQKKSFE
EKYEVMFMDVCQNFQPVFRYFCMEKFLDPAIWFEKRLAYTRSVATSSIVGYILGLGDRHV
QNILINEQSAELVHIDLGVAFEQGKILPTPETVPFRLTRDIVDGMGITGVEGVFRRCCCKT
MEVMRNSQETLLTIVEVLLYDPLFDWTMNPALKALYLQQRPEDETELHPTLNADDQECK

RNLSDIDQSFDKVAERVLMLRLQEKLKGVVEEGTVLSVGGQVNLLIQQAIDPKNLSRLFPG
WKAWV

SEQID No:104

MDLEGDRNGGAKKKNFFKLNNKSEKDKKEKKPTVSVFSMFRYSNWLDKLYMVVGTLA
AIIHGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSDINDTGFFMNLEEDMTRYAYY
YSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQFFHAIMRQEIGWFDVHDVGELNTRLTD
DVSKINEGIGDKIGMFFQSMATFFTGFIVGFTRGWKLTLVILAI SPVLGLSAAVWAKILSSF
TDKELLAYAKAGAVAEVLAARTVIAFGGQKELERYNKNLEEAKRIGIKKAITANISIGA
AFLLIYASYALAFWYGTTLVLSGEYSIGQVLTVFFSVLIGAFSVGQASPSIEAFANARGAA
YEIFKIIDNKPSIDSYSGHKKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKVQSGQTV
ALVGNSGCGKSTTVQLMQRLYDPTEGMVSVDGQDIRTINVRFLREIIGVVSQEPVLFAT
TIAENIRYGRENVMTDEIEKAVKEANAYDFIMKLP HKFDTLVGERGAQLSGGQKQRIIA
RALVRNPKILLLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIA GFDD
GVIVEKGNHDELMKEKGIYFKLVMTAGNEVELENAADESKSEIDALEMSSNDSRSSLI
RKRSTRRSVRGSQAQDRKLSTKEALDESIPPVSFWRIMKLNLTWPYFVVGVFCAIING
GLQPAFAIIFSKIIGVFTRIDDPETKRQNSNLFSLFLALGIISFITFFLQGFTFGKAGEILTK
RLRYMVFRSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKGAIGSRLAVITQNIANLGT
GIIISFIYGWQLTLLLLAIVPIIAIAGVVEMKMLSGQALKDKKELEGAGKIA TEAIENFRTVVS
LTQEQQFEHMYAQS LQVPYRNSLRKAHIFGITFSFTQAMMYFSYAGCFRFGAYLV AHKL
MSFEDVLLVFS AVVFGAMAVGQVSSFAPDYAKAKISAAHIIMIEKTPLIDSYSTEGLMPN
TLEGNVTFGEVVFNYPTRPDIPVLQGLSLEVKKGQTLALVGSSGCGKSTVVQLLERFYD
PLAGKVLLDGKEIKRLNVQWLRAHLGIVSQEPILFDCSIAENIAYGDNSRVVSQEEIVRAA
KEANIHAFIESLPNKYSTKVGDKGTQLSGGQKQRIAIARALVRQPHILLLDEATSALDTE
EKVVQEALDKAREGRTCIVIAHRLSTIQNADLIVVFQNGRVKEHGTHQQLLAQKGIYFSM
VSVQAGTKRQ

SEQID No:105

MFSLSSSTVQPQFTVPLSHLINA FHTPKNTSVSLSGVSVSQNQHRDVVPEHEAPSSECM
FSDFLTCLNIVSIGKGKIFEGYRSMFM EPAKRMKKS LDTT DNWHIRPEPFSLSIPPSLNL
DLGLSELKIGQIDQLVENLLPGFCKGKNIS SHWHTSHVSAQSFFENKYGNLDIFSTLRSS
CLYRHHSRALQSICSDLQYWPVFIQSRGFKTLKSRT RRLQSTSERLAETQNIAPSFVKG
FLLRDRGSDVESLDKLMKTKNIPEAHQDAFKTGFAEGFLKAQALTQKTNDSLRRLRTRILF
VLLLFGIYGLLKNPFLSVRFRTTTGLDS AVDPVQMKNVTFEHVKGVEEAKQELQEVVEF

LKNPQKFTILGGKLPKGILLVGPPGTGKTLLARAVAGEADVPFYYASGSEFDEMFGVGVG
 ASRIRNLFREAKANAPCVIFIDELDSVGGKRIESPMHPYSRQTINQLLAEMDGFKNPNEG
 IIGATNFPEALDNALIRPGRFDMQVTVPRPDVKGRTEILKWYLNKIKFDQSVDPETIARGT
 VGFSGALENLVNQAALKAADVKGEMVTMKELEFSKDKILMGPERRSVEIDNKNKTITA
 YHESGHAIAYYTKDAMPINKATIMPRGPTLGHVSLLPENDRWNETRAQLLAQMDVSMG
 GRVAEELIFGTDHITTGASSDFDNATKIAKRMVTKFGMSEKLGVMYSDTGKLSPETQS
 AIEQEIRILLRDSYERAKHILKTHAKEHKNLAEALLTYETLDAKEIQIVLEGKKLEVR

SEQID No:106

MDPSMGVNSVTISVEGMTCNNSCVWTIEQQIGKVNGVHHIKVSLEEKNATIIYDPKLQTPK
 TLQEAIDDMGFDVAIHNPDPPLVLTDTLFTVTASLTLPWDHIQSTLLKTKGVTDIKIYPQK
 RTVAVTIIPSIVNANQIKELVPELSLDTGTLEKKSGACEDHSMAGAGEVVLKMKVEGMTC
 HSCTSTIEGKIGKLQGVQRIKVS LDNQEATIVYQPHLISVEEMKKQIEAMGFPAFVKKQP
 KYLKLGAIDVERLKNTPVKSSEGSQQRSPSYTNDSTATFIIDGMHCKSCVSNIESTLSAL
 QYVSSIVVSLENRSAIVKYNASSVTPESLRKAIEAVSPGLYRVISITSEVESTSNPSSSSSL
 QKIPLNVVSQPLTQETVINIDGMTCNNSCVQSIEGVISKKPGVKSI RVS LANSNGTVEYDPL
 LTSPETLRGAIEDMGFDATLSDTNEPLVVIAQPSSEMPLLTSTNEFYTKGMTPVQDKEE
 GKNSSKCYIQVTGMTCASCVANIERNLRREEGIYSILVALMAGKAEVRYNPAVIQPPMIA
 EFIRELGFGATVIENADEGDGVLELVVRGMTCASCVHKIESSLTKHRGILYCSVALATNK
 AHIKYDPEIIGPRDIIHTIESLGFEASLVKKDRSASHLDHKREIRQWRRSFLVSLFFCIPVM
 GLMTYMMVMMDHFFATLHHNQNSKEEMINLHSSMFLE RQILPGLSVMNLLSFLLCVPV
 QFFGGWYFYIQAYKALKHKTANMDVLIVLATTIAFAYSLIILLVAMYERAKVNPITFFDTPP
 MLFVFIALGRWLEHIAKGTSEALAKLISLQATEATIVTLDS DNILLSEEQVDVELVQRGDII
 KVVPGGKFPVDGRVIEGHSMVDESLITGEAMPVAKKPGSTVIAGSINQNGSLLICATHVG
 ADTTL SQIVKLVEEAQTSKAPIQQFADKLSGYFVPFIVFSIATLLVWIVIGFLNFEIVETYF
 PGNRSISRTETIIRFAFQASITVLCIACPCSLGLATPTAVMVGTGVGAQN GILIKGGEPL
 MAHKVKVVVFDKTGTITHGTPVVNQVKVLTESNRISHHKILAIVGTAESNSEHPLGTAITK
 YCKQELDTETLGT CIDFQVVP GCGISCKVTNIEGLLHKNNWNIEDNNIKNASLVQIDASN
 EQSSTSSSMIIDAQISNALNAQQHKVLIGNREWMIRNGLVINNDVNDFMTEHERKGRTA
 VLVAVDDELGLIAIADTVKPEAE LAIHILKSMGLEVV LMTGDNSKTARSIASQVGITKVFA
 EVLP SHKVAKVKQLQEEGKRVAMVGDGINDSPALAMANVGIAIGTGT DVAIEAADVVLIR
 NDLLDVVASIDLSRKTVKRIRINFVFALIYNLVGIPIAAGVFMPIGLVLPWMGSAAMAAS
 SVSVVLSSLFLKLYRKPTYESYELPARSQIGQKSPSEISVHV GIDDTSRNSPKLGLLDRIV
 NYSRASINSLSDKRSLNSVVTSEPDKHSLLVGDFREDDDTAL

SEQID No:107

METPAAAAPAGSLFPSFLLACGTLVAALLGAAHRLGLFYQLLHKVDKASVRHGGENVA
 AVLRAHGVRFIFTLVGGHISPLLVACEKLGIRVVDTRHEVTAVFAADAMARLSGTVGVAA
 VTAGPGLTNTVTAVKNAQMAQSPILLGGAASTLLQNRGALQAVDQLSLFRPLCKFCVS
 VRRVRDIVPTLRAAMAAAQSGTPGPVFVELPVDVLYPYFMVQKEMVPAKPPKGLVGRV
 VSWYLENYLANLFAGAWEPQPEGPLPLDIPQASPQQVQRCVEILSRAKRPLMVLGSQA
 LLTPTSADKLRAAVETLGVPCFLGGMARGLLGRNHPLHIRENRSAAKKADVIVLAGTVC
 DFRLSYGRVLSHSSKIIIVNRNREEMLLNSDIFWKPQEAVQGDVGSFVLKLVEGLQGQT
 WAPDWVEELREADRQKEQTFREKAAMPVAQHLNPVQVLQQLVEETLPDNSILVVDGGD
 FVGTAHLVQPRGPLRWLDPGAFTLGVGAGFALGAKLRPDAEVWCLFGDGAFGYS
 LIEFDTFVRHKIPVMALVGNDAGWTQISREQVPSLGSNVACGLAYTDYHKAAMGLGAR
 GLLLSRENEDQVVKVLHDAQQQCRDGHVNVNIGRTDFRDGSIIV

SEQID No:108

MPVLSRPRPWGNTLKRTAVLLALAAYGAHKVYPLVRQCLAPARGLQAPAGEPTQEAS
 GVAAAKAGMNRVFLQRLLWLLRLLFPRVLCRETGLLALHSAALVSRTFLSVYVARLDGR
 LARCIARKDPRAFGWQLLQWLLIALPATFVNSAIRYLEGQLALSFRSRLVAHAYRLYFSQ
 QTYRVSNDGRLRNPDQSLTEDVVAFAASVAHLYSNLTKPLLDVAVTSYTLLRAARSR
 GAGTAWPSAIALGVFLTANVLRAFSPKFGELVAEEARRKGELRYMHSRVVANSEEIAF
 YGGHEVELALLQRSYQDLASQINLILLERLWYVMLEQFLMKYVWSASGLLMVAVPIITAT
 GYSESDAEAVKKAALKKEEELVSE RTEAFTIARNLLTAAADAIERIMSSYKEVTELAGYT
 ARVHEMFQVFEDVQRCHFKRPRELEDAQAGSGTIGRSGVRVEGPKIRGQVVDVEQGI
 ICENIPIVTPSGEVVVASLNIRVEEGMHLLITGPNGCGKSSLFRILGGLWPTYGGVLYKPP
 PQRMFYIPQRPYMSVGLSLRDQVIYPDSVEDMQRKGYSEQDLEAILDVVHLHHILQREG
 GWEAMCDWKDVLSGGEKQRIGMARMFYHRPKYALLDECTSAVSIDVEGKIFQAAKDA
 GIALLSITHRPSLWKYHTHLLQFDGEGGWKFELDSAARLSLTEEKQRLEQQLAGIPKM
 QRRLQELCQILGEAVAPAHVPAPSPQGPGLQAST

SEQID No:109

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVILVAGAFFWLVSLLASVWVILVHVTD
 RSDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDGRSPISIRQMAYVS
 GLSFGIISGVFSVINILADALGPGVVGIIHGDSPPYYFLTSAFLTAAIILLHTFWGVVFFDACE

RRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRS
LLCRRQEDSRVMVYSALRIPPED

SEQID No:110

MYEGKKTKNMFLTRALEKILADKEVKKAHHSQLRKACEVALEEIKAETEKQSPPHGEAK
AGSSTLPPVKSKTNFIEADKYFLPFELACQSKCPRIVSTSLDCLQKLIAYGHLTGNAPDST
TPGKKLIDRIIETICGCFQGPQTDEGVQLQIIKALLTAVTSQHIEIHEGTVLQAVRTCYNIL
ASKNLINQTTAKATLTQMLNVIFARMENQALQEAKQMEKERHRQHHLHPSPVSHHEP
ESPQLRYLPPQTVDHISQEHEGDLHTNDVDKSLQDDTEPENGS DISSAENEQTEAD
QATAAETLSKNEVLYDGENHDCEEKPDIVQNIVEEMVNIVVGDMGEGTTINASADGNI
GTIEDGSDSENIQANGIPGTPISVAYTPSLPDDRSLVSSNDTQESGNSSGPSPGAKFSHI
LQKDAFLVFRSLCKLSMKPLSDGPPDPKSHELRSKILSLQLLL SILQNAGPIFRTNEMFIN
AIKQYLCVALSKNGVSSVPEVFELSLSIFLTLLSNFKTHLKMQIEVFFKEIFLYILETSTSSF
DHKWMVIQTLTRICADAQSVVDIYVNYDCDLNAANIFERLVNDLSKIAQGRGSQELGMS
NVQELSLRKKGLECLVSISKCMVEWSKDQYVNPNSQTTLGQKEPSEQEMSEIKHPETIN
RYGSLNSLESTSSSGIGSYSTQMSGTDNPEQFEVLKQQKEIEQGIDLFNKKPKRGIQYL
QEQQMLGTTTPEDIAQFLHQEERLDSTQVGEFLGDNDKFNKEVMYAYVDQHDFSGKDF
VSALRMFLEGFRLPGEAQKIDRLMEKFAARYLECNQGQTLFASADTAYVLAYSIIMLTTD
LHSPQVKNKMTKEQYIKMNRGINDSKDLPEEYLSAIYNEIAGKKISMKETKELTIPTKSSK
QNVASEKQRRLLYNLEMEQMAKTAKALMEAVSHVQAPFTSATHLEHVRPMPFKLAWTP
FLAAFSVGLQDCDDTEVASLCLEGIRCAIRIACIFS IQLERDAYVQALARFTLLTVSSGITE
MKQKNIDTIKTLITVAHTDGNYLGNWHEILKCISQLKLAQLIGTGVPKPRYISGTVRGRG
SLTGT KDQAPDEFVGLGLVGGNV DWKQIASIQESIGETSSQS VVVAVDRIFTGSTRLDG
NAIVDFVRWLCAVSMDELLSTTHPRMFSLQKIVEISYYNMGRIRLQWSRIWEVIGDHFNK
VGCNP NEDVAIFAVDSL RQLSMKFLEKGELANFRFQKDFLRPF EHIMKRNRSP TIRDMV
VRCIAQMVNSQAANIRSGWKNIFS VFHLAASDQDESIVELAFQTTGHIVTLVFEKHFPATI
DSFQDAVKCLSEFACNAAFPDTSM EAIRLIRHCAKYVSDRPQAFKEYTSDDMNVAPED
RVWVRGWFPILFELSCIINRCKLDVRTRGLTVMFEIMKTYGHTYEKHHWWQDLFRIVFRIF
DNMKLPEQQTEKA EWMTTTCNHALYAICDVFTQYLEVLSDVLLDDIFAQLYWCVQQDN
EQLARSGTNCLENVVILNGEKFTLEIWDKTCNCTLDIFKTTIPHALLTWRPN SGETAPPP
PSPVSEKPLDTISQKSVDIHDSIQPRSV DNRQPAPLV SASAVNEEVSKIKSTAKFPEQKL
FAALLIKCVVQLELIQTIDNIVFFPATSKKEDAENLAAAQRDAVDFDVRVDTQDQGM YRF
LTSQQLFKLLDCLLESHRFAKAFNSNNEQRTALWKAGFKGKSKPNLLKQETSSLACGLR

ILFRMYMDESRSVAWEEVQQRLLNVCSEALSYFLTLTSESHREAWTNLLLLFLTQVLKIS
DNRFKAHASFYYPPLLCEIMQFDLPELRVLRFFLRIGVVFQISQPPEQELGINKQ

SEQID No:111

MAVSRLDRLFILLDTGTPVTRKAAAQQLGEVVKLHPHELNNLLSKVLIYLRSANWDTRI
AAGQAVEAIVKNVPEWNPVPRTRQEPTSESSMEDSPTTERLNFDREFDICRLLQH GASLL
GSAGAEFEVQDEKSGEVDPKERARQRKLLQKKLGLNMGEAIGMSTEELFNDEDLDYT
PTSASFVNKQPTLQAAELIDSEFRAGMSNRQKNKAKRMAKLFKQSRSDAVETNEKSN
DSTDGEPEEKRRKIANVVINQSANDSKVLIDNIPDSSSLIEETNEWPLESFCEELCNDLFN
PSWEVRHGAGTGLREILKAHGKSGGKMGDSTLEEMIQQHGEWLEDLVIRLLCVFALDR
FGDFVSDEVVAPVRETCAQTLGVVLKHMNETGVHKTVDVLLKLLTQEQWEVRHGGLLG
IKYALAVRQDVINTLLPKVLTRIIIEGLQDLDDVRAVAAASLVPVVESLVYLQTQKVPFIIN
TLWDALLELDDLTASTNSIMTLLSSLLTYPQVQQCSIQQSLTVLVPVWPFLHHTISSVR
RAALETFLTLLSTQDQNSSSWLIPILPDMLRHIFQFCVLESSQEILDLHKVWMELLSKAS
VQYVVAACPWMGAWLCLMMQPSHLPIDLNMLLEVKARAKEKTGGKVRQGQSQNKE
VLQEYIAGADTIMEDPATRDFVVMRARMMAAKLLGALCCCICDPGVNVVTQEIKPAESL
GQLLLFHLNSKSALQRISVALVICEWAALQKECKAVTLAVQPRLLDILSEHLYYDEIAVPF
TRMQNECKQLISSLADVHIEVGNRVNNNVLTIDQASDLVTTVFNEATSSFDLNPQVLQQ
LDSKRQQVQMTVTETNQEWQVLQLRVHTFAACAVVSLQQLPEKLNPIIKPLMETIKKEE
NTLVQNYAAQCIALLQOCTTRTPCPNSKIIKNLCSSLCVDPYLTPCVTCPVPTQSGQEN
SKGSTSEKDGMHHTVTKHRGIITLYRHQKAFAITSRRGPTPKAVKAQIADLPAGSSGNI
LVELDEAQKPYLVQRRGAEFALTIVKHFGGEMAVKLPHLWDAMVGPLRNTIDINNFDG
KSLLDKGDSPAQELVNSLQVFETAAASMDSELHPLLQHLPHLYMCLQYPSTAVRHMA
ARCVGVMSKIATMETMNIFLEKVLWPWLGAIDDSVKQEGAIEALACVMEQLDVGIVPYIVLL
VVPVLGRMSDQTDVRFMATQCFATLIRLMPLEAGIPDPPNMSAELIQLKAKERHFLEQ
LLDGKKLENYKIPVPINAELRKYQQDGVNWLAFNLKYKLHGILCDDMGLGKTLQSIKILA
GDHCHRAQEYARSKLAECMPLPSLVCPPTLTGHWVDEVGKFCSREYLNPLHYTGPP
TERIRLQHQQVCRHNLIVASYDVVRNDIDFFRNIKFNYCILDEGHVINGKTKLSKAVKQLT
ANYRIILSGTPIQNNVLELWSLFDLMPGFLGTERQFAARYGKPILASRDARSSSREQEA
GVLAMDALHRQVLPFLLRRMKEDVLQDLPPKIIQDYCYCTLSPLQVQLYEDFAKSRAKCD
VDETSSATLSEETEKPKLKATGHVFQALQYLRLCNHPALVLTPOHPEFKTTAEKLAV
QNSSLHDIQHAPKLSALKQLLLDLGLGNGSTSESGTESVVAQHRILFCQLKSMLDIVEH
DLLKPHLPSVTYLRLDGSIPPGQRHSIVSRFNNDPIDVLLLTTHVGGLGLNLTGADTVV
FVEHDWNPMRDLQAMDRAHRIGQKRVVNVYRLITRGTTLEEKIMGLQKFKMNIANTVISQ

ENSSLQSMGTDQLLDLFTLDKDGKAEKADTSTSGKASMKSILENLSDLWDQEQYDSEY
SLENFMHSLK

SEQID No:112

MGGRVFLAFCVWLTLPGAETQDSRGCARWCPQNSSCVNATACRCNPGFSSSFSEIITTP
TETCDDINECATPSKVSCGKFSDCWNTGSGYDCVCSPGYEPVSGAKTFKNESENTCQ
DVDECQQNPRLCKSYGTCVNTLGSYTCQCLPGFKFIPEDPKVCTDVNECTSGQNPCH
SSTHCLNNVGSYQCRCPGWQPIPGSPNGPNNTVCEDVDECSSGQHQCDSSTVCFN
TVGSYSCRCRPGWKPRHGIPNNQKDTVCEDMTFSTWTPPPGVHSQTLRFFDKVQDL
GRDSKTSSAEVTIQNVIKLVDELMEAPGDVEALAPPVRHLIATQLLSNLEDIMRILAKSLP
KGPFTYISPSNTELTLMIQERGDKNVTMGQSSARMKLNWAVAAGAEDPGPAVAGILSIQ
NMTTLLANASLNLHSHKKQAELEEIYESSIRGVQLRRLSAVNSIFLSHNNTKELNSPILFAF
SHLESSDGEAGRDPAPKDVMPGPRQELLCAFWKSDSDRGHGWATEVCQVLGSKNGS
TTCQCSSLSSFTILMAHYDVEDWKLTLITRVGLALSFLCLLLCILTFLVRPIQGSRTTIHL
HLCICLFGVSTIFLAGIENEGGQVGLRCLVAGLLHYCFLAFCWMSLEGLELYFLVVRV
FQQGGLSTRWLCLIGYGVPLLIVGVSAAIYSKGYGRPRYCWLDFEQGFLWSFLGPVTFII
LCONAVIFVTTVWKLTKQFSEINPDMKKLKKARALTITAIQFLLLGCTWVFGLFIFDDRSLV
LTYVFTILNCLQGAFLYLLHCLLNKKVREEYRKWACLVAGGSKYSEFTSTTSGTGHNQT
RALRASESGI

SEQID No:113

SLQWTAVATFLYAEVFVLLLCIPFISPKRWQKIFKSRLVELLVSYGNTFFVVLIVILVLLVI
DAVREIRKYDDVTEKVNLONNPGAMEHFHMKLFRAQRNLYIAGFSLLLSFLLRRLVTLIS
QQATLLASNEAFKKQAESASEAAKKYMEENDQLKKGAADVGGKLDVGNAEVKLEEN
RSLKADLQKLKDELASTKQKLEKAENQVLAMRKQSEGLTKEYDRLLLEEHAQLQAAVDG
PMDKKEE

SEQID No:114

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEIL
GVLNSSSRYFHWKMNLVCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF
WKLGDPPFIPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTD
ILALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSEN
TLIQQEVDAL EELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATI
NIVFDRVGKTDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAI

SSKSSNVIVLLLAQIMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVS
ALSSILFLYLAHKQAPEKQMAP

SEQID No:115

GEGGESWPPPVFRVRGVGVALTCSSATADPPSALSSRRSVPPGQLCEAAAGEGTMG
TVHARSLEPLPSSGPDFGGLGEEAEFVEVEPEAKQEILENKDVVVQHVHFDGLGR TKD
DIIICEIGDVFKAKNLIEMRKSHEAREKLLRLGIFRQVDVLIDTCQGDDALPNGLDVTFEV
TELRRLTGSYNTMVGNNEGSMVLGLKLPNLLGRAEKVTFQFSYGTKETSYGLSFFKPR
PGNFERNFSVNLYKVTGQFPWSSLRETDRGMSAEYSFPIWKTSHTVKWEGVWRELGC
LSRTASFAVRKESGHSLSKSSLSHAMVIDSRNSSILPRRGALLKVNQELAGYTGGDVFSIK
EDFELQLNKQLIFDSVFSASFVGGMVLPIGDKPSSIADRFYLG GPTSIRGFSMHSIGPQS
EGDYLGGEAYWAGGLHLYTPLFRPGQGGFGELFRTHFFLNAGNLCNLNYGEGPKAHI
RKLAECIRWSYGAGIVLRLGNIRLELNYCVP MGVQTDGRICDGVQFGAGIRFL

SEQID No:116

MALAVSLPLALSPPRLLLLLLSLLPVARASEAEHRLFEDYNEIIRPVANVSDPVIIHF
EVSMSQLVKVDEVNQIMETNLWLKQIWNDYKLKWNPSDYGGAEFMRVPAQKIWKPDIV
LYNNAVGDFQVDDKTKALLKYTG EVTWIPPAIFKSSCKIDVTYFPFDYQNCTMKFGSWS
YDKAKIDLVLIGSSMNLKDYWESGEWAIKAPGYKHDIKYNCC EEIYPDITYSLYIRRLPLF
YTINLIIPCLLISFLT VLVFYLPSCDCGEKVTLCISVLLSLTVFLLVITETIPSTSLVIPLIGEYLLF
TMIFVTL SIVITVFVLNVHYRTP THTMPSWVKTVFLNLLPRVMFMTRPTSNEGNAQKPR
PLYGAELSNLNCFSRAESKGCKEGYPCQDGMCGYCHHRIKISNFSANLTRSSSSES V
DAVLSLSALSPEIKEAIQSVKYIAENMKAQNEAKEIQDDWKYVAMVIDRIFLWVFTLVCIL
GTAGLFLQPLMAREDA

SEQID No:117

MGSRASTLLRDEELEEIKKETGFSHSQITRLYSRFTSLDKGENGTLSREDFQRIPELAINP
LGDRIINAFFPEGEDQVNFRGFMRTLAHFRPIEDNEKSKDVNGPEPLNSRSNKLHFAFR
LYDLDKDEKISRDELLQVLRMMVGVNISDEQLGSIADRTIQEADQDGD SAISFTEFVKVL
EKVDVEQKMSIRFLH

SEQID No:118

MASESSPLLAYRLLGEEGVALPANGAGGPGGASARKLSTFLGVVVPTVLSMFSIVVFLRI
GFVVGHAGLLQALAMLLVAYFILALT VLSVCAIATNGAVQGGGAYFMISRTLGP EVGGS I

GLMFYLANVCGCAVSLLGLVESVLDVFGADATGPSGLRVLPQGYGWNLLYGSLLLGLV
 GGVCTLGAGLYARASFLTFLVSGSLASVLISFVAVGPRDIRLTPRPGPNGSSLPPRFGH
 FTGFNSSTLKDNLGAGYAEDYTTGAVMNFANVFAVLFNGCTGIMAGANMSGELKDPSR
 AIPLGTIVAVAYTFFVYVLLFFLSSFTCDRTLQEDYGFFRAISLWPPLVLIGIYATALSAS
 MSSLIGASRILHALARDDDLFGVILAPAKVVSRRGNPWAAVLYSWGLVQLVLLAGKLNTLA
 AVVTVFYLVAYAAMDLSCLSLEWASAPNFRPTFSLSWHTCLLGVAŠCLLMMFLISPGA
 AGGSLLLMGLLAALLTARGGPSSWGYVSQALLFHQVRKYLLRLDVRKDHVKFWRPQLL
 LLVGNPRGALPLLRLANQLKKGGLYVLGHVTLGDLDLSPSDPVQPQYGAWLSLVDRAQ
 VKAFVDLTFSPSVRQGAQHLLRISGLGGMKPNTLVLGfyDDAPPQDHFLTDPAFSEPAD
 STREGSSPALSTLFPPPRAPGSPRALNPQDYVATVADALKMNKNVVLARASGALPPER
 LSRGSGGTSQLHHVDVWPLNLLRPRGGPGYVDVCGLFLLQMATILGMVPAWHSARLRI
 FLCLGPREAPGAAEGRLRALLSQLRIRAEVQEVVWGEAGAGEPEAEEEGDFVNSGR
 GDAEAEALARSANALVRAQQGRGTGGGPGGPEGGAEGPITALTFLYLPRPPADPAR
 YPRYLALLETLTRDLGPTLLVHGVTPTCTDL

SEQID No:119

MASFVTEVLAHSGRLEKEDLGTRISRLTRRVEEIKGEVCNMISKKYSEFLPSMQSAQGLI
 TQVDKLSIDIDLLKSRIESEVRRDLHVSTGEFTDLKQQLERDSVVLSELLKQLQEFSTAIEE
 YNCALTEKKYVTGAQRLEEAQKCLKLLKSARKCFDLKILKSLSMELTIQKQNILYHLGEEW
 QKLIVWKFPFSKDTSSLESYLQTELHLYTEQSHKEEKTMPPISSVLLAFSVLGELHSLK
 KSFGQMLLKYLRLPLASCPSLHAVIESQPNIVIRFESIMTNLEYPSPSEVFTKIRLVLEVLO
 KQLDLPLDLDLENEKTSTVPLAEMLGDMIWEDLSECLIKNCLVYSIPTNSSKLQQYEEII
 QSTEEFENALKEMRFLKGDITDLLKYARNINSHFANKKCQDVIVAARNLMTSEIHNTVKII
 PDSKINVPELPTPDEDNKLEVQKVSNTQYHEVMNLEPENTLDQHSFSLPTCRISESVKK
 LMELAYQTLLEATTSSDQCAVQLFYSVRNIFHLFHDVVPTYHKENLQKLPQLAAIHHNNC
 MYIAHHLLTLGHQFRRLRLAPILCDGTATFVDLVPGFRRLGTECFLAQMRAQKGELLERLS
 SARNFSNMDDEENYSAASKAVRQVLHQLKRLGIVWQDVLPVNIYCKAMGTLLNTAISEV
 IGKITALEDISTEDGDRLYSLCKTVMDEGPQVFAPLSEESKNKKYQEEVPVYVPKWMPF
 KELMMMLQASLQEIGDRWADGKGPLAAAFSSSEVKALIRALFQNTERRAAALAKIK

SEQID No:120

MSRLGALGGARAGLGLLLGTAAGLGFLCLLYSQRWKRTQRHGRSQSLPNSLDYTQTS
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 RGLAGEIVGEVRCHMEENQRVARRRRFPFVRERSDSTGSSSVYFTASSGATFTDAESE

GGYTTANAESDNERDSKESEDGEDEVSCETVKMGRKDSLDLEEEAASGASSALEAG
 GSSGLEDVLP LLQQADELHRGDEQ GKREGFQ LLLNNKL VYGSRQDFLWRLARAYSDM
 CELTEEVSEKKSYALDGKEEAEAALEKGDDESADCHLWYAVLCGQLAEHESIQRRIQSGF
 SFKEHVDKAIALQPENPMAHFLGRWCYQVSHLSWLEKKTATALLSPLSATVEDALQS
 FLKAEELQPGFSKAGRVYISKCYRELGKNSEARWWMKLALP DVT KEDLAIQKDLEEL
 EVILRD

SEQID No:121

EIEQNSAMAPRKRGGRGISFIFCCFRNNDHPEITYRLRND SNFALQTM EPALPMP PVEE
 LDVMFSELVDELDTDKHREAMFALPAEKKWQIYCSKKKDQEENKGATSWPEFYIDQL
 NSMAARKSLLALEKEEEEEERSKTIESLKTALRTKPMRFVTRFIDLDGLSCILNFLKTMDYE
 TSESRIHTSLIGCIKALMNNSQGRAHVLAHSESINVIAQSLSTENIKTKVAVLEILGAVCLV
 PGGHKKVLQAMLHYQKYASERTRFQTLINDLDKSTGRYRDEVSLKTAIMSFINAVLSQG
 AGVESLDFRLHLRYEFLMLGIQPVIDKLREHENSTLDRHLDFFEMLRNEDELEFAKRFEL
 VHIDTKSATQMFELTRKRLTHSEAYPHFMSILHHCLQMPYKRSGNTVQYWLLLDRIIQQI
 VIQNDKGQDPDSTPLENFNIKNVVRMLVNENEVKQWKEQAEKMRKEHNELQQKLEKK
 ERECDAKTQEKEEMMQTLNKMKEKLEKETTEHKQVKQQVADLTAQLHEL SRRAVCASI
 PGGPSPGAPGGPFPSSVPGSLLPPPPPPPLPGGMLPPPPPPPLPPGGPPPPPPGPPPLG
 AIMPPPGAPMGLALKKKSIPQPTNALKSFNWSKLPENKLEGTWTEIDDTKVFKILDLED
 LERTFSAYQRQQDFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRR AQNCNILLSRLK
 LSND EIKRAILTMDEQEDLPKDMLEQLLKFVPEKSDIDLLEEHKHELD RMAKADRFLFEM
 SRINHYQQRLQSLYFKKKFAERVAEVKPKVEAIRSGSEEVFRSGALKQLLEVVLAFGN Y
 MNKGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP SVLNLNEELRDIPQAA
 KVNMTELDKEISTLRSGLKAVETELEYQKSQPPQPGDKFVSVVSQFITVASFSFSDVEDL
 LAEAKDLFTKAVKHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEEEERRA
 RMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEVFDKDL SKLKRNRKRITN
 QMTDSSRERPITKLN F

SEQID No:122

MTVFRQENVDDYYDTGEELGSGQFAVVKKCREKSTGLQYAAKFIKKRRTKSSRRGVSR
 EDIEREVSILKEIQHPNVITLHEVYENKTDVILILELVAGGELFD FLAEKESLTEEEATEFLK
 QILNGVYYLHSLQIAHFDLKPENIMLLDRNVPKPRIKIIDFGLAHKIDFGNEFKNIFGTPEFV
 APEIVNYEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANVSAVN YEFED EYFSNT
 SALAKDFIRRLLVKDPKKRMTIQDSLQHPWIKPKDTQQALS RKASAVNMEKFKKFAARK

KWKQSVRLISLCQRLSRFSLRSNMSVARSDDTLDEEDSFVMKAIHAINDDNVPGLQH
 LLGSLSNYDVNQPNKHGTPPLLIAAGCGNIQILQLLIKRGSRIDVQDKGGSNAVYWAARH
 GHVDTLKFLSENKCPDVDKSGEMALHVAARYGHADVAQVTCAASAQIPISRTKEEET
 PLHCAAWHGYYSVAKALCEAGCNVNIKNREGETPLLTASARGYHDIVECLAHEHGADLN
 ACDKDGHIHLAVRRRCQMEVIKTLLSQGCFVDYQDRHGNTPLHVACKDGNMPIVVAL
 CEANCNLDISNKYGRTPHLAANNGILDVVRYLCLMGASVEALTTDGKTAEDLARSEQH
 EHVAGLLARLRKDTHRGLFIQQLRPTQNLQPRIKLLFGHSGSGKTTLVESLKCGLLRSF
 FRRRRPRLSSTNSSRFPPSPASKPTVSVSINNLYPGCENVSVRSRSMMFEPGLTKGM
 LEVFAVAPTHHPHCSADDQSTKAIDIQNAYLNGVGDVSVWFEFSGNPVYFCCYDYFAAND
 PTSIHVVVFSLEEPYEIQLNPVIFWLSFLKSLVPVEEPIAFGGKLNPLQVVLVATHADIMN
 VPRPAGGEFGYDKDTSLLKEIRNRFGNDLHISNKLFLVDAGASGSKDMKVLNRNHLQEIR
 SQIVSVCPPMTHLCEKIISTLPSWRKLNGPNQLMSLQQFVYDVQDQLNPLASEEDLRRI
 AQQHSTGEINIMQSETVQDVLLLDPRWLCTNVLGKLLSVETPRALHHYRGRYTVEDIQ
 RLVPDSDVEELLQILDAMDICARDLSSGTMVDVPALIKTDNLHRSWADEEDEVMVYGGV
 RIVPVEHLTPFPCGIFHKVQVNLCRWIHQQSTEGDADIRLWVNGCKLANRGAELLVLLV
 NHGQGIEVQVRGLETEKIKCCLLLDSVCSTIENVMATTLPGLLTVKHLYSPQQLREHHEP
 VMIYQPRDFFRAQTLKETSLTNTMGYKESFSSIMCFGCHDVYSQASLGMDIHASDLNL
 LTRRKLRLDPPDPLGKDWCLLAMNLGLPDLVAKYNTNNGAPKDFLPSPLHALLREW
 TTYPESTVGTLSKRLRELGRDAADLLLKASSVFKINLDGNGQEAYASSCNSGTSYNSI
 SSVVSR

SEQID No:123

MWTPTEEEKYGVVICSFRGSVPQGLVLEIGETVQILEKCEGWYRGVSTKKPNVKGIFPA
 NYIHLKKAIVSNRGQYETVVPLEDSIVTEVTATLQEWASLWKQLYVKHKVDLFYKLRHV
 MNELIDLRRQLLSGHLTQDQVREVKRHITVRLDWGNEHLGLDLVPRKDFEVVDSQISV
 SDLYKMHLSRQSVQQSTSQVDTMRRHGETCRMPVPHHFFLSLKSFTYNTIGEDTDV
 FFSLYDMREGKQISERFLVRLNKNNGGPRNPEKIERMCALFTDLSSKDMKRDLYIVAHVIR
 IGRMLLNDSSKKGPPHLHYRRPYGCAVLSILDVLQSLTEVKEEKDFVLKVYTCNNESEWS
 QIHENIIRKSSAKYSAPSASHGLIISLQLLRGDMEQIRRENPMIFNRGLAITRKLGFDPVIM
 PGDIRNDLYLTLEKGDFFERGGKSVQKNIEVTMYVLYADGEILKDCISLGSSEPNRSSYHS
 FVLYHSNSPRWGEIILPIPIDRFRGSHLRFEFRHCSTKDKGEKKLFGFAFSTLMRDDGT
 TLSDDIHELYVYKCDENSTFNNHALYLGLPCKEDYNGCPNIPSSLIFQRSTKESFFISTQ
 LSSTKLTQNVDLLALLKWKAFPDRIIMDLGRLRHVSCEEIVKFLQDILDITLFLVILDDNTEK
 YGLLVFQSLVFIINLLRDIKYFHRPVMPTYIQKHFA GALAYKELIRCLKWYMDCSAELIR

QDHIQEAMRALEYLFKFIVQSRILYSRATCGMEEEQFRSSIQELFQSIRFVLSLDSRNSET
 LLFTQAALLNSFPTIFDELLQMFTVQEVAFVRGTLGSMPTSTVHIGQSMDEVVKLQSIART
 VDSRLFSFSESRRILLPVVLHHIHLHLRQQKELLICSGILGSIFSIVKTSSLEADVMEEVEM
 MVESLLDVLLQTLLTIMSKSHAQEA VRGQRCPQCTAEITGEYVSCLLSLLRQMCDTHFQ
 HLLDNFQSKDELKEFLLKIFCVFRNLMKMSVFPRDWMVMRLLTSNIIVTTVQYLSSALHK
 NFTETDFDFKVVNSYFSLAVLFINQPSLQLEIITSAKRKKILDKYGDMRVM MAYELFSMW
 QNLGEHKKIHFIPGMIGPFLGVTLPQPEVRNIMIPIFHDMMDWEQRKNGNFQVEAELID
 KLDSMVSEGKGDESYRELFSLLTQLFGPYPSLLEKVEQETWRETGISFVTSVTRLMERL
 LDYRDCMKGEETENKKIGCTVNL MNFYKSEINKEEMYIRYIHKLCDMHLQAENYTEAAF
 TLLLYCELLQWEDRPLREFLHYPSTEWQRKEGLCRKIIHYFNKGKSWFEGIPLCRELA
 CQYESLYDYQSLSWIRKMEASYD NIMEQQRLEPEFFRVGFYGRKFPPFLRNKEYVCR
 GHDYERLEAFQQRMLSEFPQAVAMQHNPNDAILQCDAQYLQIYAVTPIPDYVDVLQ
 MDRV PDRVKSFYRVNNVRKFRYDRPFHKGPKDKENEFKSLWIERTTLTLTHSLPGISR
 WFEVERRELVEVSPL ENAIQVVENKNQELRSLISQYQHKQVHGNINLLSMCLNGVIDAA
 VNGGIARYQEAFD KDIYINKHPGDAEKITQLKELMQEQVHVLGVGLAVHEKFVHPEMR
 PLHKKLIDQFQMMRASLYHEFPGLDKLSPACSGTSTPRGNVLASHSPMSPESIKMTHR
 HSPMNL MGTGRHSSSSSLSSHASSEAGNMVMLGDGSMGDAPEDLYHMQLAYPNPRY
 QGSVTNVSVLSSSSQASPSSSSSLSTHSAPSQMITSAPSSARGSPSLPDKYRHAREMML
 LLPTYRDRPSSAMYPAAILENGQPPNFQRALFQQVVGACKPCSDPNLSVAEKGHYSLH
 FDAFHHLPLGDTPPALPARTLRKSPLHIPASPTSPQSGLDGSNSTLSGSASSGVSSLSE
 SNFGHSSEAPPRTDTMDSMPSQAWN ADEDLEPPYLPVHYSLSSES AVLDSIKAQPCRSH
 SAPGCVIPQDPMDPPALPPKPYHPRLPALEHDEGVLLREETERPRGLHRKAPLPPGSA
 KEEQARMAWEHGRGEQ

SEQID No:124

MAATFFGEVVKAPCRAGTEDEEEEEEGRRETPEDREVRLQLARKREVRLRRQTKTSL
 EVS LLEKYPCKSKFIIAIGNNAVAFLSSFVMNSGVWEEVGC AKLWNEWCRTTDTTHLSST
 EAF CVFYHLKSNPSVFLCQCSCYVAEDQQYQWLEKVFGSCPRKNMQITILTCRHVTDY
 KTSESTGSLPSPFLRALKTQNFKDSACCP LLEQPNIVHDLPAAVLSYCQVWKIPAILYLC
 YTDVMKLDLITVEAFKPILSTRSLKGLVKNIPQSTEILKKLMTTNEIQSNIYT

SEQID No:125

MSWVQATLLARGLCRAWGGT CGAALTGTSISQVPRRLPRGLHCSAAAHSSSEQSLVPS
 PPEPRQRPTKALVPFEDLFGQAPGGERDKASFLQTVQKFAEHSVRKRGHIDFIYLALRK

MREYGVERDLAVYNQLLNIFPKEVFRPRNIIQRIFVHYPRQQEAGIIVLEQMENHGVMP
 NKETEFLLIQIFGRKSYPMKLKLVRLKLWFFRPMNVNPPFVPRDLPQDPVELAMFGLRHM
 EPDLSARVTIYQVPLPKDSTGAADPPQPHIVGIQSPDQQAALARHNPARPVFVEGPFSL
 WLRNKCYYYHILRADLLPPEEREVEETPEEWNLYYPMQLDLEYVRSQWDNYEFDINEV
 EEGPVFAMCMAGAHQATMAKWIQGLQETNPTLAQIPVVFRLAGSTRELQTSSAGLEE
 PPLPEDHQEEDDNLQRQQQGS

SEQID No:126

MQAHELFRYFRMPELVDFRQCVTLPNTLMGFGAFSRRLTTFWRPRHPKPLKPPWHL
 SMQSVEVAGSGGARRSALLDSDEPLVYFYDDVTTLYEGFQRGIQVSNNGPCLGSRKP
 DQPYEWLSYKQVAELSECIGSALIQKGFKTAPDQFIGIFAQNRPEWVIEQGCFAYSMVI
 VPLYDTLGNEAITIYVKNKAELSLVFVDKPEKAKLLEGVENKLIPGLKIIVMDSYGSELVE
 RGQRCGVEVTSMKAMEDLGRANRRKPKPPAPEDLAVICFTSGTTGNPKGAMVTHRNIV
 SDCSAFVKATENTVNPCPDDTLISFLPLAHMFERVVECVMLCHGAKIGFFQGDIRLLMD
 DLKVLQPTVFPVPRLLNRMFDRIFGQANTTVKRWLLDFASKRKEADVRSQIIRNNSLW
 DRLIFHKVQSSLGGRVRLMVTGAAPVSATVLTFLRAALGCQFYEGYGQTECTAGCCLT
 MPGDWTTGHVGAPMPCNLIKLGWQLEEMNYMASEGEGEVCVKGNVVFQGYLKDPAK
 TAEALDKDOWLHTGDIGKWLPNGTLKIIDRKKHIFKLAQGEYIAPEKIENIYMRSEPAQV
 FVHGESLQAFLIAIVPDVETLCSWAQKRGFEQSFEELCRNKDVKKAILEDMVRLGKDS
 GLKPFEQVKGITLHPELFSIDNGLLTPTMKAKRPELRNYFRSQIDDLYSIIKV

SEQID No:127

MPSASCDTLLDDIEDIVSQEDSKPQDRHFVRKDVVPKVRRRNTQKYLQEEENSPPSDS
 TIPGIQKIWIRTWGCSHNSDGEYMAGQLAAYGYKITENASDADLWLLNSCTVKNPAED
 HFRNSIKKAQEENKKIVLAGCVPQAQPRQDYLKGLSIIQVQIDRVVEVVEETIKGHSVR
 LLGQKKDNGRRLGGARLDLPKIRKNPLIEIISISTGCLNACTYCKTKHARGNLASYPIDEL
 VDRAKQSFQEGVCEIWLTS EDTGAYGRDIGTNLPTLLWKLVEVIPEGAMLRLGMTNPPY
 ILEHLEEMAKILNHPRVYAFHLIPVQSASDSVLMEMKREYCVADFKRVVDFLKEKVPGITI
 ATDIICGFPGETDQDFQETVKLVEEYKFPSLFINQFYPRPGTPAAKMEQVPAQVKKQRT
 KDLSRVFHSYSPYDHKIGERQQVLVTEESFDSKFYVAHNQFYEQVLVPKNPAFMGKMV
 EVDIYESGKHFMKGQPVSADKVYTPSISKPLAKGEVSGLT KDFRNLGNLQLSSGSHTS
 AASQCDSASSRMVLPMPRLHQDCALRMSVGLALLGLLFAFFVKVYN

SEQID No:128

MGGTTSTRRTFEADENENITVVKGIRLSENVIDRMKESSPSGSKSQRYSGAYGASVS
 DEELKRRVAEELALEQAKKESEDQKRLKQAKELDRERAANEQLTRAILRERICSEEER
 AKAKHLARQLEEKDRVLLKKQDAFYKEQLARLEERSSEFYRVTTTEQYQKAAEEVEAKFK
 RYESHPVCADLQAKILQCYRENTHTQTLKCSALATQYMHCVNHAKQSMLEKGG

SEQID No:129

MALAAARLLPQFLHSRSLPCGAVRLRTPAVAEVRLPSATLCYFCRCRLGLGAALFPR SAR
 ALAASALPAQGSRWVPLSSPGLPAAFASFPACPQRSYSTEEKPQQHQKTKMIVLGFSN
 PINWVRTRIKAFLIWAYFDKEFSITEFSEGAKQAFAHVSKLLSQCKFDLLEELVAKEVLHA
 LKEKVTSLPDNHKNALANIDEIVFTSTGDISIYYDEKGRKFVNILMCFWYLTSANIPSETL
 RGASVFQVKLGNQNVETKQLLSASYEFQREFTQGVKPDWTIARIEHSKLE

SEQID No:130

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNA
 ARRPNSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKKAVRTRYISTELGI
 RQRLLVAVLTSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPI
 GHLHLALRHLLSEQHGDDFDWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFI
 GGEPTPGRYCHGGFGVLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCIL DATGVG
 CTGDHEGVHYSHLELSPGEPVQEGDPHFRSALTAHPVRDPVHMYQLHKAFARAELE
 TYQEIQELQWEIQNTSHLAVDGDRAAAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSC
 ADGSPRCPLRGADRADVADVLTGTALEELNRRYHPALRLQKQQLVNGYRRFDPARGME
 YTLDLQLEALTPQGGRRLTRRVQLLRPLSRVEILVPYVTEASRLTVLLPLAAAERDLA
 PGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVAHADVFAPVKAHVAELERRFPGAR
 VPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVLTPDFLNRCRMHAISGWQAFF
 PMHFQAFHPAVAPPQGPPELGRDTGRFDRQAASEACFYNSDYVAARGRLAAASEQ
 EEEELLES LDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDLYHRCLOQSVLEGL
 GSRTQLAMLLFEQEQGNST

SEQID No:131

MKLKLNKVNFLAYFLVSIAGLLYALVQLGQPCDCLPPLRAAAEQLRQKDLRISQLQAELRR
 PPPAPAQPPEPEALPTIYVVTPTYARLVQKAELVRLSQTLSLVPRLHWLLVEDAEGPTPL
 VSGLLAASGLLFTHLVVLTPKAQRLREGEPGWVHPRGVEQRNKALDWLRGRGGAVGG
 EKDP PPPGTQGVVYFADDDNTYSRELSEEMRWTRGVSVPVGLVGGLRFEGPQVQD

GRVVGFTAWEPSRPFVDMAGFAVALPLLLDKPNAQFDSTAPRGHLESSLLSHLVDP
KDLEPRAANCTRVLVWHTRTEKPKMKQEEQLQRQGRGSDPAIEV

SEQID No:132

MAAPRAGRGAGWSLRAWRALGGIRWGRRPRLTPDLRALLTSGTSDPRARVTYGTPSL
WARLSVGVTEPRACLTSGTPGPRAQLTAVTPDTRTREASENSGTRSRAWLAVALGAG
GAVLLLLWGGGRGPPAVLAAVPSPPPASPRSQYNFIADVVEKTAPAVVYIEILDRHPFLG
REVPISNGSGFVVAADGLIVTNAHVADRRRVRVRLLSGDTYEAVVTAVDPVADIATLRI
QTKEPLPTLPLGRSADVROGEFVAMGSPFALQNTITSGIVSSAQRPARDLGLPQTNVE
YIQTDAIDFGNSGGPLVNLDEGIVGVNTMKVTAGISFAIPSDRLREFLHRGEKKNSSSGI
SGSQRRYIGVMMLTLSPSILAEQLREPSFPDVQHGVLIHKVILGSPAHRAGLRPGDVIL
AIGQMVMQNAEDVYEAVRTQSQLAVQIRRGRETLTLYVTPEVTE

SEQID No:133

MTQLFLWEYGDHLFEGPNQRPAPCYDPCEAVLVESIPEGLDFPNASTGNPSTSQAWLG
LLAGAHSSLDIASFYWTLTNNDTHTQEPSAQQGEEVLRQLQTLAPKGVNVRIAVSKPSG
PQPQADLQALLQSGAQVRMMDQKLTHGVLHTKFWVVDQTHFYLG SANMDWRSLTQ
VKELGVVMYNCSC LARDLT KIFEAYWFLGQAGSSIPSTWPRFYDTRYNQETPMEICLNG
TPALAYLASAPPPLCPSGRTPDLKALLNVVDNARSFIYVAVMNYLPTLEFSHPHRFWPAI
DDGLRRATYERGVKVRLLISCWGHSEPSMRAFLLSLAALRDNHTHSDIQVKLFVVPAD E
AQARIPYARVNH NKYMVTERATYIGTSNWSGNYFTETAGTSLLVTQNGRGGLRSQLEAI
FLRDWDSPYIHDLDTSADSVGNACRL

SEQID No:134

MRYFLLRPETLFLLCISLALWSYFFHTDEVKTIVKSSRDAVKMVKGKVAEIMQNDR LGGL
DVLEAEFSKTWEFKNHNVAVYSIQGRRDHMEDRFEVLTDLANKTHPSIFGIFDGHGGE
GGIRGAALRFFPTLSTLQVQSGQLTGAPRWPLVFTRISERDLDPGLCRGGYARKGGG
ALTSPLRPGGLRGADVLLLD SFVCGSSGSRR

SEQID No:135

MEKQPQNSRRGLAPREVPPAVGLLLIMALMNTLLYLCLDHFFIAPRQSTVDPTHCPYGH
FRIGQMKNCS PWLSCEELRTEVRQLKRVGEGAVKRVFLSEWKEHKVALS QLTSLEMKD
DFLHGLQMLKSLQGTHVVTLLGYCEDDNTMLTEYHPLGSLSNLEETLNLSKYQNVNTW
QHRLELAMDYVSIINY LHHS PVGTRVMCD SNDLPKTL SQYLLTSNFSILANDLDALPLVN

HSSGMLVKCGHRELHGDFVAPEQLWPYGEDVPFHDDLMPHYDEKIDIWKIPDISSFLLG
HIEGSDMVRFHFLFDIHKACKSQTPSERPTAQDVLETYQKVLDTLRDAMMSQAREML

SEQID No:136

MQRAGSSGGRGECDISGAGRLGLEEAARLSCAVHTSPGGGRRPGQAAGMSAKERPK
GKVIKDSVTLLPCFYFVELPILASSVVSlyFLELTDVFKPVHSGFSCYDRSLSMPIEPTQ
EAIPFLMLLSLAFAGPAITIMVGEgILYCCLSKRRNGVGLEPNINAGGCNfNSFLRRAVRF
VGvHVfGLCSTALITDIIQLSTGYQAPYFLTVCkPNYtSLNVsCKENSyIVEDICSGSDLT
VINSGRKSfPSPQHATLAAFAAVYVSMYFNSTLTDSskLLKPLLvFTFIICGIICGLTRITQY
KNHPVDVYcGFLIGGGIALYLGLYAVGNFLPSDESMFQHRDALRSLTDLNQDPNRLLSA
KNGSSSDGIAHTEGILNRNHRDASSLTNLKRANADVEITPRSPMGKENMVTfSNTLPRA
NTPSVEDPVRrNASIHASMDsARsKQLLTQWKNKNEsRKLSLQVIEPEPGQSPPRSIE
MRSSSEPSRVGVNGDHHGPGNQYLKIQPGAVPGCNNSMPGGPRVSIQSRPGSSQLV
HIPEETQENISTSPKSSSARAKWLKAAEKTvACNRSNSQPRIMQVIAMSKQQGVlQSSP
KNTegSTVScTGSIRYKTLTDHEPSGIVrVEAHpENNRPIIQIPSTEGEGSGSWKWKAP
EKGS LRQTYELNDLNrDSESCESLKDSFGSGDRKRSNIDSNEHHHHGITTIRVTPVEGS
EIGSETLSISSSRDSTLRRKGNILIPERSNSPENTRNIFYKGTSPTRAYKD

SEQID No:137

MLTTLKPFGSVSVESKMNNKAGSFFWNLRQFSTLVSTSRTMRLCCLGLCKPKIVHSNW
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VPVDKSDDELKKVNLNHEVSNEDVLTKETKPNRISSRKLSSEECNSLSDVLDafSKAPTF
PSSNYFTAMWTIAKRLSDDQKRFEKRLMFShPAFNQLCEHMMREAKIMQYKYLlFSLH
AIVKLGIpQNTILVQTLLRVTQERINECDEICLSVLSTVLEAMEPCKNVHVLRTGFRILVDQ
QVWKIEDVFTLQVVMKCIGKDAPIALKRKLEMKALRELDrfSVLNSQHMFevLAAMNHR
SLILLDECSKVVLdNIHGcPLRIMINILQsCKDLQYHNLDLFKGLADYVAATFDIWKFRKVL
FILILFENLGFRPVGLMDLFMKRIVEDPEsLNMKNILSILHTYSSLNHVYKCQNKEQFVEV
MASALTGYLHTISSENLLDAVYSFCLMNYFPLAPFNQLLQKDIISELLTSDDMKNAYKLHT
LDTCLKLDDTVYLRDIALSLPQLPRELPSSHTNAKVAEVLSSLLGGEGHfSKDVHLPHNY
HIDFEIRMDTNRNQVLPLSDVDTTsATDIQRVAVLCVSRsAYCLGSSHPRGFLAMKMRH
LNAMEGFHVILVNNWEMDKLEMEDAVTFLKTKIYSVEALPVAAVNVQSTQ

SEQID No:138

RVYADAPAKLLLPPPAAWDLAVRLRGAEAAserQVYSVTMKLLLLHPAFQSCLLLTLG

LWRTTPEAHASSLGAPAIASAASFLQDLIHRYGEGDSLTLQQLKALLNHLDVDGVGRGNVT
 QHVQGHRLNSTCFSSGDLFTAHNFSEQSRIGSSSELQEFCTILQQLDSRACTSENQEN
 EENEQTEEGRPSAVEVWGYGLLCVTVISLCSLLGASVVPFMKKTIFYKRLLLYFIALAIGTL
 YSNALFQLIPEAFGFNPLEDYYVSKSAVVFGGFYLFFFTEKILKILLKQKNEHHHGHSHYA
 SESLPSKKDQEEGVMEKLQNGDLDMIPQHCSSELDGKAPMVDEKVIVGSLSVQDLQA
 SQSACYWLKGVRYSDIGTLAWMITLSDGLHNFIDGLAIGASFTVSVFQGISSTVAILCEE
 PHELGDVFILLNAGMSIQQALFFNFLSACCCYLGLAFGILAGSHFSANWIFALAGGMFLYI
 SLADMFPENNEVCQEDERKGSILIPFIQNLGLLTGFTIMVVLTMYSGQIQIG

SEQID No:139

MAAEWASRFWLWATLLIPAAVYEDQVGKFDWRQQYVGKVKFASLEFSPGSKKLVA
 TEKNVIAALNSRTGEILWRHVDKGTAEGAVDAMLLHGQDVITVSNGGRIMRSWETNIGG
 LNWEITLDSGSFQALGLVGLQESVRYIAVLKKTTLALHHLSSGHLKWVEHLPESDSIHYQ
 MVYSYSGSVVWALGVVPFSHVNIKFNVEDGEIVQQVRVSTPWLQHLSGACGVVDEA
 VLVCPDPSSRSLQTLALETEWELRQIPLQSLDLEFGSGFQPRVLPQTQPNPVDASRAQFF
 LHLSPSHYALLQYHYGTLSLLKNFPQTALVSFATTGEKTVAAMACRNEVQKSSSSSEDG
 SMGSFSEKSSSKDSLACFNQTYTINLYLVETGRRLLDTTITFSLEQSGTRPERLYIQVFLK
 KDDSVGYRALVQTEDHLLLFLQQLAGKVVLWSREESLAEVVCEMVDLPLTGAQAELE
 GEFGKKADGLLGMFLKRLSSQLILLQAWTSHLWKMIFYDARKPRSQIKNEINIDTLARDEF
 NLQKMMVMVTASGKLFGIESSSGTILWKQYLPNVKPDSSFKLMVQRTTAHFPHPPQCT
 LLVKDKESGMSSLYVFNPFGKWSQVAPPVLKRPIQLSLLLPVMDQDYAKVLLIDDEYK
 VTAFPATRNVLRLHELAPSIFFYLVDAEQGRLCGYRLRKDLTTELSWELTIPPEVQRIV
 KVKGKRSEHVHSQGRVMGDRSVLYKSLNPNLLAVVTESTDAHHERTFIGIFLIDGVTG
 RIIHSSVQKKAKGPVHIVHSENWVYQYWNTKARRNEFTVLELYEGTEQYNATAFSSLD
 RPQLPQVLQQSYIFPSSISAMEATITERGITSRHLLIGLPSGAILSLPKALLDPRRPEIPTE
 QSREENLIPYSPDVQIHAERFINYNQTVSRMRGIYTAPSGLESTCLVVAYGLDIYQTRVY
 PSKQFDVLKDDYDYVLISSVLFGLVFATMITKRLAQVKLLNRAWR

SEQID No:140

MAKVSELYDVTWEEMRDKMRKWREENSRNSEQIVEVGEELINEYASKLGDDIWIIYEQV
 MIAALDYGRDDLALFCLQELRRQFPGSHRVKRLTGMRFEAMERYDDAIQLYDRILQEDP
 TNTAARKRKIAIRKAQGKNVEAIRELNEYLEQFVGQDEAWHELAELYINEHDYAKAAFCL
 EELMMTNPHNHLYCQQYAEVKYTQGGLENLELSRKYFAQALKLNNRNMRALFGLYMS

ASHIASNPKASAKTKKDNMKYASWAASQINRAYQFAGRSKKETKYSLKAVEDMLETLOI
TQS

SEQID No:141

MWSIGAGALGAAALALLANTDVFLSKPQKAALEYLEDIDLKTLEKEPRTFKAKELWEKN
GAVIMAVRRPGCFLCREEAADLSSLKSMQLDQLGVPLYAVVKEHIRTEVKDFQPYFKGEI
FLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGFILGGVFVVG
GKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

SEQID No:142

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLQPSTPTPSQPSAAMAAT
DSMRGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVA
RAWPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCVLHCHVSTRV
GPPNPPCPPGSEPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLL
SLLAFAMYRP

SEQID No:143

MASGSNWLSGVNVVLVMAYGSLVFVLLFIFVKRQIMRFAMKSRRGPHVPVGHNAKDL
KEEIDIRLSRVQDIKYEPQLLADDDARLLQLETQGNQSCYNLYRMKALDAIRTSEIPFHS
EGRHPRSLMGKNFRSYLLDLRNTSTPFKGVRKALIDTLLDGYETARYGTGVFGQNEYL
RYQEALSELATAVKARIGSSQRHHQSAAKDLTQSPEVSPTTIQVTYLPSSQKSKRAKHF
LELKSFKDNYNTLESTL

SEQID No:144

MTARGLALGLLLLLLLCPAQVFSQSCVWYGECEGIAYGDKRYNCEYSGPPKPLPKDGYDL
VQELCPGFFFFGNVSLCCDVRQLQTLKDNLQLPLQLFLSRCPSCFYNNLFCELTCSPRQ
SQFLNVTATEDYVDPVTNQTCTNVKELQYYVGQS FANAMYNACRDVEAPSSNDKALGL
LCGKDADACNATNWIEYMFNKDNGQAPFTITPVFSDFPVHGMPEPMNNATKGCDDESVD
EVTAPCSCQDCSIVCGPKPQPPPPAPWTILGLDAMYVIMWITYMAFLLVFFGAFFAVW
CYRKRYFVSEYTPIDSNIAFSVNASDKGEASCCDPVSAAFEGCLRRLFTRWGSFCVRN
PGCVIFFSLVFITACSSGLVFVRVTTNPVDLWSAPSSQARLEKEYFDQHFGPFFRTEQLII
RAPLTDKHIYQPYPSGADVPPGPPLDIQLHQVLDLQIAIENITASYNETVTLQDICLAPL
SPYNTNCTILSVLNIFYQNSHSLVDHKKGDDFFVYADYHTHFLYCVRAPASLNDTSLLHD
PCLGTFGGPVFPWLVLGGYDDQNYNNATALVITFPVNNYYNDTEKLQRAQAWKEKEFIN

FVKNYKNPNLTISFTAERSIEDELNRESDSVFTVVISYAIMFLYISLALGHIKSCRRLVD
 SKVSLGIAGILIVLSSVACSLGVFSYIGLPLTLIVIEVIPFLVLAVGVDNIFILVQAYQRDERL
 QGETLDQQLGRVLGEVAPSMFLSSFSETVAFFLGALSVMMPAVHTFSLFAGLAVFIDFLL
 QITCFVSLLGLDIKRQEKNRLDIFCCVRGAEDGTSVQASESCLFRFFKNSYSPLLLKDW
 MRPIVIAIFVGVLSFSIAVLNKVDIGLDQSLSMPPDDSYMVDYFKSISQYLHAGPPVYFVLE
 EGHDTSSKGGQNMVCGGMGCNNDLSLVQQIFNAAQLDNYTRIGFAPSSWIDDYFDWVK
 PQSSCCRVDNITDQFCNASVVDPAVCVRCLTPEGKQRPQGGDFMRFLPMFLSDNPN
 PKCGKGGHAAAYSSAVNILLGHGTRVGATYFMTYHTVLQTSADFIDALKKARLIASNVTTET
 MGINGSAYRVFPYSVFYVFYEQYLTIIDDTIFNLGVSLGAIFLVTMVLLGCELWSAVIMCA
 TIAMVLVNMFGVMWLWGISLNAVSLVNLVMSCGISVEFCSHITRAFTVSMKGSRVERAE
 EALAHMGSSVFSGITLTKEGGIVVLAFAKSQIFQIFYFRMYLAMVLLGATHGLIFLPVLLSY
 IGPSVNKAKSCATEERYKGTERERLLNF

SEQID No:145

MSGCGLFLRTTAAARACRGLVVSTANRRLLRTSPPVRAFAKELFLGKIKKKEVFPFPEV
 SQDELNEINQFLGPVEKFFTEEVDNRKIDQEGKIPDETLEKLKSLGLFGLQVPPEYGGGLG
 FSNTMYSRLGEIISMDGSITVTLAAHQAIKGLKGIILAGTEEQKAKYLPKLASGEHIAAFCLT
 EPASGSDAASIRSRLTSEDKKHYILNGSKVWITNGGLANIFTVFAKTEVVDSGDSVKDK
 ITAFIVERDFGGVTNGKPEDKLGIRGSNTCEVHFENTKIPVENILGEVGDGFKVAMNINLS
 GRFSMGSVVAGLLKRLIEMTAEYACTRKQFNKRLSEFGLIQEKFALMAQKAYVMESMT
 YLTAGMLDQPGFPDCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDT
 RILLIFEGTNEILRMYIALTGLQHAGRILTTRIHELKQAKVSTVMDTVGRRLRDSLGRTVDL
 GLTGNHGVVHPSLADSANKFEENTYCFGRTVETLLLRFGKTIMEEQVLKRVANILINLY
 GMTAVLSRASRSIRIGLRNHDHEVLLANTFCVEAYLQNLFSLSQLDKYAPENLDEQIKKV
 SQQILEKRAYICAHPLDRTC

SEQID No:146

LERRWRRRREAGAGAEAAAAGSARPLGRQAAAARGSSPEAGAAAMAESIIIRVQSPDGV
 KRITATKRETAATFLKKVAKEFGFQNNGFSVYINRNKTGEITASSNKSLLKIKHGDLLF
 LFPSSLAGPSSEMETSVPFGFKVFGAPNVVEDEIDQYLSKQDGKIYRSRDPQLCRHGPL
 GKCVHCVPLEPFDEEDYLNHLEPPVKHMSFHAYIRKLTGGADKGKFVALENISCKIKSGC
 EGHLPWPNGICTKCQPSAITLNRQKYRHVDNIMFENHTVADRFLDFWRKTGNQHFGYL
 YGRYTEHKDIPLGIRAEVAAIYEPPIGTQNSLELLEDPKAEVVDEIAAKLGLRKVGWIFT
 DLVSEDTRKGTVRYSRNKDITYFLSSEECITAGDFQNKHPNMCRLSPDGHFGSKFVTAV

ATGGPDNQVHFEGYQVSNQCMALVRDECLLPCKDAPELGYAKESSESEQYVPDVFYKD
 VDKFGNEITQLARPLPVEYLIIDITTTFPKDPVYTFSISQNPFIENRDVLGETQDFHSLAT
 YLSQNTSSVFLDTISDFHLLFLVTNEVMPLQDSISLLLEAVRTRNEELAQTWKRSEQWA
 TIEQLCSEYPHPLPRHPVAGAGEQPTLHSSPLPVVPWIPHPAASWQVPSAMQRVETRP
 PCQARGRLR

SEQID No:147

MATAGGGSGADPGSRGLLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQI
 GCQSSISGDTGVIHVVEKEEDLQWVLTGPNPPYMVLESKHFTRDLMKLGRTSRIA
 GLAVSLTKPSPASGFSPSVQCPNDGFGVYSNSYGPEFAHCREIQWNSLGNGLAYEDFS
 FPIFLEDENETKVIKQCYQDHNLSQNGSAPTFFPLCAMQLFSMHAVISTATCMRRSSIQ
 STFSINPEIVCDPLSDYNVWSMLKPINTTGTLKPDDRIVVAATRLDSRSFFWNVAPGAE
 SAVASFVTQLAAAEALQKAPDVTTLPNVMFVFFQGETFDYIGSSRMVYDMEKGKFPV
 QLENVDSFVELGQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVPAVI
 LRRPNQSQPLPPSSLQRFLRARNISGVVLADHSGAFHNKYYQSIYDTAENINVSYPEWL
 SPEEDLNFTDTAKALADVATVLGRALYELAGGTNFSDTVQADPQTVTRLLYGFLIKAN
 NSWFQSILRQDLRSYLGDGPLQHIAVSSPTNTTYVVQYALANLTGTVVNLTREQCQDP
 SKVPSENKDLYEYSWVQGGLHSNETDRLPRCVRSTARLARALSPAFELSQWSSTEYST
 WTESRWKDIRARIFLIASKELELITLVGFGILIFSLIVTYCINAKADVLFIAPREPGAVSY

SEQID No:148

MPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKKPPAPQQPPPPAPHPQQHPQ
 QHPQNQAHGKGGHRRGGGGGGGKSSSSSSASAAAAAAAASSSASCSRRLGRALNFLF
 YLALVAAAFAFGWCVVHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQKVQSLQATF
 GTFESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEILKDLSDGIHVVKDARERD
 FTSLENTVEERLTETKSINDNIAIFTEVQKRSQKEINDMKAKVASLEESEGNKQDLKALK
 EAVKEIQTSAKSREWDMEALRSTLQTMESDIYTEVRELVSLEKQEQQAFKEAADTERLAL
 QALTEKLLRSEESVSRLPEEIRRLLEEELRQLKSDSHGPKEDGGFRHSEAFEALQQKSQ
 GLDSRLQHVEDGVLSMQVASARQTESLESLLSKSQEHEQRLAALQGRLEGLGSSEAD
 QDGLASTVRSLGETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQAQAA
 RLPPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAYSVKIETNENNLESAGLL
 DDLRNDLDRLFVKVEKIHEKV

SEQID No:149

MFRNQYDNDVTWSPQGRIHQIEYAMEAVKQGSATVGLKSKTHAVLVALKRAQSELAA
 HQKKILHVDNHIGISIAGLTADARLLCNFMRQECLDSRFVFDRLPVSRLVSLIGSKTQIP
 TQRYGRRPYGVGLLIAGYDDMGPHIFQTCPSANYFDCRAMSIGARSQSARTYLERHMS
 EFMECNLNELVKHGLRALRETLPAEQDLTTKNVSIGIVGKDLEFTIYDDDDVSPFLEGLE
 ERPQRKAQPAQPADEPAEKADPEMEH

SEQID No:150

SSIGTGYDLSASTFSPDGRVFQVEYAMKAVERNSSTAIGIRCKDGVVFGVEKLVLSKLYEE
 GSNKRLFNVDRHVGMAGVAGLLADARSLADIAREEASNFRSNFGYNIPLKHLADRVAMY
 VHAYTLYSAVRPFGCSFMLGSYSVNDGAQLYMIDPSGVSYGYWGCAIGKARQAAKTEI
 EKLQMKEMTCRDIVKEVAKIIVHDEVKDKAFELELSWVGELTNGRHEIVPKDIREEA EK
 YAKESLKEEDESDDDNM

SEQID No:151

MSRRYDSRTTIFSPEGRLYQVEYAMEAIGHAGTCLGILANDGVLLAAERRNIHKLLDEVF
 FSEKIYKLNEDMACSVAGITSDANVLTNELRLIAQRYLLQYQEPICEQLVTALCDIKQAY
 TQFGGKRPFVGSLLYIGWDKHYGFQLYQSDPSGNYGGWKATCIGNNSAAAVSMLKQD
 YKEGEMTLKSALALAIKVLNKTMDVSKLSAEKVEIATLTRENGKTVIRVLKQKEVEQLIKK
 HEEEEAKAEREKKEKEQKEKDK

SEQID No:152

MSRGSSAGFDRHITIFSPEGRLYQVEYAFKAINQGGLTSVAVRGKDCAVIVTQKKVPDK
 LLDSSTVTHLFKITENIGCVMTGMTADSRSQVQRARYEAANWKYKYGYEIPVDMLCKRI
 ADISQVYTQNAEMRPLGCCMILIGIDEEQGPQVYKCDPAGYYCGFKATAAGVKQTESTS
 FLEKKVKKKFDWTFEQTVETAITCLSTVLSIDFKPSEIEVGVTVENPKFRILTEAEIDAH
 VALAERD

SEQID No:153

MLSSTAMYSAPGRDLGMEPHRAAGPLQLRFSPYVFNGGTILAIAGEDFAIVASDTRLSE
 GFSIHTRDSPKCYKLTDKTVIGCSGFHGDCLTLTKIIEARLKMYSNNKAMTTGAIAAM
 LSTILYSRRFFPYVYNIIGGLDEEGKGAVYSFDPVGSYQRDSFKAGGSASAMLQPLLD
 NQVGFKNMQNVEHVPLSLDRAMRLVKDVFISAAERDVYTGDAALRICIVTKEGIREETVSL
 RKD

SEQID No:154

MEYLIQIGPDYVLVASDRVAASNIVQMKDDHDKMFKMSEKILLLCVGEAGDTVQFAEYI
QKNVQLYKMRNGYELSPTAAANFTRRNADCLRSRTPYHVNLLLAGYDEHEGPALYYM
DYLAALAKAPFAAHGYGAFLTLSILDRIYPTISRERAVELLRKCLEELQKRFILNLPTFSV
RIIDKNGIHDLDNISFPKQGS

SEQID No:155

MSIMSYNGGAVMAMKGKNCVAIAADRRFGIQAQMVTTDFQKIFPMGDRLYIGLAGLATD
VQTVAQRLKFRLNLYELKEGRQIKPYTLMSMVANLLYEKRFGPYYTEPVIAGLDPKTFKP
FICSLDLIGCPMVTDDFVVS GTCAEQMYGMCESLWEPNMDPDHLFETISQAMLNAVDR
DAVSGMGVIVHIEKDKITRRTLKARM

SEQID No:156

MEAFSGSRGLWAGGPAPGQFYRIPSTPDSFMDPASALYRGPITRTQNPMVTGTSVLG
VKFEGGVVIAADMLGSYGSLARFRNISRIMRVNNSTMLGASGDYADFQYLKQVLGQMVI
DEELLGDGHSYSPRAIHSWLTRAMYSRRSKMNPLWNTMVIGGYADGESFLGYVDMLG
VAYEAPSLATGYGAYLAQPLLREVLEKQPVLSQTEARDLVERCMRVLYYRDARSYNRF
QTATVTEKGVEIEGPLSTETNWDIAHMISGFE

SEQID No:157

MALASVLERPLPVNQRGFFGLGGRADLLDLGPGSLSDGLSLAAPGWGVPEEPGIEMHL
GTTTLAFKFRHGVIVAADSRATAGAYIASQTVKKVIEINPYLLGTMAGGAADCSFWERLL
ARQCRIYELRNKERISVAAASKLLANMVYQYKGMGLSMGTMICGWDKRGPGLYYVDSE
GNRISGATFSVGSGSVYAYGVMDRGYSYDLEVEQAYDLARRAIYQATYRDAYS GGAVN
LYHVREDGWIRVSSDNVADLHEKYSGSTP

SEQID No:158

MAATLLAARGAGPAPAWGPEAFTPDWESREVSTGTTIMAVQFDGGVVLGADSRTTTG
SYIANRVTDKLTPIHDRIFCCRS GSAADTQAVADAVTYQLGFHSELNEPPLVHTAASL FK
EMCYRYREDLMAGIIIAGWDPQEGGQVYSVPMGGMMVRQSFAIGGSGSSYIYG YVDA
TYREGMTKEECLQFTANALALAMERDGSSGGVIRLAAIAESGVERQVLLGDQIPKFAVA
TLPPA

SEQID No:159

MGQSQSGGHGPGGGKKDDKDKKKKYEPVPTRVGKKKKKTKGPDAASKLPLVTPHT
 QCRLKLLKLERIKDYLLMEEEFIRNQEOMKPLEEKQEEERSKVDDLRGTPMSVGTLEEII
 DDNHAIVSTSVGSEHYVSILSFVDKDLLEPGCSVLLNHKVVHAVIGVLMDDTDPLVTVMKV
 EKAPQETYADIGGLDNQIQEIKESVELPLTHPEYYEEMGIKPPKGVILYGPPGTGKTLLAK
 AVANQTSATFLRVVGSELIQKYLGDGPKLVRELFRVAEEHAPSIVFIDEIDAIGTKRYDSN
 SGGEREIQRTMLELLNQLDGFDSRGDVKVIMATNRIETLDPALIRPGRIDRKIEFPLPDEK
 TKKRIFIHTSRMTLADDVTLDDLIMAKDDLSGADIKAICTEAGLMALRERRMKVTNEDF
 KSKENVLYKKQEGTPEGLYL

SEQID No:160

MPDYLGADQRKTKEDKDDKPIRALDEGDIALLKTYGQSTYSRQIKQVEDDIQQLLKIN
 ELTGIKESDTGLAPPALWDLAADKQTLQSEQPLQVARCTKIINADSEDPKYIINVKQFAKF
 VVDLSDQVAPTDIEEGMRVGVDRNKYQIHIPLPPKIDPTVTMMQVEEKPDVTYSVGGC
 KEQIEKLREVVETPLLHPERFVNLGIEPPKGVLLFGPPGTGKTLCAVANRTDACFIRVI
 GSELVQKYVGEGARMVRELFEMARTKKACLIFFDEIDAIGGARFDDGAGGDNEVQRTM
 LELINQLDGFDPGRNIKVLMTNRPDTLDPALMRPGRILDRKIEFSLPDLEGRTHIFKI HAR
 SMSVERDIRFELLARLCPNSTGAEIRSVCTEAGMFAIRARRKIA TEKDFLEAVNKVKS YA
 KFSATPRYMTYN

SEQID No:161

MNLLPNIESPVTRQEKMATVWDEAEQDGIGEEVLKMSTEEIIQRTRLLDSEIKIMKSEVL
 RVTHELQAMKDKIKENSEKIKVNKTLPYLVS NVIELLDVDPNDQEEDGANIDLDSQRK GK
 CAVIKTSTRQTYFLPVIGLVDAEKLKPGDLVGVNKDSYLILETLPT EYDSRVKAMEVDER
 PTEQYSDIGGLDKQIQELVEAIVLPMNHKEKFENLGIQPPKGVLMY GPPGTGKTLLARAC
 AAQTKATFLKLAGPQLVQMFIGDGAKLV RDAFALAKEKAPSIIFIDELDAIGTKRFDSEKA
 GDREVQRTMLELLNQLDGFQPN TQVKVIAATNRVDILDPALLRSGRLDRKIEFPMPNEE
 ARARIMQIH SRKMNVSPDVNYEELARCTDDFNGAQCKAVCVEAGMIALRRGATELTHE
 DYMEGILEVQA KKKANLQYYA

SEQID No:162

MEEIGILVEKAQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSRYKKLQQE LEFLEVQEEYI
 KDEQKNLKKEFLHAQEEVKRIQSIPLVIGQFLEAVDQNTAIVGSTTGSNYYVRILSTIDRE
 LLKPNASVALHKHSNALVDVLPPEADSSIMMLTSDQKPDVMYADIGGMDIQKQEVREAV

ELPLTHFELYKQIGIDPPRGVLMYGPPGCGKTMLAKAVAHHTTAAFIRVVGSEFVQKYL
 GEGPRMVRDVFRLAKENAPAIIFIDEIDAIATKRFDQAQTGADREVQRILLELLNQMDGFD
 QNVNVKVIMATNRADTLDPALLRPGRRLDRKIEFPLPDRRQKRLIFSTITSKMNLSEEVDL
 EDYVARPDKISGADINSICQESGMLAVRENRYIVLAKDFEKAYKTVIKKDEQEHEFYK

SEQID No:163

MALDGPEQMELEEGKAGSGLRQYYLSKIEELQLIVNDKSQNLRRRLQAQRNELNAKVRL
 REELQLLQEQGSYVGEVVRAMDKKKVLVKVHPEGKFVVDVDKNIDINDVTPNCRVALR
 NDSYTLHKILPNKVDPLVSLMMVEKVPDSTYEMIGGLDKQIKEIKEVIELPVKHPELFEAL
 GIAQPKGVLVLYGPPGTGKTLLARAVAHHTDCTFIRVSGSELVQKFIGEGARMVRELFVM
 AREHAPSIIFMDEIDSIGSSRLEGGSGGDSEVQRTMLELLNQLDGFEATKNIKVIMATNRI
 DILDSALLRPGRIDRKIEFPPPNEEARLDILKIHRSRKMNLTRGINLRKIAELMPGASGAEVK
 GVCTEAGMYALRERRRVHVTQEDFEMAVAKVMQKDSEKNMSIKKLWK

SEQID No:164

MADPRDKALQDYRKLLLEHKEIDGRLKELREQLKELTKQYEKSENDLKALQSVGQIVGE
 VLKQLTEEFIVKATNGPRYVVGCRRLDKSKLKPGRVALDMTTLTIMRYLPREVDPL
 VYNMSHEDPGNVSYSEIGGLSEQIRELREVIELPLTNPELFQRVGIIPPKGCLLYGPPGT
 GKTLLARAVASQLDCNFLKVVSSSIVDKYIGESARLIREMFNYARDHQPCIIFMDEIDAIG
 GRRFSEGTSADREIQRTLMELLNQMDGFDTLHRVKMIMATNRPDTLDPALLRPGRRLDR
 KIHIDLPNEQARLDILKIHAGPITKHGEIDYEAIVKLSDGFNGADLRNVCTEAGMFAIRADH
 DFVVQEDFMKAVRKVADSKKLESKLDYKPV

SEQID No:165

MITSAAGIISLLDEDEPQLKEFALHKLNAVVNDFWAEISESVDKIEVLYEDEGFRSRQFAA
 LVASKVIFYHLGAFEESLNYALGARDLFNVNDNSEYVETIIAKCIDHYTKQCVENADLPEG
 EKKPIDQRLEGIVNKMFORCLDDHKYKQAIGIALETRRLDVFEKTILESNDVPGMLAYSL
 KLCMSLMQNKQFRNKVLRVLVKIYMNLEKPDFINVCQCLIFLDDPQAVSDILEKLVKEDN
 LLMAYQICFDLYESASQQFLSSVIQNLRTVGTPIASVPGSTNTGTVPGSEKDSDSMETE
 EKTSSAFVGKTPEASPEPKDQTLKMIKILSGEMAIELHLQFLIRNNNTDLMILKNTKDAVR
 NSVCHTATVIANSFMHCGTTSQQLRDNLEWLARATNWAKFTATASLGVIHKGHEKEAL
 QLMATYLPKDTSPGSAYQEGGGLYALGLIHANHGDIIDYLLNQLKNASNDIVRHGGSL
 GLGLAAMGTARQDVYDLLKTNLYQDDAVTGEAAGLALGLVMLGSKNAQAIEDMVGYYAQ
 ETQHEKILRGLAVGIALVMYGRMEEADALIESLCRDKDPILRRSGMYTVAMAYCGSGNN

KAIRRLHVAVSDVNDDVRSAAVESLGFI LFRTP EQCPSVVSLLSESYNPHVRYGAAMA
 LGICCAGTGNKEAINLLEPMTNDPVNYVRQGALIASALIMIQQTEITCPKVNQFRQLYSKV
 INDKHDDVMAKFGAILAQGILDAGGHNV TISLQSR TGHTHMP SVVGVLVFTQFWFWFPL
 SHFLSLAYTPTCVIGLNKDLKMPKVQYKSNCKPSTFAYPAPLEVPKEKEKEKEKVSTAVLSI
 TAKAKKKEKEKEKEKEEKEMEVDEAEKKEEKEKKKEPEPNFQLLDNPARVMPAQLKVLT
 MPETCRYQPFKPLSIGGIILKDTSEDI EELVEPVAAHGPKIEEEEQEPEPEPEFEYIDD

SEQID No:166

MAAAAVVEFQRAQSLLSTDREASIDILHSIVKRDIQENDEEAVQVKEQSILELGSLLAKTG
 QAAELGGLLKYVRPFLNSISKAKAARLVRSLLDLFLDMEAA TGQEVELCLECIEWAKSEK
 RTFLRQALEARLVSLYFDTKRYQEALHLGSQLLRELKKMDDKALLVEVQLLESKTYHAL
 SNLPKARAALTSARTTANAIYCPPKLQATLDMQSGIIHAAEEKDWKTAYSIFYEAFEGYD
 SIDSPKAITS LKYM LLLCKIMLNTPEDVQALVSGKLALRYAGRQTEALKCVAQASKNRSLA
 DFEKALTDYRAELRDDPIISTHLAKLYDNLLEQNLIRVIEPFSRVQIEHISSLIKLSKADVER
 KLSQMILDKKFH GILDQ GEGVLIIFDEPPVDKTYEAALETIQNMSKVVD SLYNKAKKLT

SEQID No:167

MADGGSERADGRIVKMEVDYSATVDQRLPECAKLAKEGRLQEVIETLLSLEKQTRTASD
 MVSTSRILVAVVKMCYEAK EWDL LNENIMLLSKRRSQLKQAVAKMVQQCCTYVEEITDL
 PIKLRLIDTLRMVTEGKIYVEIERARLT KT LATIKEQNGDVKEAASILQELQVETYGSMEKK
 ERVEFILEQMRLCLAVKDYIRTQIISKINTKFFQEENTEKLKLKYYNLMIQLDQHEGSYLS
 ICKHYRAIYDTPCQAESEK WQQALKSVVLYVILAPFDNEQSDLVHRISGDKKLEEIPKYK
 DLLKLFTTMELMRWSTLVEDYGMELRKGSLESPATDVFGSTEEGEKRWKDLKNRVVE
 HNIRIMAKYYTRITMKRMAQLLDLSVDESEAFLSNLVVNKTIFAKVDRLAGIINFQRPKDP
 NNLLNDWSQKLNSLMSLVNKTTHLIAKEEMIHNLQ

SEQID No:168

MKDVPGLQSQNSGPGQPAVWHRLEELYTKKLWHQLTLQVLDFVQDPCFAQGDGLI
 KLYENFISEFEHRVNPLSLVEIILHVVRQMTDPNVALTFLEKTREKVKSSDEAVILCKTAIG
 ALKLNIGDLQVTKETIEDVEEMLNNLPGVTSVHSRFYDLSSKYYYQTIGNHASYYKDALRF
 LGCVDIKDLPVSEQQERAFTLGLAGLLGEGVFNF GELLMHPVLESLRNTDRQWLIDTLY
 AFNSGNVERFQTLKTAWGQQPD LAANE AQLLRKIQLLCLMEMTFTRPANHRQLTFEEIA
 KSAKITVNEVELLMKALSVGLVKGSIDEVDKRVHMTWVQPRVLDLQQIKGMKDRLEF
 WCTDVKSMEMLVEHQAHDILT

SEQID No:169

MEEGGRDKAPVQPQQSPAAAPGGTDEKPSGKERRDAGDKDKEQELSEEDKQLQDEL
 EMLVERLGEKDTSLYRPALEELRRQIRSSTTSMTSVPKPLKFLRPHYGKLKEIYENMAP
 GENKRFAADIISVLAMTMSGERECLKYRLVGSQEELASWGHEYVRHLAGEVAKEWQEL
 DDAEKVQREPLTLVKEIVPYNMAHNAEHEACDLLMEIEQVDMLEKDIDENAYAKVCLYL
 TSCVNYVPEPENSALLRCALGVFRKFSRFPEALRLALMLNDMELVEDIFTSCKD VVVQK
 QMAFMLGRHGVFLELSEEDVEEYEDLTEIMSNVQLNSNFLALARELDIMEPKVPDDIYKT
 HLENNRFGGSGSQVDSARMNLASSFVNGFVNAAFQGDKLLTDDGNKWLYKNKDHGM
 LSAAASLGMILLWDVDGGLTQIDKYLYSSEDIKSGALLACGIVNSGVRNECDPALALLS
 DYVLHNSNTMRLGSIFGLGLAYAGSNREDVLTLLLPVMGDSKSSMEVAGVTALACGMIA
 VGSCNGDVTSTILQTIMEKSETELKDTYARWLPLGLGLNHLGKGEAIEAILAALEVSEPF
 RSFANTLVDCAYAGSGNVLKVQQLLHICSEHFDSKEKEEDKDKKEKKDKDKKEAPAD
 MGAHQGVAVLGIALIAMGEEIGAEMALRTFGHLLRYGEPTLRRVPLALALISVSNPRLNI
 LDTLSKFSHDADPEVSYSNIFAMGMVSGGTNNARLAAMLRLQLAQYHAKDPNNLFMVRL
 AQGLTHLGKGTTLCPYHSDRQLMSQVAVAGLLTVLVSFLDVRNIILGKSHYVLYGLVAA
 MQPRMLVTFDEELRPLPVSVRVGQAVDVVGQAGPKTITGFQTHHTTPVLLAHGERAEL
 ATEEFLPVTPILEGFVILRKNPNYDL

SEQID No:170

MKQEGSARRRGADKAKPPPGGGEQEPPPPAPQDVEMKEEAATGGGSTGEADGKTA
 AAAAEHSQRELDTVTLEDIKEHVQLEKAVSGKEPRFVLRALRMLPSTSRRLNHVLYK
 AVQGGFTSNNATRDFLLPFLEEDMDTEADLQFRPRTGKAASTPLLPEVEAYLQLLVVIFM
 MNSKRYKEAQKISDDLMOQKISTQNRALDLVAAKCYYYHARVYEFDLKLDVRSFLHAR
 LRTATLRHDADGQATLLNLLLRNYLHYSLYDQAEKLVSKSVFPEQANNNEWARYLYT
 GRIKAIQLEYSEARRTMTNALRKAPQHTAVGFKQTVHKLLIVVELLLGEIPDRLQFRQPSL
 KRSLMPYFLLTQAVRTGNLAKFNQVLDQFGEKFQADGTYTLIIRLRHNVIKTGVRMISLS
 YSRISLADIAQKLQLDSPEDADEFIVAKAIRDGVIEASINHEKGYVQSKEMIDIYSTREPQLA
 FHQRISFCLDIHNMSVKAMRFPPKSYNKDLESAEERREREQQDLEFAKEMAEDDDDSF
 P

SEQID No:171

MVLESTMVCVDNSEYMRNGDFLPTRLQAQQDAVNIVCHSKTRSNPENNVGLITLANDC
 EVLTTLTPTDGRILSKLHTVQPKGKITFCTGIRVAHLALKHRQGKNHKMRIIAFVGSPVED

NEKDLVKLAKRLKKEKVNVDIINFGEEEVNTEKLTAFVNTLNGKDGTGSHLVTVPPGPSL
ADALISSPILAGEGGAMLGLGASDFEFGVDPSADPELALALRVSMEEQRQRQEEEEARR
AAAASAAEAGIATTGTEDSDDALLKMTISQQEFGRTGLPDLSSMTEEEQIAYAMQMSLQ
GAIEFGQAESADIDASSAMDTSEPAKEEDDYDVMQDPEFLQSVLENLPGVDPNNEAIRN
AMGSLASQATKDGKKDKKEEDKK

SEQID No:172

MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEEDG
EEDPDRYVCSGVPGRPPGLEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRFYTEKN
GQLIYTPFTEDTPSVGQRLNLSVLNLTIMISVIVMTIFLVVLYKYRCYKFIHGWLIMSSLM
LLFLFTYIYLGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWKGPLVLQQAYLIMISAL
MALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRMLVETAQERNEPIFPALIYSSAMV
WTVGMAKLDPSSQGALQLPYDPEMEEDSYDSFGEPSYPEVFEPPLTGYPGEELEEEE
ERGVKLGLGDFIFYSVLVGKAAATGSGDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPI
SITFGLIFYFSTDNLVRPFMDTLASHQLYI

SEQID No:173

MAAKVFESIGKFGLALAVAGGVVNSALYNVDAGHRAVIFDRFRGVQDIVVGEGTHFLIP
WVQKPIIFDCRSRPRNPVITGSKDLQNVNITLRILFRPVASQLPRIFTSIGEDYDERVLPS
ITTEILKSVVARFDAGELITQRELVSQVSDDLTERAATFGLILDDVSLTHLTFGKEFTEAV
EAKQVAQQEAERARFVVEKAEQQKKAIIISAEGDSKAAELIANSLATAGDGLIELRKLEA
AEDIAYQLSRSRNITYLPAGQSVLLQLPQ

SEQID No:174

MPLAQLADPWQKMAVESPSDSAENGQQIMDEPMGEEEINPQTEEVSKEIAITHHVKEG
HEKADPSQFELLKVLGQGSFGKVFLVKKISGSDARQLYAMKVLKKATLKVRDRVRTKM
ERDILVEVNHPFIVKLHYAFQTEGKLYLILDFLRGGDLFTRLSKEVMFTEEDVKFYLAELA
LALDHLHSLGIIYRDLKPENILLDEEGHIKLTDFGLSKESIDHEKKAYSFCGTVEYMAPEV
VNRRGHTQSADWWSFGVLMFEMLTGTLPFQGKDRKETMTMILKAKLGMPQFLSPEAQ
SLLRMLFKRNPANRLGAGPDGVVEIKRHSFFSTIDWNKLYRREIHPPFKPATGRPEDTF
YFDPEFTAKTPKDSPGIPPSANAHQLFRGFSFVAITSDDSQAMQTVGVHSIVQQLHRN
SIQFTDGYEVKEDIGVGSYSVCKRCIHKATNMEFAVKIIDKSKRDPTEEIEILLRYGQHPNI
ITLKD VYDDGKYVYVVTLMKGGELLDKILRQKFFSEREASAVLFTITKTVEYLHAQGVV
HRDLKPSNILYVDESGNPESIRICDFGFAKQLRAENGLLMTPCYTANFVAPEVLKRQGY

DAACDIWSLGVLLYTMLTGYTPFANGPDDTPEEILARIGSGKFSLSGGYWNSVSPTAKD
 LVSKMLHVDPHQRLTAALVLRHPWIVHWDQLPQYQLNRQDAPHLVKGAMAATYSALN
 RNQSPVLEPVGRSTLAQRRGIKKITSTAL

SEQID No:175

SVTQPAGSVMGRWSLTASPVTLTSLLPMTAGPAAGKSSSSTSWDTVLTAITCASTVQ
 LISTTLGASASGARMPTTCCSGTTVFLTALQDTMQREELVKNATPPAEPARAEDLSPAP
 HVTPTSCCPTLAPAAPPASLGTILMTIMFASTQSQWSIEVGVDDHFLDLQQKTSLFKKV
 WPHQDVCVSTTCNTHCGSCDSQASCTSCRDPNKVLLFGECQYESCAPQYYLDFSTNT
 CKAADRVLINELLGLRVDRKEDNLMQTTFFLECDWSCSACSGPLKTDCLQCMDGYVLQD
 GACVEQCLSSFYQDSGLCKNCDSYCLQCQGPHECTRCKGPFLLLEAQCQVQECGKGYF
 ADHAKHKCTACPQGCLQCShRDRCHLCDHGFFLKSGLCVYNCVPGFSVHTSNETCSG
 KIHTPSLHVNGSLILPIGSIKPLDFSLLNVQDQEGRVEDLLFHVVSTPTNGQLVLSRNGKE
 VQLDKAGRFSWKDVNEKKVRFVHSKEKLRKGYLFLKISDQQFFSEPQLINIQAFSTQAP
 YVLRNEVLHISRGERATITTQMLDIRDDDNPDVVEIIDPPLHGQLLQTLQSPATPIYQF
 QLDELSRGLLHYAHDGSDSTSDVAVLQANDGHSFHNILFQVKTPQNDRGLQLVANSM
 VVWPEGGMLQITNRILQAEAPGASAEIYKITQDYPQFGEVLLVNMPADSPADEGQH
 LPDGRATATPTSTFTQQDINEGIVWYRHSGAPAQSDSFRFEVSSASNAQTRLESHMFNIA
 ILPQTPEAPKVSLEASLHMTAREDGLTVIQPHSLSFINSEKPSGKIVYNITLPLHPNQGIIE
 HRDHPHSPIRYFTQEDINQGKVMYRPPPAAPHLQELMAFSFA

SEQID No:176

MSSQPAGNQTS PGATEDYSYGSWYIDEPQGGEELOPEGEVPSCHTSIPPGLYHACLA
 SLSILVLLLLLAMLVRRRQLWPDCVRGRPLPSPVDFLAGDRPRAVPAAVFMVLLSSLCL
 LLPDEDALPFLTLASAPSQDGKTEAPRGAWKILGLFYAAALYYPLAACATAGHTAAHLLG
 STLSWAHLGVQVWQRAECPQVPKIYKYSSLLASLPLLLGLGLFLSLWYPVQLVRSFSRRT
 GAGSKGLQSSYSEEYLRNLLCRKKLGSSYHTSKHGFLSWARVCLRHCIYTPQPGFHLP
 LKLVL SATLTGTAIYQVALLLLVGVVPTIQKVRAGVTDDVSYLLASFGIVLSEDKQEVVELV
 KHHLWALEVCYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQ
 AIFCWMSFSAYQTAFICLGLLVQQIIFLGTALAFVLMPVLHGRNLLFRSLESSWPFW
 LTLALAVILQNMAAHWVFLETHDGHQPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLL
 SALYNAIHLGQMDLSLLPPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSL
 PRTMAAPQDSL RPGEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTL
 QVFRKTALLGANGAQP

SEQID No:177

MERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRLDAPPPPAAPLPRWSGPIGVS
WGLRAAAAGGAFFPRGGRWRRSAPGEDEECGRVRDFVAKLANNTHQHVFDDLGRGSVS
LSWVG DSTGVILVLTTFHVPLVIMTFGQSKLYRSEDYGKNFKDITDLINNTFIRTEFGMAI
GPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVQTDLPFHPLTQMMYSPQNSDYLLA
LSTENGLWVSKNFGGKWEEIHKAVCLAKWGSDNTIFFTTYANGSCKADLGALELWRTS
DLGKSFKTIGVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDQGD TWSMAQLPSVGQE
QFYSILAANDDMVFMHVDEPGDTGFGTIFTSDDRGIVYSKSLDRHLYTTTGGETDFTNV
TSLRGVYITSVLSEDNSIQTMITFDQGGRWTHLRKPENSECDATAKNKNECSLHIHAS
SISQKLNVPMAPLSEPNAVGIHAGSVGDAISVMVPDVYISDDGGYSWTKMLEGPHYY
TILDSGGIIVAIHSSRPINVIKFSTDEGQCWQTYTFTTRDPIYFTGLASEPGARSMNISIWG
FTESFLT SQWVSYTIDFKDILERNCEEKDYTIWLAHSTD PEDYEDGCILGYKEQFLRLRK
SSMCQNGRDYVVT KQPSICLCSLEDFLCDFGYR PENDSKCVEQPELKGHDLEFCLYG
REEHLTTNGYRKIPGDKCQGGVNPVREV KDLKKKCTSNFLSPEKQNSKSNVPIILAIVG
LMLVTVVAGVLIVKKYVCGGRFLVHRYSVLQQHAEANGVDGVDALDTASHTNKSGYHD
DSDEDLLE

SEQID No:178

MPAHLQDDISSSYTTTTTITAPPSRVLQNGGDKLETMPLYLEDDIRPDIKDDIYDPTYKD
KEGPSPKVEYVWRNIILMSLLHLGALYGITLIPTCKFYTWLWGVFYFVSALGITAGAHRL
WSHRSYKARLPLRLFLIIANTMAFQNDVYEWARHDRAHHKFSETHADPHNSRRGFFFS
HVGWLLVRKHPAVKEKGSTLDLSDLEAEKLVMFQRRYYKPGLLMMCFILPTLVPWYFW
GETFQNSVFVATFLRYAVVLNATWLVN SAAHLFGYR PYDKNISPRENILVSLGAVGEGF
HNYHHSFPYDYSASEYRWHINFTTFFIDCMAALGLAYDRKKVSKAAILARIKRTGDGNYK
SG

SEQID No:179

MAAAPGN GRASAPRLLLLFLVPLLWAPAAVRAGPDEDLSHRNKEPPAPAQQLQPQP
AVQGPEPARVEKIFT PAAPVHTNKEDPATQTNLGFIHAFVAAISVIVSELGDKTFFIAAIM
AMRYNRLTVLAGAMLALGLMTCLSVLFGYATTVIPRVYTYVSTVLFAIFGIRMLREGLK
MSPDEGQEELEE VQAEKKKDEEFQRTKLLNGPGDVETGTSITVPQKKWLHFISPIFVQ
ALTLTFLAEWGDRSQLTTIVLAAREDPYGVAVGGTVGHCLCTGLAVIGGRMIAQKISVRT
VTIIGGIVFLAFAFSALFISPD SGF

SEQID No:180

MTSIHFVVHPLPGTEDQLNDRLREVSEKLNKYNLNSHPPLNVLEQATIKQCVVGPNHAA
FLLEDGRVCRIGFSVQPDRLLELGKPDNNDGSKLNSNSGAGRTSRPGRTSDSPWFLSG
SETLGRLAGNTLGSRWSSGVGGSGGGSSGRSSAGARDSRRQTRVIRTGRDRGSGLL
GSQPQPVIPASVIPEELISQAQVVLQGKSRSVIRELQRTNLDVNLAVNNLLSRDDEDGD
DGDDTASESYLPGEDLMSLLDADIHSAHPSVIIDADAMFSEDISYFGYPSFRRSSLSRLG
SSRVLLLPLERDSELLRERESVLRRLRERRWLDGASFDNERGSTSKEGEPNLDKKNTPV
QSPVSLGEDLQWWPDKDGTKFICIGALYSELLAVSSKGELYQWKWSESEPYRNAQNP
SLHHPRATFLGLTNEKIVLLSANSIRATVATENNKVATWVDETLSSVASKLEHTAQTYSE
LQGERIVSLHCCALYTCAQLENSLYWWGVVPFSQRKKMLEKARAKNKKPKSSAGISSM
PNITVGTQVCLRNNPLYHAGAVAFSISAGIPKVGVLMEVWNMNDSCRFQLRSPESLKN
MEKASKTTEAKPESKQEPVKTEMGPPPPSPASTCSDASSIASSASMPYKRRRSTPAPKE
EEKVNEEQWSLREVVFVEDVKNVPVGKVLKVDGAYVAVKFPGTSSNTNCQNSSGPDA
DPSSLLQDCRLLRIDELQVVKTGGTPKVPDCFQRTPKKLCIPEKTEILAVNVDSKGVHAV
LKTGNWVRYCIFDLATGKAEQENNFTSSIAFLGQNERNVAIFTAGQESPIILRDGNGTIY
PMAKDCMGGIRDPDWLDLPPISSLGMGVHSLINLPANSTIKKKAAVIIMAVEKQTLMQHIL
RCDYEACRQYLMNLEQAVVLEQNLQMLQTFISHRCDGNRNILHACVSVCFPTSNNKETK
EEEEAERSERNTFAERLSAVEAIAAISVVSSNGPGNRAGSSSSSRSLRLREMMRRSLR
AAGLGRHEAGASSSDHQDPVSPPIAPPSWVPDPPAMDPDGDIDFILAPAVGSLTTAATG
TGQGPSTSTIPGPSTEPSVVESKDRKANAHFILKLLCDSVVLQPYLRELLSAKDARGMT
PFMSAVSGRAYPAAITILETAQKIAKAEISSSEKEEDVFMGMVCPSGTNPDDSPLYVLCC
NDTCSFTWTGAEHINQDIFECRTCGLLESLLCCCTECARVCHKGHDCCLKRTSPTAYCD
CWEKCKCKTLAGQKSARLDLLYRLLTATNLVTLPNRGEHLLLFLVQTVARQTVEHCQ
YRPPRIREDRNRKTASPEDSDMPDHDLEPPRFAQLALERVLDWNALKSMIMFGSQEN
KDPLSASSRIGHLLPEEQVYLNQQSGTIRLDCFTHCLIVKCTADILLDDTLGLTLVKELQN
KYTPGRREEAIAVTMRFLRSVARVFVILSVEMASSKKKNNFIPQPIGKCKRVFQALLPYA
VEELCNVAESLIVPVRMGIARPTAPFTLASTSIDAMQGSEELFSVEPLPPRPSSDQSSSS
SQSQSSYIIRNPQQRRISQSQPVRGRDEEQDDIVSADVEEVEVVEGVAGEEDHHDEQE
EHGEENAEAEQGQHDEHDEDGSDMELDLLAAAEATESDSSESNHSNQDNASGRRSVVTAA
TAGSEAGASSVPAFFSEDDSQSNDSSSDSSSSSQSDDIEQETFMLDEPLERTTNSSHA
NGAAQAPRSMQWAVRNTQHQRRAASTAPSSSTPAASSAGLIYIDPSNLRRSGTISTSAA
AAAAALEASNASSYLTSASSLARAYSIVIRQISDLMLIPKYNHLVYSQIPAAVKLTYQDA
VNLQNYVEEKLIPTWNWMVSIMDSTEALRYGSALASAGDPGHPNHPLHASQNSARR

ERMTAREEASLRTLEGRRRATLLSARQGMMSARGDFLNYALSLMRSHNDEHSDVLPV
LDVCSLKHVAYVFQALIYWIKAMNQQTTLDTQPQLERKRTRELLELGIDNEDSEHENDDD
TNQSATLNDKDDDSLPAETGQNHPPFRRSDSMTFLGCIPPNPFEVPLAEAIPLADQPHL
LQPNARKEDLFGRPSQGLYSSSASSGKCLMEVTVDRCNLEVLPTKMSYAANLKNVMN
MQNRQKKEGEEQPVLPPEETESSKPGPSAHDLAALQKSSLLAEIGLTESEGPPLTSFRPQ
CSFMGMVISHDMLLGRWRLSLELFGRVFMEDVGAEPGSILTELGGFEVKESKFRREME
KLRNQQSRDLSLEVDRDRDLLIQQTMRQLNNHFGRRCATTPMAVHRVKVTFKDEPGE
GSGVARSFYTAIAQAFLSNEKLPNLECIQNANKGTHTSMLQRLNRGERDRERERERE
MRRSSGLRAGSRRDRDRDFRRQLSIDTRPFRPASEGNPSDDPEPLPAHRQALGERLY
PRVQAMQPAFASKITGMILLESPAQLLLLLASEDSLRRARVDEAMELIIAHGRENGADSIL
DLGLVDSSEKVQQENRKRHGSSRSVVDMDLDDTDDGDDNAPLFYQPGKRGFYTPRP
GKNTEARLNCFRNIGRILGLCLLQNELCPITLNRHVIVKVLGRKVNWHDFAFFDPVMYES
LRQLILASQSSDADAVFSAMDFAIDLCKEEGGGQVELIPNGVNIPVTPQNVYEVYRKY
AEHRMLVVAEQPLHAMRKGLLDVLPKNSLEDLTAEDFRLLVNGCGEVNVQMLISFTSFN
DESGENAEKLLQFKRWFWSIVEKMSMTERQDLVYFWTSSPSLPASEEGFQPMPSITIR
PPDDQHLPTANTCISRLYVPLYSSKQILKQKLLLAIKTKNFGFV

SEQID No:181

MATHGQTCARPMCIPPSYADLGKVARDIFNKGFGFGLVKLDVKTSCSGVEFSTSGSS
NTDTGKVTGTLETYKWCEYGLTFTEKWNTDNTLGTEIAIEDQICQGLKLTFTDTTFSPNT
GKKSGKIKSSYKRECINLGCVDVDFDFAGPAIHGSAVFGYEGWLAGYQMTFDSAQSKLT
RNNFAVGVRTGDFQLHTNVNDGTEFGGSIYQKVCEDLDTSVNLAWTSGTNCTRFGIAA
KYQLDPTASISAKVNNSSLIGVGYTQTLRPGVKLTLSALVDGKSINAGGHKVGLALELEA

SEQID No:182

MDSNTAPLGPSCPQPPAPQPQARSRLNATASLEQERSEPRAPGPQAGPGPGVRD
AAAPAEPPAQHTRSRRERADGTGPTKGDMEIPFEEVLERAKAGDPKAQTEVGKHYLQLA
GDTDEELNSCTAVDWLVLAQKGRREAVKLLRRCLADRRGITSENEREVRQLSSETDL
ERAVRKAALVMYWKLNPKKKKQVAVAELENVGVNEHDGGAQPGPVPKSLQKQRR
MLERLVSSSESKNYIALDDFVEITKKYAKGVIPSSLFLQDDEDDDELAKSPEDLPLRLKV
VKYPLHAIMEIKEYLIDMASRAGMHWLSTIIPTHHINALIFFFIISNLTIDFFAFFIPLVIFYLSF
ISMVICTLKVFQDSKAWENFRTLTDLLLRFEPNLDVEQAEVNFGWNHLEPYAHFLLSVFF
VIFSFPISKDCIPCSELAVITGFFTSTSYLSLSTHAEPYTRRALATEVTAGLLSLLPSMPL
NWPYLVKVLGQTFITVPVGHLLVNLVSVPCLLYVYLLYLFFRMAQLRNFKGTICYLVPLYV

CFMWCELSVVILLESTGLGLLRASIGYFLFLFALPILVAGLALVGVLQFARWFTSLELTkia
 VTVAVCSVPLLLRWWTkasfsvvgmvksltrssmvklilvwltaivlfcwfyvyrsegm
 kvynstltwqqygalcgpr¹¹awketnmartqilcshleghrvtwtgrfkyvrvt¹¹didn
 saesainmlpffigdwmrcl¹¹ygeaypacspgntstae¹¹eelcrlkllakhpchikkfdry
 kfeitvgmpfssgadgsrsreeddvtkdivlrassefksvllslrqgsliefstilegrlg
 skwpvfelkaisclncmaqlsptrrhvk¹¹iehdwrstv¹¹hgavkfafdffffpflsaa

SEQID No:183

MGSGPLSLPLALSPPRLLLLLLSLLPVARASEAEHRLFERLFEDYNEIIRPVANVSDPVII
 HFEVSMSQLVKVDEVNQIMETNLWLKQIWN¹¹DYKLKWNPSDYGGAEFMRVPAQKIWK¹¹P
 DIVLYNNAVGD¹¹FQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYFPFDYQNCTMKFGS
 WSYDKAKIDLVLIGSSMNLKDYWESGEWAIKAPGYKHDIKYNCC¹¹EIYPDITYSLYIRRL
 PLFYTINLIIPCLLISFLT¹¹VLV¹¹FYLPSDCGEKVTL¹¹CISVLLSLTVFLLVITETIPSTSLVIPLIGEY
 LLFTMIFVTL¹¹SIVITV¹¹FVLNVHYRTPTTHTMP¹¹SWVKTVFLNLLPRVMFMTRPTSNEGNAQ
 KPRPLYGAELSNLNCFSRAESKGCKEGYPCQDGMCGYCHHRRIKISNFSANLTRSSSS
 ESVD¹¹AVLSLSALSPEIKEAIQSVKYIAENMK¹¹AQNEAKEEQKAQEIQQLKRKEKSTETSDQ
 EPGL

SEQID No:184

MEKRETFVQAVSKELVGEFLQFVQLDKEASDPFSLNELDEL¹¹SRKQKEELWQRLKNLLT
 DVLLESPVDGWQVVEAQGEDNMETE¹¹HGSKMRKSIEIIYAITSVILASVSVINESENYEALL
 ECVIILNGILYALPESERKLQSSIQDLCVTWWEKGLPAKEDTGKTA¹¹FVMLLRRSLETKTG
 ADVCRLWRIHQALYCFDYDLEESGEIKDMLLECFININ¹¹YIKKEEGRRFLSCLFNWNINFIK
 MIHGTIKNQLQGLQKSLMVYIAEIYFRAWKKASGKILEAIENDCIQDFMFHGIHLPRRSPV
 HSKVREVLSYFHHQKKVRQGEEMLYR¹¹LYKPILWRGLKARNSEVRSNAALLFVEAFPIR
 DPNLHAIEMDSEIQKQFEELYSLLED¹¹PYPMVRSTGILGVCKITSKYWEMMPPTILIDLLKK
 VTGELAFDTSSADVRC¹¹SVFKCLPMILDNKLSHPLLEQLLPALRYSLHDNSEKVRVAFVD
 MLLKIKAVRAAKFWKICPMEHILVRLETDSRPVSRRLVSLIFNSFLPVNQPEE¹¹WCERCV
 TLVQMNHAAARRFYQYAHEHTACTNIAKLIHVIRHCLNACIQRAVREPPED¹¹EEEDGRE
 KENVTVLDKTL¹¹SVNDVACMAGLLEIIVILWKSIDRSMENNKEAKLYTINKFASVLPEYLKV
 FKDDRCKIPLFMLMSFMPASAVPPFSCGVISTLRSREEGAVDKSYCTLLDCLCSWGQV
 GHILELVDNWLPT¹¹EHQA¹¹KSNTASKGRVQIH¹¹DTRPVKPELALVYIEYLLTHPKNRECLLS
 APRKKNHLLKALET¹¹SKADLESLLQTPGGKPRGFSEAAAPRAFG¹¹LHCRLSIHLQHKFCS
 EGKVYLSMLEDTGFWLESKILSFIQDQEEDYLK¹¹HRVIYQQIIQTYLTVCKDVVMVGLGD

HQFQMQLLQSRSLGIMQTVKGFFYVSLLLDILKEITGSSLIQKTDSDDEEVAMLLDTVQKVF
 QKMLECIARSFRKQPEEGLRLLYSVQRPLHEFITAVQSRHTDTPVHRGVLSTLIAGPVVE
 ISHQLRKVSDVEELTPPEHLSDLPPFSRCLIGIIKSSNVVRSFLDELKACVASNDIEGIVCL
 TAAVHIILVINAGKHKSSKVREVAATVHRKLKTFMEITLEEDSIERFLYESSSRTLCELLNS

SEQID No:185

MAAAAVQGGRRSGGSGGCSGAGGASNCGTGSGRSGLLDKWKIDDKPVKIDKWDGSAV
 KNSLDDSAKKVLEKYKYVENFGLIDGRLTICTISCFFAIVALIWDYMHPPFESKPVLALC
 VISYFVMMGILTIYTSYKEKSIFLVAHRKDPTGMDPDDIWQLSSSLKRFDDKYTLKLTFIS
 GRTKQQREAEFTKSIKFFDHSGTLVMDAYEPEISRLHDSLAIERKIK

SEQID No:186

MAVLRQLALLLWKNYTLQKRKVLVTVLELFLPLLFPGLIWLRLKIQSENVPNATIYPGQSI
 QELPLFFTFFPPPGDTWELAYIPSHSDAAKTVTETVRRALVINMRVRGFPSEKDFEDYIRY
 DNCSSSVLAADVFEHPFNHSKEPLPLAVKYHLRFSYTRRNWMWTQTGSFFLKETEGWH
 TTSFLPLFPNPGPRELTSPDGGEPGYIREGFLAVQHAVDRAIMEYHADAATRQLFQRLT
 VTIKRFPPYPPFIADPFLVAIQYQLPLLLLLSFTYTALTARAVVQEKERRLKEYMRMMGLS
 SWLHWSAWFLLFFLFLIAASFMTLLFCVKVKPNVAVLSRSDPSLVLAFLLCFAISTISFSF
 MVSTFFSKANMAAAFGGFLYFFTYIPYFFVAPRYNWMTLSQKLCSCLLSNVAMAMGAQ
 LIGKFEAKGMGIQWRDLLSPVNVDDDFCFGQVLGMLLLDSVLYGLVTWYMEAVFPGQF
 GVPQPWYFFIMPSYWCGKPRAVAGKEEEDSDPEKALRNEYFEAEPEDLVAGIKIKHLSK
 VFRVGNKDRAAVRDLNLNLYEGQITVLLGHNGAGKTTTSLMLTGLFPPTSGRAYISGYEI
 SQDMVQIRKSLGLCPQHDLFDNLTVAEHLYFYAQLKGLSRQKCPEEVKQMLHIIGLEDK
 WNSRSRFLSGGMRRKLSIGIALIAGSKVLILDEPTSGMDAISRRAIWDLQRQKSDRTIVL
 TTHFMDEADLLGDRIAIMAKGELQCCGSSLFLKQKYGAGYHMTLVKEPHCNPEDISQLV
 HHHVPNATLESSAGAELSIFLPRESTHRFEGLFAKLEKKQKELGASFGASITTEEVFLR
 VGKLVDSMDIQAIQLPALQYQHERRASDWAVDSNLCGAMDPDGDIGALIEEERTAVKL
 NTGLALHCQQFWAMFLKKAAYSWREWKMVAAQVLVPLTCVTLALLAINYSSELFDDPM
 LRLTLGEYGRTVVPFSVPGTSQLGQQLSEHLKDALQAEGQEPREVLGDLEEFLIFRASV
 EGGGFNERCLVAASFRDVGERTVVNALFNNQAYHSPATALAVVDNLLFKLLCGPHASIV
 VSNFPQPRSAALQAAKDQFNEGRKGFIDIALNLLFAMAFLASTFSILAVSERAVQAKHVQF
 VSGVHVASFWLSALLWDLISFLIPSLLLLTVFKAFDVRAFTRDGHMADTLLLLLLYGWAI
 PLMYLMNFFFLGAATAYTRLTIFNILSGIATFLMVTIMRIPAVKLEELSKTLDHVFLVLPNH
 CLGMAVSSFYENYETRRYCTSSSEVAAHYCKKYNIQYQENFYAWSAPGVGRFVASMAA

SGCAYLILLFLIETNLLQRLRGILCALRRRRTLTELYTRMPVLPEDQDVADERTRILAPSP
 DSSLHTPLIIKELSKVYEQRVPLLAVDRLSLAVQKGECFLLGFNGAGKTTTFKMLTGEE
 SLTSGDAFVGGHRISSDV¹¹GKVRQRIGYCPQFDALLDHMTGREMLVMYARLRGIPERHI
 GACVENTLRGLLLEPHANKLVRTYSGGNKRKLSTGIALIGEPAVIFLDEPSTGMDPVARR
 LLWDTVARARESGKAIITSHSMEECEALCTRLAIMVQQGQFKCLGSPQHLKSKFGSGGYSL
 RAKVQSEGQQEALEEFKAFVDLTFPGSVLEDEHQGMVHYHLPGRDLSWAKVFGILEKA
 KEKYGVDDYSVSQISLEQVFLSFAHLQPPTAEGR

SEQID No:187

MAQALPWLLLWMGAGVLPAGHTQHGIPLRSLGLGGAPLGLRLPRETDEEPEEPGRR
 GSFVEMVDNLRGKSGQGYVEMTVGSPQTLNILVDTGSSNFAVGAAPHPFLHRYYQ
 RQLSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGS
 NWEIGILGLAYAEIARPDSDLEPFFDSL VKQTHVPNLFSLQLCGAGFPLNQSEVLASVGG
 SMIIGGIDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTN
 LRLPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVT
 NQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRI
 GFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDESTLMTIAYVMAAICALFMLP
 LCLMVCQWRCLRCLRQQHDDFADDISLLK

SEQID No:188

MSEADGLRQRRPLRPQVVTDDDGQAPEAKDGSSFSGRVFRVTFLMLAVSLTVPLLGA
 MMLLESPIDPQPLSFKEPPLLLGVLHPNTKLRQAERLFENQLVGPESIAHIGDVMFTGTA
 DGRVVKLENGEIETIARFGSGPCKTRDDEPVCGRPLGIRAGPNGTLFVADAYKGLFEVN
 PWKREVKLLLSSETPIEGKNMSFVNDLTVTQDGRKIYFTDSSSKWQRRDYLLLVMEGT
 DDGRLLEYDTVTREVKVLLDQLRFPNGVQLSPAEDFVLVAETTMARIRRVYVSGLMKG
 GADLFVENMPGFPDNIRPSSSGGYWVGMSTIRPNPGFSMLDFLSERPWIKRMIFKLFS
 QETVMKFVPRYSLVLELSDSGAFRRSLHDPDGLVATYISEVHEHDGHLVLSFRSPFLC
 RLSLQAV

SEQID No:189

MLKVTVPSCSASSCSSVTASAAPGTASLVPDYWIDGSNRDALSDFFEVESELGRGATSI
 VYRCKQKGTQKPYALKVLKKTVDKKIVRTEIGVLLRLSHPNIIKLKEIFETPTEISLVLELVT
 GGELFDRIVEKGYYSERDAADAVKQILEAVAYLHENGIVHRDLKPENLLYATPAPDAPLK
 IADFGLSKIVEHQVLMKTVCGTPGYCAPEILRGAYGPEVDMWSVGIITYILLCGFEFPY

DERGDQFMFRRILNCEYYFISPWWDEVSLNAKDLVRKLIVLDPKKRLTTFQALQHPWVT
 GKAANFVHMDTAQKKLQEFNARRKLKAAVKAVVASSRLGSASSSHGSIQESHKASRDP
 SPIQDGNEDMKAIPEGEKIQGDGAQAQAAVKGAQAELMKVQALEKVKGADINAEAEAPKMV
 PKAVEDGIKVADLEEEGLAEKLTVEEAAAAPREGQGSSAVGFEVPQQDVILPEY

SEQID No:190

MSSSEEVSWISWFCGLRGNEFFCEVDEDYIQDKFNLTGLNEQVPHYRQALDMILDLEP
 DEELEDNPNQSDLIEQAAEMLYGLIHARYILTNRGIAQMLEKYQQGDFGYCPRVYCENQ
 PMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRRHHHTDGAYFGTGFPHMLFMVHPEYR
 PKRPNQFVPRLYGFKIHPMAYQLQLQAASNFKSPVKTIR

SEQID No:191

MWQLWASLCCLLVLANARSRPSFHPVSDLVNYVKNRNTTWQAGHNFYNVDMSYLKR
 LCGTFLGGPKPPQRMFTEDLKLPASFDAREQWPQCPTIKEIRDQGSCGSCWAFGAV
 EAISDRICHTNAHVSVEVSAEDLLTCCGSMCGDGCNGGYPAEAWNFWTRKGLVSGGL
 YESHVGCPRYSIPPCEHHVNGSRPPCTGEGDTPKCSKICEPGYSPTYKQDKHYGYNSY
 SVSNSEKDIMAIEIYKNGPVEGAFSVYSDFLLYKSGVYQHVTGEMMGHAIIRILGWGVE
 NGTPYWLANSWNTDWGDNGFFKILRGQDHCGIESEVVAGIPRTDQYWEKI

SEQID No:192

MMRQAPTARKTTTTRRPKPTRPASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLA
 APIIPTPVLTSFGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRRLKRAEDKAKLKELEKHKI
 QLEQVQEWKSKMQEQQADLQRRRLKEARKEAKEALEAKERYMEEMADTADAIEMATLD
 KEMAEERAESLQQEVEALKERVDELTTDLEILKAEIEEKGSDDGAASSYQLKQLEEQNAR
 LKDALVRMRDLSSEKQEHVKLQKLMEKKNQELEVVRQQRERLQEELSQAESTIDELK
 EQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVGDLEAMNEMNDELQENARETELEL
 REQLDMAGARVREAQKRVEAAQETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASV
 ERQQQPPPETFDKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPDSFLRPG
 GDHDCVLVLLLMPLICKAELIRKQAQEKFELSENCSERPGLRGAAGEQLSFAAGLVYS
 LSLQATLHRYEHALSQCSVDVYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETNNVE
 PLTKAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVGRRLRAFLQGGQEA
 TDIALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAALAFGPQVSDTLLDCRKHLTWV
 VAVLQEVAASAAAQLIAPLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNILIS
 TMNKLATAMQEGEYDAERPPSKPPPVELRAAALRAEITDAEGLGLKLEDRETVIKELKK

SLKIKGEELSEANVRLSLLEKKLDSAAKDADERIEKVQTRLEETQALLRKKEKEFEETMD
 ALQADIDQLEAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQRGAI PGQA
 PGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSILKGAQMKASLASLPPLHVAKLSHE
 GPGSELPAGALYRKTSQLETLNQLSTHTHVVDITRTSPA AKSPSAQLMEQVAQLKSLS
 DTVEKLKDEV LKETVSQRPGATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAA
 GFGQRHRLVLTQEQLHQLHSRLIS

SEQID No:193

MGKGGNQGE GAAEREVSVP TFSWEEIQKHNLRTDRWLVIDRKVYNITKWSIQHPGGQ
 RVIGHYAGEDATDAFRAFHPDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALR
 KTAEDMNLFKTNHVFLLLLAHIIALESIAWFTVFYFGNGWIPTLITAFVLATSQAQAGWL
 QHDYGHLSVYRKPKWNHLVHKFVIGHLKGASANWWNHRHFQHHAKPNIFHKDPDVNM
 LHV FVLGEWQPIEYGKKKLYLPYNHQHEYFFLIGPPLLIPMYFQYQIIMTMIVHKNWVDL
 AWAVSYYIRFFITYIPFYGILGALLFLNFIRFLESHWFVWVTQMNHIVMEIDQEAYRDWFS
 SQLTATCNVEQSFFNDWFSGHLNFQIEHHLFPTMPRHNHKKIAPLVKSLCAKHGIEYQE
 KPLL RALLDIIRSLKKSGKLWLDAYLHK

SEQID No:194

MASLDRVKVLVLGD SGVGKSSLVHLLCQNQVLGNPSWTVGCSVDVRVHDYKEGTPEE
 KTCYIELWDVGGSVGSASSVKSTRAVFYNSVNGIIFVHDLTNKKSSQNLRRWSLEALNR
 DLVPTGVLVTNGDYDQEQFADNQIPLL VIGTKLDQIHETKRHEVLT TTAFLAEDFNPEEIN
 LDCTNPRYLAAGSSNAVKLSRFFDKVIEKRYFLREGNQIPGFPDRKRFGAGTLKSLHYD

SEQID No:195

MNNHVSSK PSTMKLKHTINPILLYFIHFLISLYTILTYIPFYFFSES RQEKS NRKAKPVNSK
 PDSAYRSVNSLDGLASVLYPGCDTLDKVFTYAKNKFKNRLLGTREVLNEEDEVPNG
 KIFKKVILGQYNWLSYEDVFVRAFNFNGNGLQMLGQKPKTNIAIFCETRAEWMIAAQACF
 MYNFQLVTLYATLGGPAIVHALNETEVTNIITSKELLQTKLKDIVSLVPRLRHIITVDGKPPT
 WSDFPKGIIVHTMAAVEALGAKASMENQPHSKPLPSDIAVIMYTS GSTGLPKGVMISHS
 NIIAGITGMAERIP ELGEEDVYIGYLPLAHVLELSAELVCLSHGCRIGYSSPQTLADQSSKI
 KKGSKGDT SMLKPTLMAAVPEIMDRIYKNVMNKVSEMSSFQRNLFILAYNYKMEQISKG
 RNTPLCDSFVFRKVR SLLGGNIRLLLCGGAPLSATTQRFMNICFC CPVGQGYGLTESAG
 AGTISEVWDYNTGRVGAPLVCCEIKLKNWEEGGYFNTDKPHPRGEILIGGQSVTMGY
 KNEAKTKADFS EDENGQRWLCTGDIGEFEPDGCLKIIDRKKDLVKLQAGEYVSLGKVEA

ALKNLPLVDNICAYANSYHSYVIGFVVPNQKELTELARKKGLKGTWEELCNSCEMENEV
LKVLSEAAISASLEKFEIPVKIRLSPEPWTPETGLVTDFAKLKRKELKTHYQADIERMYGR
K

SEQID No:196

MKLKLNVLTIILLPVHLLITIYSALIFIPWYFLTNAKKKNAMAKRIKAKPTSDKPGSPYRSVT
HFDSLAVIDIPGADTLDKLFDHAVSKFGKKDSLGTREILSEENEMQPNGKVFKKLILGNY
KWMNYLEVNRVNNFGSGLTALGLKPKNTIAIFCETRAEWMIAAQTCFKYNFPLVTLYA
TLGKEAVVHGLNESEASYLITSVELLESKLKTALLDISCVKHIIYVDNKAINKAEYPEGFEIH
SMQSVEELGSPENLGIPPSRPTPSDMAIVMYTSGSTGRPKGVMMHHSNLIAGMTGQ
CERIPGLGPKDITYIGYLPLAHVLELTAEISCFTYGCRIGYSSPLTSDQSSKIKKGSKGDC
TVLKPTLMAAVPEIMDRIYKNVMSKVQEMNYIQKTLFKIGYDYKLEQIKKGYDAPLCNLLL
FKKVKALLGGNVRMMLSGGAPLSPQTHRFMNVCFCCPIGQGYGLTESCGAGTVTEVT
DYTTGRVGAPLICCEIKLDWQEGGYTINDKPNPRGEIVIGGQNISMGYFKNEEKTAEDY
SVDENGQRWFCTGDIGEFHPDGCLQIIDRKKDLVKLQAGEYVSLGKVEAALKNCPLIDNI
CAFAKSDQSYVISFVVPNQKRLTLAQQKGVEGTWVDICNNPAMEAEILKEIREANAM
KLERFEIPIKVRLSPEPWTPETGLVTDFAKLKRKELRNHYLKDIERMYGGK

SEQID No:197

MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPEVQTPKPSDADWDDLWDQFDE
RRYLNAAKWRVGDDPYKLYAFNQRESERISSNRAIPDTRHLSVLNRTPTHLIREIILVDDF
SNPDDDCKQLIKLPKVKCLRNNERQGLVRSRIRGADIAQGTTLTFLDSHCEVNRDWLQP
LLHRVKEDYTRVVCVIDIINLDTFTYIESASELRGGFDWSLHFQWEQLSPEQKARRLDP
TEPIRTPIIAGGLFVIDKAWFDYLGKYDMDMDIWGGGENFEISFRVWMCGGSLEIVPCSRV
GHVFRKKHPYVFPDGNANTYIKNTKRTAEVWMDEYKRYYYAARPFALERPFGNVESRL
DLRKNLRCQSFKWYLENIYPELSIPKESSIQKGNIRQRQKCLESQANGTTGSSGQRPAG
GTSEIWVQKPRVRNRRHAAPQGFDPGAKPSQHWRRPEHPAAE

SEQID No:198

MFFSMGFIVAVKGKIASPLEAPVFVAAPHSTFFDGIACVVAGLPSMVSRNENAQVPLIGR
LLRAVQPVLVSRVDPDSRKNTINEIIRKRTTSGGEWPQILVFPEGTCTNRSLITFKPGAFI
PGVPVQPVLRLYPNKLDTVTWTWQGYTFIQLCMLTFCQLFTKVEVEFMPVQVPNDEEK
NDPVLFAKVRNLMAEALGIPVTDHTYEDCRLMISAGQLTLPMEAGLVEFTKISRKLKLD
WDGVRKHLDEYASIASSSKGGRIIEEFAKYLKLPVSDVLRQLFALFDRNHDGSIDFREY

VIGLAVLCNPSNTEEEIIQVAFKLFVDVDEDEGYITEEEFSTILQASLGVPDLVDVSGLFKEIAQG
 DSISYEEFKSFALKHPEYAKIFTTYLDLQCHVFSLPKEVQTTTPSTASNKVSPEKHEEST
 SDKKDD

SEQID No:199

MRPRRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEKKVKATNFRPNIVISGCD
 VYAEDSWDELLIGDVELKRVMACSRCILTTVPDPTGVMSRKEPLETLKSYRQCPSERK
 LYGKSPLFGQYFVLENPGTIKVGDPVYLLGQ

SEQID No:200

MSSFGYRTLTVALTICCPGSDEKVFVHVRPKKLAVEPKGSLEVNCSTTCNQPEVGG
 LETSLNKILLDEQAQWKHYLVSNISHDTVLCQCHFTCSGKQESMNSNVSVYQPPRQVILT
 LQPTLVAVGKSFTIECRVPTVEPLDSLTLFLFRGNETLHYETFGKAAPAPQEATATFNST
 ADREDGHRNFSCLAVLDLMSRGGNIFHKHSAPKMLEIYEPVSDSQMVIIIVTVVSVLLSLF
 VTSVLLCFIFGQHLRQQRMGTYGVRAAWRRLPQAFRP

SEQID No:201

MDTEGFGELLQQAEQLAAETEGISELPHVERNQLQEIQQAGERLRSRTLTRTSQETADV
 ASVLLGSRGLDISHISQRLESLSAATTFEPLPVKDTDIQGFLKNEKDNALLSAIEESRKR
 TFGMAEEYHRESMLVEWEQVKQRILHTLLASGEDALDFTQESEPSYISDVGPPGRSSL
 DNIEMAYARQIYIYNEKIVNGHLQPNLVDLCASVAELDDKSISDMWMTVMKQMTDVLLTPA
 TDALKNRSSVEVRMEFVRQALAYLEQSYKNYTLVTVFGNLHQAQLGGVPGTYQLVRSF
 LNIKLPAPLPGLQDGEVEGHPVWALIYYCMRCGDLLAASQVVNRAQHQLGEFKTWFOE
 YMNSKDRRLSPATENKLRLHYRRALRNNTDPYKRAVYCIIGRCDVTDNQSEVADKTED
 YLWLKLNQVCFDDGTSSPQDRLTSLSQFQKQLLEDYGESHTVNQQPFLYFQVLFLTA
 QFEAAVAFLFRMERLRCHAVHVALVLFELKLLKSSGQSAQLLSHEPGDPPCLRLNFV
 RLLMLYTRKFESTDPREALQYFYFLRDEKDSQGENMFLRCVSELVIESREFDMILGKLE
 NDGSRKPGVIDKFTSDTKPIINKVASVAENKGLFEEAAKLYDLAKNADKVLELMNKLLSP
 VVPQISAPQSNKERLKNMALSIAERYRAQGISANKFVDSTFYLLLDLITFFDEYHSGHIDR
 AFDIIERLKLVLPLNQESVEERVAEFRNFSDEIRHNLSEVLLATMNILFTQFKRLKGTSPSS
 SSRPQRVIEDRDSQLRSQARTLITFAGMIPYRTSGDTNARLVQMEVLMN

SEQID No:202

MLLVLECVLFSVAQGYFRMDSSATQFHIETHENTSGLWSIWYRNHFDRSVVLNDVFLSK

ETKHMLKILNFTGPLFLPPGCWNIFSLKLAVKDIAINLFTNVFLTNTNIGAIFAIPLOIYSAPTK
 EGSLGFEVIAHCGMHYFMGKSKAGNPWNWNGSLSDQSTWNVDSELANKLYERWKY
 KNGDVCKRNVLGTTTRFAHLKKSKESESVFFLPRLIAEPGLMLNFSATALRSRMIKYFVV
 QNPSSWPVSLQLLPLSLYPKPEALVHLLHRWFGTDMQMINFTTGEFQLTEACPYLGTH
 SEESRFGILHLHLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFGARELLK
 VGGRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSITKNFKVENIGPLPITVSSLKINGY
 NCQGYGFEVLDCHQFSLDPNTSRDISIVFTPDTSSWVIRDLSLVTAADLEFRFTLNVT
 PHHLLPLCADVVPGPSWEESFWRLTVFFVSLSLGVLIAFQQAQYILMEFMKTRQRQN
 ASSSSQQNNGPMDVISPHSYKSNCKNFLDTYGPSDKGRGKNCLPVNTPQSRIQNAAK
 RSPATYGHSQKKHKCSVYYSKHKTSTAAASSTSTTTEEKQTSPLGSSSLPAKEDICTDA
 MRENWISLRYASGINVNLOKNLTLPKNLLNKEENTLKNITVFSNPSSECSMKEGIQTCMF
 PKETDIKTSENTAEFKERELCPLKTSKKLPENHLPRNSPQYHQPDLPEISRKNNGNNQQ
 VPVKNEVDHCENLKKVDTKPSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEK
 EGNLQNLNWSKSRCTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELSSDINVRSWCI
 QESTREVCKADAEIASSLPAAQREAEGYYQKPEKKCVDFKFCSDSSSDCGSSSGSVRAS
 RGSWGSWSSTSSSDGDKKPMVDAQHFLPAGDSVSQNDPSEAPISLNLSHNICNPMT
 VNSLPQYAEPPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLENGVPCVI
 QESAPVHNSFIDWSATCEGQFSSAYCPELNDYNAFPEENMNYANGFPCPADVQTDFI
 DHNSQSTWNTPPNMPAAWGHASFISSPPYLTSTRSLSPMSGFLGSIWAPQSDVYENC
 CPINPTTEHSTHMENQAVVCKEYYPGFNPFRAVMNLDIWTANRANFPLSRDSSYC
 GNV

SEQID No:203

ASGEWRVSGGRPAGAGRPEEALAAGSDPRGAAARLACSAPTPGGGTMPFDFRRFDIY
 RKVPKDLTQPTYTGAIISICCLFILFLFLSELTGFITTEVVNELYVDDPDKDSGGKIDVSL
 NISLPNLHCELVLGDIQDEMGRHEVGHIDNSMKIPLNNGAGCRFEGQFSINKVPGNFHV
 STHSATAQPQNPDMTTHVIHKLSFGDTLQVQNIHGAFNALGGADRLTSNPLASHDYILKIV
 PTVYEDKSGKQRYSYQYTVANKEYVAYSHTGRIIPAIWFRYDLSPITVKYTERRQPLYRF
 ITTICAIIGGTFTVAGILDSCIFTASEAWKKIQLGKMH

SEQID No:204

NSKKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALQREILLQGRLYLSEN
 WICFYSNIFRWETTISIQLKEVTCLKKEKTAKLIPNAIQICTESEKHFFTSFGARDRCFLIF
 RLWQNALLEKTLSPRELWHLVHQCYGSELGLTSEDEDYVSPLQLNGLGTPKEVGDVIA

LSDITSSGAADRSQEPPSPVGSRRGHVTPNLSRASSDADHGAEEDKEEQVDSQPDASS
 SQTVTPVAEPPSTEPTQPDGPTTLGPLDLLPSEELLTDTSNSSSSSTGEEADLAALLPDL
 GRLLINSVFHVGAERLQQMLFSDSPFLQGFLQCKFTDVTLSPWSGDSKCHQRRVLT
 TIPISNPLGPKSASVVETQTLFRRGPQAGGCVDSEVLTQGIPYQDYFYTAHRYCILGLA
 RNKARLRVSSEIRYRKQPWSLVKSLIEKNSWSGIEDYFHHLERELAKAEKLSLEEGGKD
 ARGLLSGLRRRKRPPLSWRAHGDGPQHDPDP CARAGIHTSGSLSSRFSEPSVDQGGP
 AGIPSALVLISIVSLIILIALNVLLFYRLWSLERTAHTFESWHSLALAKGKFPQTATEWAEIL
 ALQKQFHSVEVHKWRQILRASVELLDEMKFSLEKLHQGITVSDPPFDTQPRPDDSF

SEQID No:205

MLGLLVALLALGLAVFALLDVWYLVRLPCAVLRARLLQPRVRDLLAEQRFPGRVLP
 DLLLHMNNARYLREADFARVAHLTRCGVLGALRELRAHTVLAASCARHRRSLRLLPEP
 VRTRLLGWDDRAFYLEARFVSLRDGFVCALLRFRQHLLGTSPERVVQHLCQRRVEP
 LPADLQHWISYNEASSQLLRMESGLSDVTKDQ

SEQID No:206

MTLARFVLALMLGALPEVVGFDVSLNDSLHSHRHSPAGPHYPPYYLPTQQRPPPTTRP
 PPPLPRFPRPPRALPAQRPHALQAGHTPRPHPWGPCPAGEPWVSVTDFGAPCLRWAE
 VPPFLERSPPASWAQLRGQRHNFCRSPDGAGRPWCFYGDARGKVDWGYCDCRHS
 VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIKQTPFSG
 LGLIPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCSFSHGPTFPIIRLAGGS
 SVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGSGPV
 MLDEVRCCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCTPLTDGVIRLAGGKGSHEGR
 LEVYYRGQWGTVCDDGWTELNTYVVCRLGFKYKQASANHFEESTGPIWLDDVSCS
 GKETRFLQCSRRQWGRHDCSHREDVSIACYPGGEGHRLSLGFPVRLMDGENKKEGR
 VEVFINGQWGTICDDGWTDKDAVICRQLGYKGPARTMAYFGEGKGPIHVDNVKCT
 GNERSLADCIKQDIGRHNCRHSEDAGVICDYFGKKASGNSNKESSLSSVCGLRLLHRRQ
 KRIIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTR
 SYAVRVGDYHTLVPEEFEEEEIGVQQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSH
 VLPACLPLWRERPQKTASNCYITGWGDTGRAYSRTLQQAAPLLPKRFCEERYKGRFT
 GRMLCAGNLHEHKRVDSCQGDSSGGLMCPGSGSWVVGVTWVGYGCGVKDSPGV
 YTKVSAFVPWIKSVTKL

SEQID No:207

MEDGGLTAFEEDQRCLSQSLPLPVSAEGPAAQTAEPSRSFSSAHRHLSRRNGLSRLC
 QSRTALSEDRWSSYCLSSLA AQNICTSKLHCPAAPEHTDPSEPRGSVSCCSLLRGLSS
 GWSSPLL PAPVCNPNKAIFTVDAKTTEILVANDKACGLLGYSSQDLIGQKLTQFFLRSDS
 DVVEALSEEHEADGHA AVVFGTVVDIISRSGEKIPVSVWMKRMQRERRLCCVVVLEP
 VERVSTWVAFQSDGTVTSCDSLFAHLHG YVSGEDVAGQHITDLIPSVQLPPSGQHIPKN
 LKIQRSVGRARDGTTFFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISGLITLLP
 DGTIHGINHSFALTFLGYGKTELLGKNITFLIPGFYSYMDLAYNSSLQLPDLASCLDVGNE
 SGCGERTLDPWQQQDPAEGGQDPRINVL AGGHVVP RDEIRKLMESQDIFTGTQTELI
 AGGQLLSCLSPQPAPGVDNVPEGSLPVHGEQALPKDQQITALGREEPVAIESPGQDLL
 GESRSEPVDVKPFASCEDSEAPVPAEDGGSDAGMCGLCQKAQLERMGVSGPSGSDL
 WAGAAVAKPQAKGQLAGGSLLMHCPCYGSEWGLW WRSQDLAPSPSGMAGLSFGTP
 TLDEPWLG VENDORREELQTCLIKEQLSQLSLAGALDVPHAELVPTECQAVTAPVSSCDLG
 GRDLCGGCTGSSSACYALATDLP GGLEAVEAQEVDVNSFSWNLKELFFSDQTDQTSS
 NCSCATSELRETPSSLAVGSDPDVGS LQEQQGSCVLDDRELLLLTGTCVDLGQGRRFRE
 SCVGHDPTEPLEVCLVSSEHYAASDRESPGHVPSTLDAGPEDTCPSAEEPRLNVQVTS
 TPVIVMRGAAGLQREIQEGAYSGSCHHRDGLRLSIQFEVRRVELQGPTPLFCCWL VKD
 LLHSQRDSAARTRLFLASLP GSTHSTAAELTGPSLVEVLRARPWFEEPPKAVELEGLAA
 CEGEYSQKYSTMSP LGSGAFGFVWTAVDKEKNKEVVVKFIKKEKVLEDCWIEDPKLGK
 VTLEIAILSRVEHANIIVLDIFENQGGFFQLVMEKHGSGLDLFAFIDRHPRLDEPLASYIFR
 QLVSAVGYLRLKDIIHRDIKDENVIAEDFTIKLIDFGSAAYLERGKLFYTFCGTIEYCAPEV
 LMGNPYRGPELEMWSLGVTLTYTLVFEENPFCELEETVEAAIHPPYLVSKEMLSLVSGLL
 QPVPERRTTLEKLVTDPWVTQPVNLADYTWE EVCVRVKNKPESGVL SAASLEMGNRSL
 DVAQAQELCGGPVPGEAPNGQGCLHPGDPRLTS

SEQID No:208

MEPGTGGSRKRLGPRAGFRFWPPFFPRRSQAGSSKFPTPLGPENSGNPTLLSSAQPE
 TRVSYWTKLLSQLLAPLPGLLQKVL IWSQLFGGMFPTRWLDFAGVYSALRALKGREKP
 APTAQKSLSSLQLDSSDPSVTSP LDWLEEGIHWQYSPPDLKLELKAKGSALDPAAQAF
 LLEQQLWGV ELLPSSLQSRLYSNREL GSSPSGPLNIQRIDDFS VVS YLLNPSYLD CFPRL
 EVSYQNSDGNSEVVGFQTLTP ESSCLREDHCHPQPLSAELIPASWQGCPLSTEGLPEI
 HHLRMKRLEFLQQASKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQFVPAA
 GDIPGNTQESTEEKIELLTTEVPLALEEESPSEGCPSS EIPMEKEPGEGRISVVDYSYLE
 GDLPI SAR PACSNKLIDYILGGASSDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLE

QDPEGLHLWNSFCSDPYNPQNFTATIQTAARIVPEEPSDSEKDLSGKSDLENSSSQSG
 SLPETPEHSSGEEDDWESSADEAESLKLWNSFCNSDDPYNPLNFKAPFQTSGENEKG
 CRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVKRKKVTF
 LEEVTEYYISGDEDRKGPWEEFARDGCRFQKRIQETEDAIGYCLTFEHRERMFNRLQG
 TCFKGLNVLKQC

SEQID No:209

MNLERSVNEEKLNLCKRYYLGGFAFLPFLWLVNIFWFFREAFVLPAYTEQSQIKGYVWR
 SAVGFLFWVIVLTSWITIFQIYRPRWGALGDYLSFTIPLGTP

SEQID No:210

MTELPAPLSYFQNAQMSEDNHLSENTNDNRERQEHNDRRLGHPEPLSNGRPQGNSR
 QVVEQDEEEDEELTLKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLIYTPFTE
 DTETVGQRALHSILNAAIMISVIVVMTILLVVLYKYRCYKVIHAWLISSLLLLFFFSFIYLGE
 VFKTYNVAVDYITVALLIWNLGVVGMISIHVKGPLRLQQAYLIMISALMALVFIKYLPEWT
 AWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFPALIYSSTMVWLVNMAEGDPEA
 QRRVSKNSKYNAESTERESQDTVAENDDGGFSEWEAQRDShLGPHRSTPESRAAV
 QELSSSILAGEDPEERGVLGLGDFIFYSVLVGKASATASGDWNTTIACFVAILIGLCLTL
 LLLAIFKKALPALPISITFGLVFYFATDYLVPFMDQLAFHQFYI

SEQID No:211

MAAETLLSSLLGLLLLGLLLLPASLTGGVGSLNLEELSEMRYGIEILPLPVMGGQSQSSDV
 VIVSSKYKQRYECRLPAGAIHFQREREETPAYQGPGIPELLSPMRDAPCLLKTCDWWT
 YEFQYGRHIQQYHMEDSEIKGEVLYLGYYSQSAFDWDDDETAKASKQHRLKRYHSQTYG
 NGSKCDLNGRPREAIEVRFLCDEGAGISGDYIDRVDEPLSCSYVLTIRTPRLCPHPLLRP
 PPSAAPQAILCHPSLQPEEY MAYVQRQADSKQYGDKIIEELQDLGPQVWSETKSGVAP
 QKMAGASPTKDDSKDSDFWKMLNEPEDQAPGGEEVPAEEQDPSPEAADSASGAPND
 FQNNVQVKVIRSPADLIRFIEELKGGTKKGKPNIGQEPPVDDAAEVPQREPEKERGDPE
 RQREMEEEDEDEDEDEDEDERQLLGEFEKELEGILLPSDRDRLRSEVKAGMERELN
 IIQETEKELDPDGLKKESERDRAMLALTSTLNKLIKRLKQSPKLVKKHKKRVPKPKP
 PPSPQPTTEDEPHRVRVRVTKLRLGGPNQDLTVLEMKRENPKLQKQIEGLVKELLEREG
 LTAAGKIEIKIVRPWAEGTEEGARWLTDEDTRNLKEIFFNILVPGAEAAQKERQRQKELE
 SNYRRVWGSPGGEGTGDLDEFDF

SEQID No:212

MAVVPLLLLGGGLWSAVGASSLGVVTCGSVVKLLNTRHNVRLHSHDVRYGSGSGQQSV
TGVTSVDDSNYSYWRIRGKSATVCERGTPIKCGQPIRLTHVNTGRNLHSHHFTSPLSGN
QEVSAFGEEGEGDYLDDWTVLCNGPYWVRDGEVRFKHSSTEVLVSVTGEQYGRPISG
QKEVHGMAQPSQNNYWKAMEGIFMKPSELLKAEAHHAEL

SEQID No:213

MEASGKLICRQRQVLFSLFLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQRE
FSRRGVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRQVLLLESPFEFF
QAEHQVIDINDHSPVFLDKQMLVKVSESSPPGTAFPLKNAEDLDIGQNNIENYIISPNSYF
RVLTRKRS DGRKYPELVLDNALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVVDVND
NAPEFQQPFYRVQISEDSPISFLVVKVSATDVDTGVNGEISYSLFQASDEISKTFKVDFLT
GEIRLKKQLDFEFKFSYEVNIEARDAGGFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPE
NAPETVVALFSVSDLDSENGKISCSIQEDLPFLKSSVGNFYTLTETPLDRESRAEYN
VTITVTDLGTPRLTTHLNMTVLVSDVNDNAPAFQTQTSYTLFVRENNSPALHIGSVSATDR
DSGTNAQVTYSLLPPQDPHLPLASLVSINTDNHGLFALRSLDYEALQAFEFVRVGASDRG
SPALSSEALVRVLVDANDNSPFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDS
GQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLLSERDAAKQRLVVLVKDNGEPPCS
ATATLHLLLVDGFSQPYLPLPEAAPAQGQADSLTVYLVVALASVSSLFLFSVLLFVAVLLC
RRSRAASVGRCSVPEGPFGHLVDVRGTGSLSQNYQYEVCLAGGSGTNEFQFLKPVL
PNIQGHSGPEMEQNSNFRNGFGFSLQLK

SEQID No:214

MASRGVVGIFFLSAVPLVCLELRRGIPDIGIKDFLLLCGRILLLLALLTLISVTTSWLNSFKS
PQVYLKEEEEKNEKRQKLVRKKQQEAQGEKASRYIENVLKPHQEMKLRKLEERFYQMT
GEAWKLSSGHKLGGDEGTSQTSFETSNREAAKSQNLPKPLTEFPSPAEQPTCKEIPDL
PEEPSQTAEVVTVALRCPSGNVLRRRFLKSYSSQVLFDWMTRIGYHISLYSLSTSFP
RPLAVEGGQSLEDIGITVDTVLILEEKEQTN

SEQID No:215

MAAAEEEDGGPEGPNRERGGAGATFECNICLETAREAVVSVCGHLYCWPC LHQWLET
RPERQECPVCKAGISREKVVPLYGRGSQKPQDPRLKTPPRPQGQRPAPE SRGGFQPF
GDTGGFHFSFGVGAFPF GFFTTVFNAHEPFRRGTGVDLGQGH PASSWQDSLFLFLAIF
FFFWLLSI

SEQID No:216

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSKL
 VLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGV
 VYTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLL
 AYCSSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVV
 NRLMHGILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQAQ

SEQID No:217

MWSAGRGGAAWPVLLGLLLALLVPGGGAAGTGAELVTCGSVLKLLNTHHRVRLHSHDI
 KYGSGSGQQSVTGVEASDDANSYWRIRGGSEGGCPCGSPVRCGQAVRLTHVLTGKN
 LHTHHFPSPLSNNQEVSAFGEDGEGDDLDLWTVRCSGQHWEREAAVRLQHVGTSVFL
 SVTGEQYGSPIRGQHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

SEQID No:218

GRWASGEMAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIE
 FYAPWCPACQNLQPEWESFAEWGEDLEVNIKVDVTEQPGLSGRIFIITALPTIYHCKDG
 EFRRYQGPRTKKDFINFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHN
 YFIEDLGLPVWGSYTVFALATLFSGLLLGLCMIFVADCLCPSKRRRRPQPYPYPSKKLLSE
 SAQPLKKVEEEQEADEEDVSEEEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

SEQID No:219

HPAGLAAAAAGTPRLPSKRRIPVSQPGMADPHQLFDDTSSAQSRGYGAQRAPGGLSY
 PAASPTPHAAFLADPVSNMAMAYGSSLAQAQKELVDKNIDRFIPITKLKYFAVDTMYV
 GRKLGLLFFPYLHQDWEVQYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQD
 RFSPDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDLVAFLGYKYVGMIGGVLMG
 LLFGKIGYYLVLGWCCVAIFVFMIRTLRLKILADAAAEGVPVRGARNQLRMYLTMAVAAA
 QPMLMYWLTFHLVR

SEQID No:220

MAATALLEAGLARVLFYPTLLYTLFRGKVPGRAHRDWYHRIDPTVLLGALPLRSLTRQLV
 QDENVRGVITMNEEYETRFLCNSSQEWKRLGVEQLRLSTVDMTGIPITLDNLQKGVQFA
 LKYQSLGQCYYVHCKAGRSRSATMVAAYLIQVHKWSPEEAVRAIAKIRSYIHIRPGQLDV
 LKEFHKQITARATKDGTFVISK

SEQID No:221

MNTVLSRANSLFAFSLSVMAALTFGCFITTAFKDRSVPVRLHVSRIMLKNVEDFTGPRER
SDLGFITSDITADLENIFDWNVKQLFLYLSEAESTKNNALNQVVLWDKIVLRGDNPKLLK
DMKTKYFFDDGNGLKGNRNVTLTLSWNVVPNAGILPLVTGSGHVSVPFPDYEITKSY

SEQID No:222

MALRGFCSADGSDPLWDWNVTWNTSNPDFTKCFQNTVLVWVPCFYLWACFPFYFLYL
SRHDRGYIQMTPLNKTKTALGFLWIVCWADLFYSFWERSRGIFLAPVFLVSPTLLGITT
LLATFLIQLERRKGVQSSGIMLTFWLVALVCALAILRSKIMTALKEDAQVDLFRDITFYVYF
SLLLIQLVLSCFSDRSPLFSETHDPNPCPESSASFLSRITFWWITGLIVRGYRQPLEGSD
LWSLNKEDTSEQVVPVLVKNWKKECAKTRKQPVKVYSSKDPAPKESKVDANEEV
EALIVKSPQKEWNPSLKFVLYKTFGPYFLMSFFFKAIHDLMMFSGPQILKLLIKFVNDTKA
PDWQGYFYTVLLFVTACLQTLVLHQYFHICFVSGMRIKTAVIGAVYRKALVITNSARKSS
TVGEIVNLMSVDAQRFMDLATYINMIWSAPLQVILALYLLWLNLGPSVLAVVAVMLMVP
VNAVMAKTKTYQVAHMKSKDNRIKLMNEILNGIKVLKLYAWELAFKDKVLAIRQEELKV
LKKSAYLSAVGTFTWVCTPFLVALCTFAVYVTIDENNILDAQTAFVSLALFNILRFPLNILP
MVISSIVQASVSLKRLRIFLSHEELEPDSIERRPVKDGGGTNSITVRNATFTWARSDPPTL
NGITFSIPEGALVAVVGQVGCGKSSLLSALLAEMDKVEGHVAIKGVNLSSGGQKQRVSLA
RAVYSNADIYLFDDPLSAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIV
MSGGKISEMGSYQELLARDGAFAEFLRTYASTEQQEQAENGVTGVSGPGKEAKQME
NGMLVTD SAGKQLQRQLSSSSSSYSGDISRHHNSTAELQKAEAKKEETWKLMEADKAQ
TGQVKLSVYWDYMKAIGLFISFLSIFLMCNHVSALASNYWLSLWTDDPIVNGTQEHTK
VRLSVYGALGISQGIAVFGYSMAVSI GGILASRCLHVDLLHSILRSPMSFFERTPSGNLVN
RFSKELDTVDSMIPEVIKMFMSGSLFNVIGACIVILLATPIAAIIPPLGLIYFFVQRFYVASSR
QLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKVDENQKAYYPSIVANR
WLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSEMET
NIVAVERLKEYSETEKEAPWQIQETAPPSSWPQVGRVEFRNYCLRYREDLDFVLRHINV
TINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGINIAKIGLHDLRFKITIIPQDPVLF
SGSLRMNLD PFSQYSDEEVWTSLELAHLKDFVSALPKLDHECAEGGENLSVGQRQLV
CLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVLTIAHRLNTIMDYTRVIVLD
KGEIQEYGAPSDLLQQRGLFY SMAKDAGLV

SEQID No:223

MARGKAKEEGSWKKFIWNSEKKEFLGRTGGSWFKILLFYVIFYGCLAGIFIGTIQVMLLTI
SEFKPTYQDRVAPPGLTQIPQIQKTEISFRPNDPKSYEAYVLNIVRFLEKYKDSAQRDDM
IFEDCGDVPSEPKERGDFNHERGERKVCRFKLEWLGNCSSGLNDETYGYKEGKPCIIKL
NRVLGFKPKPPKNESLETYPVMKYNPVLPVQCTGKRDEDKDKVGNVEYFGLGNSPG
FPLQYYPPYGGKLLQPKYLQPLLAVQFTNLTMDTEIRIECKAYGENIGYSEKDRFQGRFDV
KIEVKS

SEQID No:224

MKVARFQKIPNGENETMIPVLTSKKASELPVSEVASILQADLQNGLNKCEVSHRRAFHG
WNKFDISEDEPLWKKYISQFKNPLIMLLLASAVISVLMHQFDDAVSITVAILIVTVAFVQE
YRSEKSLEELSKLVPPECHCVREGKLEHTLARDLVPGDTVCLSVGDRVPADLRLFEAVD
LSIDESSLTGETTPCSKVTAPOPAATNGDLASRSNIAFMGTLVRCGKAKGVVIGTGENS
EFGEVFKMMQAEAPKTPLQKSMDLLGKQLSFYSFGIIGIIMLVGWLLGKDILEMFTISVS
LAVAAIPEGLPIVVTVTALGVMRMVKKRAIVKKLPIVETLGCCNVICSDKTGTLTKNEMT
VTHIFTSDGLHAEVTGVGYNQFGEVIVDGDVVHGFYNPAVSRIVEAGCVCNDAVIRNNT
LMGKPTEGALIALAMKMGLDGLQQDYIRKAEYFSSSEQKWMMAVKCVHRTQQDRPEICF
MKGAYEQVIKYCTTYQSKGQTLTLTQQQRDVYQQEKARMGSAGLRVLALASGPPELGQ
LTFLGLVGIIDPPRTGVKEAVTTIASGVSIMITGDSQETAVAIASRLGLYSKTSQSVSGE
EIDAMDVQQLSQIVPKVAVFYRASPRHKMKIISLQKNGSVVAMTGDGVNDAVALKAAD
IGVAMGQTGTDVCKEADMILVDDDFQTMSAIEEGKGIYNNIKNFVRFQLSTSIAALTIS
LATLMNFPNPLNAMQILWINIIMDGPAPQSLGVEPVDKDVIRKPPRNWKDSILTKNLILKIL
VSSIIIVCGTLFVFWREL RDNVITPRDTTMTFTCFVFFDMFNALSSRSQTKSVFEIGLCSN
RMFCYAVLGSIMGQLLVYFPPPLQKVFTESLSILDLLFLLGLTSSVCIVAEIHKVERSRE
KIQKHVSSTSSSFLEV

SEQID No:225

MAKNRRDRNSWGGFSEKTYEWSSEEEEPVKKAGPVQVLIVKDDHSFELDETALNRILL
SEAVRDKEVVAVSVAGAFRKGKSFLMDFMLRYMYNQESVDWVG DYNEPLTGFSWRG
GSERETTGIQIWSEIFLINKPDGKKVAVLLMDTQGTQSTLRDSATVFALSTMISSIQV
YNLSQNVQEDDLQHLQLFTEYGR LAMEETFLKPFQSLIFLVRDWSFPYEF SYGADGGA
KFLEKRLKVSGNQHEELQNV RKHIHSCFTNISCFLLPHPGLKVATNP NFDGKLKEIDDEFI
KNLKILIPWLLSPESLDIKEINGNKITCRGLVEYFKAYIKIYQGEELPHPKSM LQATAEANN
LAAVATAKDTYNKKMEEICGGDKPFLAPNDLQTKHLQLKEESVKLFRGVKKMGGE EFS

RRYLQQLESEIDELYIQYIKHNDSKNIFHAARTPATLFVVIFITYVIAGVTGFIGLDIIASLCN
MIMGLTLITLCTWAYIRYSGEYRELGAVIDQVAAALWDQGSTNEALYKLYSAAATHRHLY
HQAFTPKESESTEQSEKKKM

SEQID No:226

MGCCSSASSAAQSSKREWKPLEDRSCTDIPWLLLFI LFCIGMGFICGFSIATGAAARLVS
GYDSYGNICGQKNTKLEAIPNSGMDHTQRKYVFFLDPCNLDLINRKIKSVALCVAACPR
QELKTLSDVQKFAEINGSALCSYNLKPSEYTTSPKSSVLC PKLPVPASAPIFFHRCAPV
NISCYAKFAEALITFVSDNSVLHRLISGVMTSKEIILGLCLLSVL SMILMVIIRYISRVLVWIL
TILVILGSLGGTGVLWWLYAKQRRSPKETVTPEQLQIAEDNLRALLIYAISATVFTVILFLIM
LVMRKRVALTIALFHVAGKVFIHLPLLVFQPFWTF FALVLFWVYWIMTLLFLGTTGSPVQ
NEQGFVEFKISGPLQYMWWYHVVG LIWISEFILACQQMTVAGAVVTTYFTRDKRNLPFT
PILASVNRLIRYHLGTVAKGSFIITLVKIPRMILMYIHSQ LKGKENACARCVLKSCICCLWC
LEKCLNYLNQNAYTATAINSTNFCTSAKDAFVILVENALRVATINTVGDFMLFLGKVLIVC
STGLAGIMLLNYQQDYTVWVPLIIVCLFAFLVAHCFLSIYEMVVDVLF LCF AIDTKYNDG
SPGREFYMDKVLMEFVENS RKAMKEAGKGGVADSRELKPMLKKR

SEQID No:227

EKSGGPGTREEREREKREERQSAWGRKERGREGWVRRRERSAANPRRRRAWSPSQNS
SPSRSRSQGGGCRDRQPCMMHLRLFCILLA AVSGAEGWGYG CDEELVGPLYARSLG
ASSYYSLLTAPRFARLHGISGWSPRIGDPNPWLQIDLMKKHRIRAVATQGSFNSWDWV
TRYMLLYGDRVDSWTFYQRGHNSTFFGNVNESAVVRHDLHFHFTARYIRIVPLAWN P
RGKIGLRLGLYGCPYKADILYFDGDDAISYRFPRGVS RSLWDVFAFSFKTEEKDGLLLHA
EGAQGDYVTLELEGAHLLLHMSLGSSPIQPRPGHTTVSAGGV LNDQHWHYVRVDRFG
RDVNFTLDGYVQRFILNGDFERLNL DTEMFIGGLVGAARKNLAYRHNFRCIENVIFNRV
NIADLAVRRHSRITFEGKVAFRCLDPVPHPI NFGGPHNFVQVPGFPRRGRLAVSFRFRT
WDLTG LLLFSRLGDGLGHVELTLSEGQVNVSIAQSGRKKLQFAAGYRLNDGFWHEVNF
VAQENHAVISIDDVEGAEVRVSYPLLIRTGTSYFFGGCPKPASRWDCHSNQTA FHGCM
ELLKVDGQLVNLTLVEGRRLGFYAEVLFDTCGITDR CSPNMCEHDGRCYQSWDDFICY
CELTGYKGETCHTPLYKESCEAYRLSGKTSGNFTIDPDGSGPLKPFV VYCDIRENRAWT
VVRHDLRWTTTRVTGSSMERPF LGAIQYWNASWEEVSALANASQHCEQWIEFSCYNSR
LLNTAGGYPYSFWIGRNEEQHFYWGGSQPGIQR CACGLDRSCVDPALYCNC DADQPQ
WRTDKGLLTFVDHLPVTQVVIGDTNRSTSEAQFFLRPLRCY GDRNSWNTISFHTGAALR
FPPIRANHSLDVSFYFRTSAPSGVFLENMGGPYCQWRRPYVRVELNTSRDVVFAFDVG

NGDENLTVHSDDFEFNDDDEWHLVRAEINVKQARLRVDHRPWVLRPMPPLQTYIWMEYD
 QPLYVGSaelKRRPFVGCRLAMRLNGVTNLLEGRANASEGTSPNCTGHCAHPRLPCF
 HGGRCVERYSSYYTCDCLTAFDGPYCNHDIGGFFEPGTWMRYNLQSALRSAAREFSH
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 VSFSFSTSSAPAVLLYVSSFVRDYMALIKDDGTLQLRYQLGTSPYVYQLTTRPVTDGQ
 PHSINITRVYRNLFIQVDYFPLTEQKFSLLVDSQLDSPKALYLGRVMETGVIDPEIQRYNT
 PGFSGCLSGVRFNNAVPLKTHFRTPRPMTAEALAEALRVQGELSESNCGAMPRLVSEVP
 PELDPWYLPDPFPYHDEGWVAILLGLVAFLLGLVGMVLVLFYLNHRYKGSYHTNEP
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 EESRSE

SEQID No:228

MGNRGMEDLIPLVNRLQDAFSAIGQNADLDLPQIAVVGGQSAGKSSVLENFVGRDFLP
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 SDLANSALKVAKEVDPQGQRTIGVITKLDLMDEGTDARDVLENKLLPLRRGYIGVVNR
 SQKDIDGKKDITAALAAERKFFLSHPSYRHLADRMGTPYLQKVLNQQLTNHIRTDLPLGLR
 NKLQSQLLSIEKEVEEYKNFRPDDPARKTKALLQMVQQFAVDFEKRIEGSGDQIDTYEL
 SGGARINRIFHERFPFELVKMEFDEKELRREISYAIKNIHGIRTGLFTPDMAFETIVKKQVK
 KIREPCLKCVDMMISELISTVRQCTKKLQQYPRLREEMERIVTTHIREREGRTKEQVMLLI
 DIELAYMNTNHEDFIGFANAQQRSNQMNKKKTSGNQDEILVIRKGWLTINNIGIMKGGSK
 EYWFVLTAENLSWYKDDEEKEKKYMLSVDNLKLRDVEKGMSSKHIFALFNTEQRNVY
 KDYRQLELACETQEEVDSWKASFLRAGVYPERVGDKEKASETEENGSDSFMHSMDPQ
 LERQVETIRNLVDSYMAIVNKTVRDLMPKTIMHLMINNTKEFIFSELLANLYSCGDQNTLM
 EESAEEQAQRRDEMLRMYHALKEALSIIGNINTTTVSTPMPPPVDSDWLQVQSVPAARR
 SPTSSPTPQRRAPAVPPARPGSRGPAPGPPAGSALGGAPPVPSRPGASPDPPGPPP
 QVPSRPNRAPPVPSRSGQASPSRPESPRPPFDL

SEQID No:229

MAARRQGPARSANPRPQFPVCGREHAATLRAPGRGGGASPAQIGTRGRGGHNFAP
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 TTTSSVEGKQNLVIMGKKTWFSIPEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDAL
 KLTEQPELANKVDMVWIVGGSSVYKEAMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKY
 KLLPEYPGVLSDVQEEKGIKYKFEVYEKND

SEQID No:230

MDRGTLPLAVALLLASCSLSPTSLAETVHCDLQPVGPERGEVTTYTTSQVSKGCVAQAP
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 AYNSSLVTFQEPPGVNTTELPSFPKTOILEWAAERGPITSAAELNDPQSILLRLGQAQGS
 LSFCMLEASQDMGRTLEWRPRTPALVRGCHLEGVAGHKEAHILRVLPGHSAGPRTVTV
 KVELSCAPGDLDVAVLILQGPPYVSWLIDANHNMQIWTTGEYSFKIFPEKNIRGFKLPDTP
 QGLLGEARMLNASIVASFVELPLASIVSLHASSCGGRLQTSPAPIQTTPPKDTCSPELLM
 SLIQTCKADDAMTLVLKKELVAHLKCTITGLTFWDPSCEAEDRGDKFVLRSAVSSCGMQ
 VSASMISNEAVVNILSSSSPQRKKVHCLNMDLSLQGLYLSPHFLQASNTIEPGQGSF
 VQVRVSPSVSEFLLQLDSCHLDLGPEGGTVELIQGRAAKGNCVSLSPSPEGDPFRFSFL
 LHFYTVPIPKTGTLSCVALRPKTGSQDQEVHRTVFMRLNIISPDLSGCTSKGLVLPVAVL
 GITFGAFLIGALLTAALWYIYSHTRSPSKREPVVAVAAPASSESSSTNHSIGSTQSTPCST
 SSMA

SEQID No:231

MCASVKYNIRGPALIPRMKTKHRIYYITLFSIVLLGLIATGMFQFWPHSIESSNDWNVEKR
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 RGTNHLLFNMLPGGPPDYNTALDVPRDRALLAGGGFSTWYRQGYDVSIPVYSPLSAE
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 KRCHKHQVFDYPQVLQEATFCVVLRGARLGQAVLSDVLQAGCVPVVIADSYILPFSEVL
 DWKRASVVVPEEKMSDVYSILQSIPQRQIEEMQRQARWFWEAYFQSIKAIALATLQIIND
 RIYPYAAISYEEWNDPPAVKWGSVSNPLFLPLIPPQSQGFTAIVLTYDRVESLFRVITEVS
 KVPSLSKLLVVWNNQNKNPPEDSLWPKIRVPLKVVRTAENKLSNRFFPYDEIETEAVLAI
 DDDIIMLTSDQLQFGYEVWREFPDRLVGYPGRLHLWDHEMNKWKYESEWTNEVSMVL
 TGAIFYHXYFNYLYTYKMPGDIKNWVDAHMNCEDIAMNFLVANVTGKAVIKVTPRKKFK
 CPECTAIDGLSLDQTHMVERSEKINFASVFGTMPLKVVEHRADPVLYKDDFPEKLKSF
 PNIGSL

SEQID No:232

MTGYTMLRNGGAGNGGQTCMLRWSNRIRLTWLSFTLFVILVFFPLIAHYLTTLDEADE
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 IENAKQDLLQLKNVISQTEHSYKELMAQNQPKLSLPIRLLPEKDDAGLPPPKATRGCRLH

NCFDYSRCPLTSGFPVYVYDSQFVFGSYLDPLVKQAFQATARANVYVTENADIACLYV
 ILVGEMQEPVVLRPAAELEKQLYSLPHWRTDGHNHVIINLSRKSDTQNLLYNVSTGRAMV
 AQSTFYTVQYRPGFDLVV^{III}SPLVHAMSEPNFMEIPPQVPVKRKYLFTFQGEKIESLRSSL
 QEARSFEEEMEGDPPADYDDRIIATLKAVQDSKLDQVLVEFTCKNQPKPSLPTEWALC
 GEREDRLELLKLSTFALIITPGDPRLVISSGCATRLFEALEVGAVPVVLGEQVQLPYQDM
 LQWNEAALVVPKPRVTEVHFLLRSLSDSLLAMRRQGRFLWETYFSTADSIFNTVLAMI
 RTRIQIPAAPIREEAAAEIPHRSGKAAGTDPNMADNGDLDLGPVETEPYASPRYLRNFT
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 IGVPIMVVRTEKNSLNNRFLPWNEIETEAILSIDDAHLRHDEIMFGFRVWREARDRIVGF
 PGRYHAWDIPHQSWLYNSNYSCELSMVLTGAFFHKYYAYLYSYVMPQAIRDMVDEYI
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SEQID No:233

MGPGRPAPAPWPRHLLRCVLLGCLHLGRPGAPGDAALPEPNVFLIFSHGLQGCLQAQ
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 PIKSNDCETFWDKDQLTDSCYQFNQSTLSWREAWASCEQQGADLLSITEIHEQTYING
 LLTGYSSTLWIGLNDLDTSGGWQWSDNSPLKYLNWESDQPDNPSEENCGVIRTESSG
 GWQNRDCSIALPYVCKKKPNATAEPTPPDRWANVKVECEPSWQPFQGH CYRLQAEK
 RSWQESKKACLRGGGDLVSIHSMAELEFITKQIKQEVEELWIGLNDLKLQMNFEWSDG
 SLVSFTHWHPFEPNPNFRDSLEDCVTIWGPEGRWNDSPCNQSLPSICKKAGQLSQGAA
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 YNWEGEYFWTALQDLNSTGSFFWLSGDEVMYTHWNRDQPGYSRGGCVALATGSAM
 GLWEVKNCTSFRRARYICRQSLGTPVTPELPGPDPTPSLTGSCPQG WASDTKLRYCYKV
 FSSERLQDKKSWVQAQGACQELGAQLLSLASYEEEEHFVANMLNKIFGESEPEIHEQHW
 FWIGLNRDRDPRGGQSWRWSDGVGFSYHNFD RSRHDDDDIRGCAVLDLASLQWVAMQ
 CDTQLDWICKIPRGTDVREPDDSPQGRREWLR FQEAEYKFFEHHSTWAQAQRIC TW F
 QAELTSVHSQAELDFLSHNLQKFSRAQEQHWWIGLHTSESDGRFRWTDGSIINFISWA
 PGKPRPVGKDKKCVYMTASREDWGDQRCLTALPYICKRSNVTKETQPPDLPTTALGG
 CPSDWIQFLNKCFQVQGQEPQSRVKWSEAQFSCEQQEAQLVTITNPLEQAFITASLPN
 VTFDLWIGLHASQRDFQWVEQEPLMYANWAPGEPSPGSPAPSGNKP TSCAVVLHSPS

AHFTGRWDDRSCTEETHGFICQKGTDPSSLSPSPAALPPAPGTELSYLNGTFRLLQKPLR
 WHDALLLCESHNASLAYVPDPYTQAFLTQAARGLRTPWIGLAGEEGSRRYSWVSEEP
 LNYVGWQDGEPPQPGGCTYVDVDGAWRTTSCDTKLQGAVCGVSSGPPPPRRISYHG
 SCPQGLADSAWIPFREHCYSFHMELLGHKEARQRCQRAGGAVLSILDEMENVFVWE
 HLQSYEGQSRGAWLGMNFNPKGGTLVWQDNTAVNYSNWGPPGLGPSMLSHNSCYW
 IQSNSGLWRPGACTNITMGVVCKLPRAEQSSFSPPSALPENPAALVVVLMVLLLLALLTA
 ALILYRRRQSIERGAFEGARYSRSSSSPTEATEKNILVSDMEMNEQQE

SEQID No:234

MEDHQHVPIDIQTSKLLDWLVDRRHCSLKWQSLVLTIREKINAAIQDMPESSEEIAQLLSG
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 VNYEIPSLKKQIAKCCQLQOEYSRKEEECCAGAAEMREQFYHSCKQYGITGENVRGEL
 LALVKDLPSQLAEIGAAAQQLGEAIDVYQASVGFVCESPTEQVLPMLRFVQKRGNSTV
 YEWRTGTEPSVVERPHLEELPEQVAEDAIDWGDGFGVEAVSEGTDSGISAEAAAGIDWGI
 FPESDSKDPGGDGIDWGDDAVALQITVLEAGTQAEQVARGPDALTLLLEYTETRNQFL
 DELMELEIFLAQRAVELSEEADVLSVSQFQLAPAILQGQTKEKMVTMVSVLEDLIGKLT
 LQLQHLFMILASPRYVDRVTEFLQQKLKQSQLLALKKELMVQKQQAEEQAALPKLD
 LLEKTKELQKLIADISKRYSGRPVNLMTSL

SEQID No:235

MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPHCHCEPDGRMLLRVDCSDLGLS
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 MLQNNQLRHVPTEALQNLRSLSRLDANHISYVPPSCFSGLSRLHLWLDDNALTEIP
 VQAFRSLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGLHSLET
 LDLYNNNLDEFPTAIRTLNLKELGFHSNNIRSIPEKAFVGNPSLITIFHDNPIQFVGRSA
 FQHLPELRTLTLNGASQITEFPDLTGANLESLTLTGAQISSLPQTVCNQLPNLQVLDLSY
 NLLDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQLSLRSLNLAWNKAIIHPNAFSTLPS
 LIKLDLSSNLLSSFPITGLHGLTHLKLGTGNHALQSLISSENFPELKVIEMPYAYQCCAFGV
 CENAYKISNQWNKGDNSSMDDLHKKDAGMFQAQDERDLEDFLDFFEDLKALHSVQC
 SPSPGPFKPCHELLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYISPIKLLIGVIAAVN
 MLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLTLAALER
 GFSVKYSAKFETKAPFSSLKVIILLCALLTMAAVPLLGGSKYGASPLCLPLPFGEPTM
 GYMVALILLNSLCFLMMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNCPVAF

LSFSSLINLTFISPEVIKFILLVVVPLPACLNPLLYILFNPHFKEDLVSLRKQTYVWTRSKHP
SLMSINSDDVEKQSCDSTQALVTFTSSSITYDLPPSSVPSPAYPVTESCHLSSVAFVPCL

SEQID No:236

MIASHLLAYFFTELNDQVQKVDQYLYHMRLSDETLLEISKRFRKEMEKGLGATTHPTA
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MRGSGTQLFDHIAECLANFMDKLQIKDKKLPLGFTFSFPCHQTKLDESFLVSWTKGFKS
SGVEGRDVVALIRKAIQRRGDFDIDIVAVVNDTVGTMTCGYDDHNCEIGLIVGTGSNA
CYMEEMRHIDMVEGDEGRMCINMEWGAFGDDGSLNDRTEFDQEIDMGSLNPGKQLF
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EVLMLRLGLDPTQEDCVATHRICQIVSTRSASLCAATLAAVLQRIKENKGEERLRSTIGVD
GSVYKKHPHFAKRLHKTVRRLVPGCDVRFLRSEDGSGKGAAMVTAVAYRLADQHRAR
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LALDLGGTNFRVLLVRVRNGKWGGVEMHNKIYAIPQEVMMHGTGDELFDHIVQCIADFLE
YMGMKGVSLPLGFTFSFPCQQNSLDESILLKWTGFKASGCEGEDVVTLLKEAIHRREE
FDLDVVAVVNDTVGTMTCGFEDPHCEVGLIVGTGSNACYMEEMRNVELVEGEEGRM
CVNMEWGAFGDNGCLDDFRTEFDVAVDELSLNPGRFEKMGMYLGEIVRNILIDFT
KRGLLFRGRISERLKTRGIFETKFLSQIESDCLALLQVRATLQHLGLESTCDDSIIVKEVCT
VVARRAAQLCGAGMAAVVDRIENRGLDALKVTVGVDGTLYKLHPHFAKVMHETVKDL
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SEQID No:237

CDGQPCADGSDEWDCSYVLPRKVITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIF
APLSRMEAEIVQQQAPPSYGQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDM
TPGGGPGARRRQRGRMLMRRLVHRLRRWGLLPRTNTPARASEARSQVTPSAAPLEALD
GGTGPAREGGAVGGQDGEQAPPLPIKAPLSASTSPAPTTVPEAPGPLPSLPLEPSLLS
GVVQALRGRLPSLGPPGPTRSPPGPHTAVLALEDEDDVLLVPLAEPGVWVAEAEDEP
LLT

SEQID No:238

VTIAFLRLITTLVKGQLGSTQSQGLVPCVMFVLKEMPLPSYHKWRYNSHGVREQIGCLILE
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GAEGQGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLAQALSQHGAGHNNLIAVLAKYI
YHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAAIRDAFLTRLQSKIEDMRIKVMILE

FLTVAVETQPGLIELFLNLEVKDGSDGSKEFSLGMWSC LHAVLELIDSQQQDRYWC PPL
 LHRAAIAFLHALWQDRRDSAMLVLR TKPKFWENLTSPLFGT LSPSETSEPSILETCALI
 MKIICLEIYYVVKGS LDQSLKDTLKKFSIEKR FAYWSGYVKSLAVHVAETEGSSCTSLEY
 QMLVSAWRMLLIATTHADIMHLTDSV VRRQLFLDVLDTG KALLVPASVNCLRLGSMKC
 TLLLILLRQWKRELGSVDEILGPLTEILEGVLQADQQLMEKTKAKVFSAFITVLQMKEMKV
 SDIPQYSQLVLNV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQR
 DGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTTLEVSLRMKQNLHFTEATLHL
 LLTLARTQQGATAVAGAGITQSICLPLLSVYQLSTNGTAQTPSASRKS LDAPS WPGVYR
 LSMSLMEQLLKT LRYNFLPEALDFVGVHQERTLQCLNAV RTVQSLACLEEADHTVG FIL
 QLSNFMKEWHFHLPQLMRDIQVGAQDGVLESGVMLGDREAVRSHWGTPSELQDVPE
 RGLFPWGAQGLLSCAYSG

SEQID No:239

MWERLNCAAEDFY SRLLQKFNEEKKGIRKDPFLYEADVQVQLISKGQPNPLKNILNENDI
 VFIVEKVPLEKEETSHIEELQSEETAISDFSTGENVG PLALPVGKARQLIGLYTMAHNPN
 MTHLKINLPVTALPPLWVRCDSSDPEGTCWLGAELITTNNSITGIVLYVVSCKADKNYSV
 NLENLKNLHKKRHH LSTVTSKGFAQYELFKSSALDDTITASQTAIALDISWSPVDEILQIP
 PLSSTATLNIKVESGEPRGPLNHLYRELKFLLV LADGLRTGVTEWLEPLEAKSAVELVQE
 FLNDLNKLDGFGDSTKKDTEVETLKHDTAAVDRSVKRLFKVRS DLDFAEQLWCKMSSS
 VISYQDLVKCFTLI IQSLQRGDIQPWLHSGSNSLLSKLIHQSYHGTM DTVSLSGTIPVQML
 LEIGLDKLLKDYISFFIGQELASLNHLEYFIAPSVDIQE QVYRVQKLHHILEILVSCMPFIKS
 QHELLFSLTQICIKYYKQNPLDEQHIFQLPVRPTAVKNLYQSEKPQKWRVEIYRGQKKIK
 TVWQLSDSSPIDHLNFHKPDFSELTLNGSLEERIFFTNMVTCSQVHFK

SEQID No:240

MPGMVLFGRRWAIASDDL VFPGFFELVVRVLWWIGILTLYLMHRGKLD CAGGALLSSYL
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 DGVQCDRTVVNGI IATVVVSWIIIAATVVSIIIVFDPLGGKMAPYSSAGPSHLD SHDSSQLL
 NGLKTAATSVWETRIKLLCCCIGKDDHTRVAFSSTAELFSTYFSDTDLP SDIAAGLALLH
 QQQDNIRNNQEPAQVVCHAPGSSQEADLDAELENCHHYMQFAAAAYGWPLYIYRNPL
 TGLCRIGGDCCRSRTTDYDLVGGDQLNCHFGSILHTTGLQYRDFIHVSFHDKVYELPFL
 VALDHRKESVVVAVRG TMSLQDVLTDLSAESEVLDVECEVQDRLAHKGISQAARYVYQ
 RLINDGILSQAFSIAPEYRLVIVGHS LGGGAALLATMLRAAYPQVR CYAFSPPRGLWSK
 ALQEYSQS FIVSLVLGKDVIPRLSVTNLEDLKR RILRVVAHCNKPKYKILLHGLWYELFGG

NPNNLPTELDGGDQEVLTQP LLGEQSLLTRWSPAYSFSSDSPLDSSPKYPPLYPPGRIL
HLQEEGASGRFGCCSAAHYSAKWSHEAEFSKILIGPKMLTDHMPDILMRALDSVVSDR
AACVSCPAQGVSSVDVA

SEQID No:241

MSSKEVKTALKSARDAIRNKEYKEALKHCKTVLKQEKNNNYNAWVFIGVAAAELEQPDQA
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VCKKLVDLYYQEKKHLEVARTWHKLIKTRQEQGAENEELHQLWRKLTQFLAESTEDQN
NETQQLLFTAFENALGLSDKIPSEDHQVLYRHFQSLSKFPHESARLKKACEGMINIYPTV
QYPLEVLCLHLIESGNLTDEGQQYCCRLVEMDSKSGPGLIGLGIKALQDKKYEDAVRNL
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HLKAEALIKLSDYDSSEEAIRTLDDQISDADNIPGLLVKSLAYRNKGSFDEAAKIMEDLLSS
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MGSSSAEDEKNTALKTIQKAALLSPGDP AIWAGLMAACHADDKLALVNNTQPKRIDLYL
ALLSAVSASIKDEKFFENYNQSLEKWSLSQAVTGLIDTGRISEAETLCTKNLKSNDQPA
VILLRQVQCKPLLESQKPLPDAVLEELQKTVM SNSTSVPAWQWLAHVYQSQGM MRA
AEMCYRKSLQLASQRGSWSGKLSSLLRLALLALKVCMANISNDHWPSLVQEATTEALK
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SEQID No:242

MGAAAGRSPHLGPAPARRPQRSLLLLQLLLLVAAPGSTQAQAAPFPELCSYTWEAVDT
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GTIPKLTAKSNCRYEIEWITEYACHRDYLESKTCSLSGEQQDVSIDLTPLAQSGGSSYIS
DGKEYLFYLNVCGETEIQFCNKKQAAVCQVKKSDTSQVKAAGRYHNQTLRYSDGDLTLI
YFGGDECSSGFQRMSVINFECKNTAGNDGKGTPVFTGEVDCTYFFTWDTEYACVKEK
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TEELKNWKPARPVGIEKSLQLSTEGFITLTYKGPLSAKGTADAFIVRFVCNDDVYSGPLK
FLHQDIDSGQGIRNTYF EFETALACVPSPVDCQVTDLAGNEYDLTGLSTVRKPWTA VDT
SVDGRKRFTYLSVCNPLPYIPGCQGS AVGSCLVSEGNSWNLGVVQMSPQAAANGSLSI
MYVNGDKCGNQRFSTRITFECAQISGSPAFQLQDGCEYVFIWRTVEACP VVRVEGDNC
EVKDPRHGNLYDLKPLGLNDTIVSAGEYTY YFRVCGKLSSDVCPTSDKSKVVSSCQEK
REPQGFHKVAGLLTQKLT YENGLLKMNFTGGDTCHKVYQRSTAIFFYCDRGTQRPVFL
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CPDGIRKKSTTIRFTCS ESQVNSRPMFISAVEDCEYTFAWPTATACPMKSNEHDDCQVT
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FNLSSLSTSTFKVTRDSRTYSVG VCTFAVGPEQGGCKDGGVCLLSGTKGASFGR LQS
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 FDSENPGDDGQMHKGLSERSQAVGAVLSLLLVALTCCLLALLYKKERRETIVISKLTTC
 CRRSSNVSYKYSKVNKEEETDENETEWLMEEIQLPPPRQGKEGQENGHITTKSVKALS
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 KARKGKSSSAQQKTVSSTKLVSFHDDSDDLLHI

SEQID No:243

MSDKMSSFLHIGDICSLYAEGSTNGFISTLGLVDDRCVVQPETGDLNNPPKKFRDCLFK
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 RGGAGYWNSLFRFKHLATGHYLAEEVDPDFEEECLEFQPSVDPDQDASRSRLRNAQE
 KMOVSLVSPVPEGNDISSIFELDPTTLRGGDSLVRPNYSVRLRHLCTNTWVHSTNIPIDKE
 EEKPVMLKIGTSPVKEDKEAFAIVPVSPAIEVRDLDFANDASKVLGSIAGKLEKGTITQNE
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SEFLFSDVCRVESGENCSPAPREELVPAEETEQDKEHTCETLLMCIVTVLSHGRLRSGG
GVGDVLRKPSKEEPLFAARVIYDLLFFFMVIVNLIFGVIIIDTFADLRSEKQKKEEILKTTC
FIGLERDKFDNKTVTFEHHIKEEHNMMWHYLCFIVLVKVKDSTEYTGPE SYVAEMI KERN
LDWFPRMRAMSLVSSDSEGEQNELRNLQEKLESTMKLVNLSGQLSELKDQMTEQRK
QKQRIGLLGHPPHMNVNPQQA

SEQID No:244

GGRQRCQRGRSCGAREEEVEPGTARPPPAASAMDASLEKIADPTLAEMGKNLKEAVK
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NIGEQGHMALLGHSLGAYISTLDKEKLRKL TTRILSDTTLWLCRIFRYENG CAYFHEER
EGLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQYLCNQLGLPFPCLCR
VPCNTVFGSQHQMDVAFLEKLIKDDIERGRLPLLLVANAGTAAVGHTDKIGRLKELCEQ
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EDELSSPVVFRFFQELPGSDPVFKAVPVPMNTPSGVGRERHSCDALNRWLGEQLKQ
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 IQEAQVELQKASEERLLEEGVLRQIPVVGSVLWVSPVQALQKGRTFNLTAGSLESTEPI
 YVYKAQGAGVTLPPTPSGSRTKQRLPGQKPFKRSRLRGSDALSETSSVSHIEDLEKVERL
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SEQID No:245

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 PSGSYITADGDSWASSPSCSLSLAPAEGLDFPSGWGLSPQGSMVDERELHPAGTPE
 PPSSESSLADSSSSWGQEGHFFDLDFLANDPMIPAALLPFQGS LIFQVEAVEVTPLSP
 EEEEEEA VADPD PGGDLAGEGEEDSTSASFLQSLSDLSITEGMDEAFAFRDDTSAASS
 DSDSASYAEADDERLYSGEPHAQATLLQDSVQKTEEESSGGGAKGLQAQDGTVSWAVE
 AAPQTS DRGAYLSQRQELISEVTEEGLALGQESTATVTPHTLQVAPGLQVEVATRVTPQ
 AGEETDSTAGQESAAMAMPQPSQEGISEILGQESVTA EKLPTPQEETSLTLCPDSPQ
 NLKEEGGLDLPSGRKPVAAATIVPRQAKEDLTLPQDSAMTPPLPLQD TD LSSAPKPVAA
 ATIVSQQAE EGLTLPQDSVMTPLPLQDTELSSAPKPVAAATLV SQQAE EGLTLPQDSA
 MTPPLPLQD TD LSSAPKPVAAATLV SQQAE EGLTLPQDSAMTPPLPLQD TD LSSAPKPV
 AAATLV SQQAE EGLTLPQDSAMTPPLPLQD TD LSSAPKPVAAATIV SQQAE EGLTLPQD
 SAMTPPLPLQD TD LSSAPKPVAAATIV SQQAE EGLTLPQDSAMTPPLPLQD TD LSSAPK
 PVAAATPV SQQAE EGLTLPQDSAMTPPLPLQD TD LSSAPKPVAAATPV SQQAE EGLT
 PQDSAMTAPLPLQD TGPTSGPEPLAVATPQTLQAEAGCAPGTEPVATMAQQEVGEAL
 GPRPAPEEKNAALPTVPEPAALDQVQQDDPQPAAEAGTPWAAQEDADSTLGMEALSL
 PEPASGAGEEIAEALSRPGREACLEARAHTGDGAKPDSPQKETLEVENQQEGGLKLLA
 QEHGPRSALGGAREVPDAPPAACPEVSQARLLSPAREERGLSGKSTPEPTLPSAVATE
 ASLDSCPESSVGAVSSLD RGCPDAPAPTSAPTSQQPEPVLGLGSVEQPHEVPSVLGTP
 LLQPPENLAKGQPSTPVDRPLGPDPSAPGTLAGAALPPLEPPAPCLCQDPQEDSVEDE
 EPPGSLGLPPPQAGVQPA AAAVSGTTQPLGTGPRVSLSPHSPLLSPKVASMDAKDLAL
 QILPPCQVPPPSGPQSPAGPQGLSAPEQQEDED SLEEDSPRALGSGQHSDSHGESSA
 ELDEQDILAPQTVQCPAQAPAGGSEETIAKAKQSRSEKKARKAMSKLGLRQIQGVTRITI
 QKSKNILFVIAKPDVFKSPASDTYVVFGEAKIEDLSQQVHKAAA EKFKVPSEPSALVPES

APRPRVRLECKEEEEEEEEVDEAGLELRDIELVMAQANVSRAKAVRALRDNHSDIVNA
IMELTM

SEQID No:246

MLTTLKPFSGSVSVESKMNNKAGSFFWNLRQFSTLVSTSRMRLCCLGLCKPKIVHSNW
NILNNFHNRMQSTDIIRYLFQDAFIFKSDVGFQTKGISTLTALRIERLLYAKRLFFDSKQSL
VPVDKSDDELKKVNLNHEVSNEDVLTKETKPNRISSRKLSEECNSLSDVLDAFSKAPTF
PSSNYFTAMWTIAKRLSDDQKRFEKRLMFSHPAFNQLCEHMMREAKIMQYKYLFLSLH
AIVKLGIPQNTILVQTLLRVTQERINECDEICLSVLSTVLEAMEPCKNVHVLRTGFRILVDQ
QVWKIEDVFTLQVVMKCIGKDAPIALKRKLEMKALRELD RFSVLNSQHMFEVLAAMNHR
SLILLDECSKVVL DNIHGCP LRIMINILQSC KDLQYHNLDL FKG LADYVAATFDIWKFRKVL
FILILFENLGFRPVGLMDLFMKRIVEDPESLNMKNILSILHTYSSLNHVYKCQNKEQFVEV
MASALTGYLHTISSENLLDAVYSFCLMNYFPLAPFNQLLQKDIISELLTSDDMKNAYKLHT
LDTCLKLDDTVYLRDIALSLPQLPRELPSSHTNAKVAEVLSSLLGGEGHFSKDVHLPHNY
HIDEEIRMDTNRNQVLPLSDVDTT SATDIQRLLTYISEAGLSELKS

SEQID No:247

LQLSVKMSVLISQSVINYVEEENIPALKALLEKCKDVDERNECGQTPLMIAAEQGNLEIVK
ELIKNGANCNLEDLDNWTALISASKEGHVHIVEELLKCGVNLEHRDMGGWTALMWACY
KGRTDVVELLLSHGANPSVTGLYSVYPIIWAAGRGHADIVHLLLQNGAKVNCSDKYGTT
PLVWAARKGHLECVKHLLAMGADV DQEGANSMTALIVAVKGGYTQSVKEILKRNP NVN
LTDKDGNTALMIASKEGHTEIVQDLLDAGTYVNIPDRSGDTV LIGAVRGGHVEIVRALLQ
KYADIDIRGQDNKTALY WAVEKGNATMVRDILQCNPDTEICTKDGETPLIKATKMRNIEV
VELLLDKGAKVSAVDKKGDTPLHIAIRGRSRKLAELLRNPKDGRLLYRPNKAGETPYNI
DCSHQKSILTQIFGARHLSPTETDGDMLGYDLYSSALADILSEPTMQPPICVGLYAQWG
SGKSFLLKKLEDEMKT FAGQQIEPLFQFSWLIVFLTLLLCGGLGLLFAFTVHPNLGIAVSL
SFLALLYIFFIVIYFGGRREGESWNWAWVLSTRLARHIGYLELLLKLMFVNPPPELPEQTTK
ALPVRFLFTDYNRLSSVGGETSLAEMIATLSDACEREFGLATRLFRVFKTEDTQGKKK
WKKTCCLPSFVIFLFIIGCIISGITLLAIFRVDPKHLTVNAV LISIASVVGLAFVLNCRTWWQ
VLDSLLNSQRKRLHNAASKLHKLKSEGFMKVLKCEVELMARMAKTIDSFTQNQTRLV VII
DGLDACEQDKVLQMLD TVRVLF SKGPFIAIFASDPHIIKAINQNLNSVLRDSNINGHDYM
RNIVHLPVFLNSRGLSNARKFLVTSATNGDVPCSDTTGIQEDADRRVSQNSLGEMTKLG
SKTALNRRD TYRRRQMQR TITRQMSFDLTKLLVTE DWFS DISPQTMRRLLNIVSVTGRL
LRANQISFNWDR LASWINLTEQWPYRTSWLILYLEETEGIPDQMTLKT IYERISKNIPTTK

DVEPLLEIDGDIRNFEVFLSSRTPVLVARDVKVFLPCTVNLDPKLREIIADVRAAREQISIG
 GLAYPPLPLHEGPPRAPSGYSQPPSVCSSTSFNGPFAGGVVSPQPHSSYYSGMTGPQ
 HPFYNRPFAPYLYTPRYYPGGSQHLISRPSVKTS�PRDQNNGLEVIKEDAAEGLSSPT
 DSSRGSGPAPGPVLLNSLNVDAVCEKQIEGLDQSMPLQYCTTIKKANINGRVLAQC
 NIDELKKEMNMNFGDWHLFRSTVLEMRNAESHVVPEDPRFLSESSSGPAPHGEPARR
 ASHNELPHTELSSQTPYTLNFSFEELNTLGLDEGAPRHSNLSWQSQTRRTPSLSSLNS
 QDSSIEISKLTDKVQAEYRDAYREYIAQMSQLEGGPGSTTISGRSSPHSTYYMGQSSSG
 GSIHSNLEQEKGDSEPKPDDGRKSFLMKRGDVIDYSSSGVSTNDASPLDPITEEDEKS
 DQSGSKLLPGKKSSERSLFTDLKLGSGRLRYQKLPSDEDESGTEESDNTPLLKDDK
 DRKAEGKVERVPKSPEHSAEPIRTFIKAKEYLSDALDKKDSSDSGVRSSSESSPNHSLH
 NEVADDSQLEKANLIELEDDSHSGKRGIPHSLSGLQDPIIARMSICSEDKKSPSECSLIAS
 SPEENWPACQKAYNLNRTPTSTVTLNNSAPANRANQNFDEMEGIRETSQVILRPSSSP
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SEQID No:248

MEAAPPGPWPLLLLLLLLLALCGCPAPAAASPLLLFANRRDVRLVDAGGVKLESTIVVS
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 GKPLYWTDSETNRIEVANLNGTSRKVLFWQDLQDPRAIALDPAHGYMYWTDWGETPRI
 ERAGMDGSTRKIIVDSDIYWPNGLTIDLEEQLYWADAKLSFIHRANLDGSFRQKVVEG
 SLTHPFALTLSGDTLYWTDWQTRSIHACNKRTGGKRKEILSALYSPMDIQVLSQERQPF
 FHTRCEEDNGGCSHLCLLSPSEPFYTCACPTGVQLQDNGRTCKAGAEVLLARRTDL
 RRISLDTPDFTDIVLQVDDIRHAIADYDPLEGYVYWTDDEVRAIRRAYLDGSGAQTLVNT
 EINDPDGIAVDWVARNLYWTDGTDRIEVTRLNGTSRKILVSEDLDPEPRAIALHPVMGLM
 YWTDWGENPKIECANLDGQERRVLVNASLGWPNGLALDLQEGKLYWGDAKTDKIEVIN
 VDGTKRRTLLEDKLPHFIFGFTLLGDFIYWTDWQRRSIERVHKVKASRDVIIDQLPDLMGL
 KAVNVAKVVGTPNPCADRNGGCSHLCCFTPHATRCGCPIGLELLSDMKTCIVPEAFLVFT
 SRAAIHRISLETNNNDVAIPLTGVKEASALDFDVSNNHIYWTDVSLKTISRAFMNGSSVE
 HVVEFGLDYPEGMAVDWMGKNLYWADTGTNRIEVARLDGQFRQVLVWRDLNPRSL
 ALDPTKGYIYWTEWGGKPRIVRAFMDGTNCMTLVDKVGRANDLTIDYADQRLYWTDLD
 TNMIESSNMLGQERVVIADDLPHPFGLTQYSDIYWTDWNLHSIERADKTSGRNRTLIQ
 GHLD FVMDILVFHSSRQDGLNDCMHNNGQCGQLCLAIPGGHRCGCASHYTLPSSRN
 CSPPTTFLFSQKSAISRMIPDDQHSPDLILPLHGLRNVKAIDYDPLDKFIYWVDGRQNIK
 RAKDDGTQPFVLTSLSQGQNPDRQPHDLSIDIYSRTLFWTCEATNTINVHRLSGEAMGV
 VLRGDRDKPRAIVVNAERGYLYFTNMQDRAAKIERAALDGTEREVLFTTGLIRPVALVVD

NTLGKLFWVDADLKRIESCDLSGANRLTLEDANIVQPLGLTILGKHLYWIDRQQQMIE
 EKTTGDKRTRIQQGRVAHLTGIIHAVEEVSLIEFSAHPCARDNGGCSHICIAKGDGTPRCS
 CPVHLVLLQNLLTCGEPPTCSPDQFACATGEIDCIPGAWRCDGFPECDDQSDEEGCPV
 CSAAQFPCARGQCVDLRLRCDGEADCQDRSDEVDCDAICLPNQFRCASGQCVLKQQ
 CDSFPDCIDGSDELMCEITKPPSDDSPAHSAGPVIGIILSLFVMGGVYFVCQRRVVCQR
 YAGANGPFPHEYVSGTPHVPLNFIAPGGSQHGPFPTGIACGKSMMSSVSLMGGRGGVP
 LYDRNHVTGASSSSSSSTKATLYPPILNPPSPATDPSLYNMDMFYSSNIPATARPYP
 YIIRGMAPPPTPCSTDVCDSDYSASRWKASKYYLDLNSDSDPYPPPPTPHSQYLSAEDS
 CPPSPATERSYFHLFPPPPSPCTDSS

SEQID No:249

MDMFPLTWVFLALYFSRHQVRGQPDPPCGGRLNSKDAYITSPGYQDYPSHQNCE
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 MLYIKFTSDYARQGAGFSLRYEIFKTGSEDCSKNFTSPNGTIESPGFPEKYPHNLDCTFT
 ILAKPKMEIILQFLIFDLEHDPLQVGEGDCKYDWLDIWDGIPHVGPLIGKYCGTKTPSEL
 SSTGILSLTFHTDMAVAKDGFSAARYLVHQEPLNFQCNVPLGMESGRIANEQISASST
 YSDGRWTPQQSRLHGDDNGWTPNLDNKEYLQVDLRFLTMLTAIATQGAISRETQNG
 YYVKSYSKLEVSTNGEDWMVYRHGKNHKVFQANNDATEVVLNKLHAPLLTRFVRIRPQT
 WHSGIALRLELFGCRVTDAPCSNMLGMLSGLIADSQISASSTQEYLWSPSAARLVSSRS
 GWFPRIPQAQPGEEWLQVDLGTPKTVKGVIIQGARGGDSITAVEARAFVRKFKVSYSLN
 GKDWEYIQDPRTQQPKLFEGNMHYDTPDIRRFDPIPAQYVRVYPERWSPAGIGMRLEV
 LGCDWTDKPTVETLGPTVKSEETTPYPTTEEEATECGENCSFEDDKDLQLPSGFNCN
 FDFLEPCGWMYDHAKWLRTTWASSSSPNDRTPDDRNLRLQSDSQREGQYARLIS
 PPVHLPRSPVCMEFYQATGGRGVALQVVREASQESKLLWVIREDDQGGEWKHGRILP
 SYDMEYQIVFEGVIGKGRSGEIAIDDIRISTDVPLENCMEPISAFAGENFKVDIPEIHEREG
 YEDEIDDEYEVDWSNSSSSATSGSGAPSTDKEKSWLYTLDPILITIIAMSSLGVLLGATCA
 GLLLYCTCSYSGLSSRSCTTLENYNFELYDGLKHKVKMNHQKCCSEA

SEQID No:250

MVSRCSCLGVQCCLLLSLLLLAAWEVSGQLHYSVYEEARHGTFVGRQAQDLGLELAELV
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 VEVKDINDNPPRFSVTEQKLSIPESRLLDSPFLEGASDADVGENALLTYKLSPNEYFVL
 DIINKKDKDKFPVLVLRKLLDREENPQLKLLLTATDGGKPEFTGSVLLILVLDANDNAPIF
 DRPVYEVKMYENQVNQTLVIRLNASDSDEGINKEMMYSFSSLVPPTIRRKFWINERTGEI

KVND AIDFEDSNTYEIHVDVTDKGNPPMVGHCTVLVELLDENDNSPEVIVTSLSLPVKED
 AQVGT VIALISVSDHDSGANGQVTC SLTPHVPFKLVSTYKNYYSLVLDSALDRERV SAY
 ELVVTARDGGSPPLWATASVSVEVADVNDNAPAF AQSEYTVFVKENNPPGCHIFTVSA
 WDADAQENALVSYS LVERRLGERSLSSYVSVHAESGKVYALQPLDHEELELLQFQVSA
 RDGGVPPLG SNLTLQVFVLDENDNAPALLAS PAGESAGGAVSELVLR SVVAGHV VAKVR
 AVDADSGYN AWLSYELQSAAVGARIPFRVGLYTGEISTTRALDETDSPRQRLLVLVKDH
 GEPSLTATATVLVSLVEGSQAPKASSRASVGV APEVALVDVNVYLI ICAVSSLLVLTLL
 YTALRCSAAPT EGACGPVKPTLVCSSAVG SWSYSQQRRQRVCSGEGLPKADLMAFSP
 SLPPCPMVDVDGEDQSIGGDHSRKPRQPNPDWRY SASLRAGMHSSVHLEEAGILRAG
 PGGPDQQWPTVSSATPEPEAGEVSP PVGAGVNSNSWTFKYGPGNPKQSGPGELPK
 FIIPGSPA IISIRQEPTNSQIDKSDFITFGKKEETKKKKKKKKGNKTQEKKEKGNSTTDNSD
 Q

SEQID No:251

MENGGAGTLQIRQVLLFFVLLGMSQAGSETGNFLVMEELQSGSFVGNLAKTLGLEVSE
 LSSRGARVVSNDNKECLQLD TNTGDLLLREMLDREELCGSNEPCVLYFQVLMKNPTQF
 LQIELQVRDINDHSPVFLEKEMLLEIPENSPVGAVFLLES AKDL DVGINAVKSYTINPN SH
 FHVKIRVNP DN RKYPELVLDKALDYEERPELSFILTALDGGSPPRSGTALVRVVVDIND
 NSPEFEQA FYEVKILENSILGSLVVTVSAWDLDSGTNSELSYTFSHASEDIRKTFEINQKS
 GDITLTAPLD FEAIESYSIIIQATDGGGLFGKSTVRIQVMDVNDNAPEITVSSITSPIENTP
 ETVVMVFRIRDRDSGDNGK MVCSIPEDIPFVLKSSVNYYTLETERPLDRESRAEY NITI
 TVTDLGT PRLKTEHNITVLVSDVNDNAP AFTQTSYALFVRENNSPALHIGSISATDRDSG
 TNAQVNY SLLPSQDPHLPLASLV SINADNGHLFALRSLDYEALQGFQFRVGATDHGSPA
 LSSEALVRVLVDANDNSPFVLYPLQNGSAPCTELVPWAAEPGYLVTKVVAVDGD SGQ
 NAWLSYQLLKATEPGLFGVWAHNGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATA
 TLHVLLVDGFSQPYLPLPEAAPAQAAQADSLTVYLVALASVSSLFLFSVLLFVAVRLCRR
 SRAAPVGRCSVPEGPFPGHLVDVSGTGTL SQSYHYEVCVTGGSR SNKFKFLKPIIPNFL
 PQSTGSEVEENPPFQNNLGF

SEQID No:252

MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQRE
 FSRRGV RVVSRGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLR FQVLLES PF EFF
 QAELQVIDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYF
 RVLTRKRS DGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLVDND

NAPEFEQPFYRVQISEDSPVGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPL
 TGEIELKKQLDFEKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPE
 NAPETVVALFSVSDLDSENGKISCSIQEDLPFLLKSAENFYTLTERPLDRESRAEYNIT
 ITVTDLGTPMLITQLNMTVLIADVNDNAPAFQTQSYTLFVRENNSPALHIRSVSATDRDSG
 TNAQVTYSLLPPQDPHLPLTSLVSINADNGHLFALRSLDYEALQGGFQFRVGASDHGSPA
 LSSEALVRVVVLDANDNSPFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQ
 NAWLSYQLLKATELGLFGVWAHNGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATA
 TLHVLLVDGFSQPYLPLPEAAPTQAQADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRR
 SRAASVGRCLVPEGPLPGHLVDMSGTRTLSQSYQYEVCLAGGSGTNEFKFLKPIIPNFP
 PQCPGKEIQGNSTFPNNFGFNIQ

SEQID No:253

MKKLGRIHPNRQVLAFILMVFLSQVRLEPIRYSVLEETESGSFVAHLAKDLGLGIGELASR
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 LIQDINDHSPIFPEREVLLKILENSQPGTLFPLLIAEDLDVGSNGLQKYTISPNSHFHILTRN
 HSEGKKYPDLVQDKPLDREEQPEFSLTLVALDGGSPPRSGTVMVRILIMDINDNAPEFV
 HTPYGVQVLENSPLDSPIVRVLARDIDAGNFGSVSYGLFQASDEIKQTFSINEVTGEILLK
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 IFRIRDRDSGENGKMICSIPDNLPFILKPTLKNFYTLVTERPLDRETSAEYNITIAVTDLGTP
 RLKTQQNITVQVSDVNDNAPAFQTQSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTY
 SLLPPQDPHLPLASLVINADNGHLFALRSLDYEALQAFEFVRVGASDRGSPALSSEALV
 RVLVLDTNDNSPFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQ
 LLKATEPGLFGVWAHNGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVD
 GFSQPYLPLPEAAPAQQAQADSLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVG
 RCSVPEGPFPGHLVDVSGTGTLTSQSYQYEVCLTGDSGTGEFKFLKPIFPNLLVQDTGR
 EVKENPKFRNSLVFS

SEQID No:254

MQRAREAEMMKSQVLFPFLLSLFCGAISQQIRYTIPEELANGSRVGKLAKDLGLSVREL
 PTRKLRVSAEDYFNVSLESGLLVNGRIDREKICGRKLECALEFETVAENPMNVFHVVV
 VIQDINDNAPRFVAKGIDLEICESALPGVKFSLDSAQDADVEGNSLKLYTINPNQYFSLST
 KESPDGSKYPVLLLEKPLDREHQSSHRLILTAMDGGDPPLSGTTHIWIRVTDANDNAPV
 FSQEVYRVSLQENVPWGTSVLRVMATDQDEGINAEITYAFLNSPISTSLFNLNPNTGDIT
 TNGTLDFEETSRYVLSVEAKDGGVHTAHCNVQIEIVDENDNAPEVTFMSFSNQIPEDSD

LGTVIALIKVRDKDSGQNGMVTCTQEEVPFKLESTSKNYYKLVIAGALNREQTADYNVT
 IIATDKGKPALSSRTSITLHISDINDNAPVFHQASYVVHVSENNPPGASIAQVSASDPDLG
 PNGRVSYSLASDLEPRELLSYVSVSPQSGVVFAQRAFDHEQLRAFELTLQARDQGSPA
 LSAVSLRVLVGDLNDNAPRVLYPALGPDGSAFFDMVPRSAEPGYLVTKVVAVDADSG
 HNAWLSYHVLQASEPGLFSLGLRTGEVRTARALGDRDAARQRLLVAVRDGGQPPLSA
 TATLHLIFADSLQEVLPDLSDRPEPSDPQTELQFYLVVALALISVLFLLAVILAIALRLRRS
 SLDTEGCFQTGLCSKSGPGVPPNHSEGTLPYSYNLCIAHSAKTEFNLSNLTPEMAPPQ
 DLLCDDPSMVVCASNEDHKIAYDPSLSSHQAPPNTDWRFSQAQRPGTSGSQNGDDTG
 TWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQ
 NVYIPGSNATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

SEQID No:255

MGGSCAQRRRAGPRQVLFPLLLPLFYPTLSEPIRYSIPEELAKGSVVGNLAKDLGLSVLD
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 VVIEDVNDHAPQFDKKEIHLEIFESASAGTRLSDPATDPDININSIKDYKINSNPYFSLMV
 RVNSDGGKYPELSLEKLLDREEQRSHSLILTALDGGDPPRSATAHIEISVKDTNDNPPVF
 SRDEYRISLSENLPSPVLPVLTATDQDEGVNAEINYYFRSTAQSTKHMFSLDEKTGMI
 KNNQSFD FEDVERYTMEVEAKDGGGLSTQCKVIIELDENDNSPEIIITSLSDQILENSPP
 GMVVALFKTRDLDFGGNGEVR CNIEDIPFKIYSSSNYYKLVTGDALDREQTPEYNVTI
 VATDRGKPPLSSSR SITLYVADINDNAPVFDQTSYVVHVAENNNPPGASIAQVSASDPDL
 GLNGHISYSIVASDLEPLAVSSYVSVSAQSGVVFAQRAFDHEQLRAFALTQARDHGSP
 TLANVSLRVLVGDRNDNAPRVLYPALGPDGSAFFDMVPRSAEPGYLVTKVVAVDADS
 GHNAWLSYHVLQASEPGLFSLGLRTGEVRTARALGDRDAARQRLLVAVRDGGQPPLS
 ATATLHLVFADNLQEILPDLSDRPVLSDPQAEQFYLVVALALISVLFLLAVILAIALRLRRS
 LSPATWDCFHPGLCVKSGPVVPPNYSEGTLPYSYNLCIAHTGTKEFNFLKCSVPLHSNE
 DMVCSVSPGALIPPHGGEDLTSHPETLTSQAPPNTDWRFSQAQRPGTSGSQNGDDTG
 TWPNNQFDTEMLQAMILASASEAADGSSTLGGGAGTMGLSARYGPQFTLQHVPDYRQ
 NVYIPGSNATLTNAAGKRDGKAPAGGNGNKKKSGKKEKK

SEQID No:256

MAAAAARVVLSSAARGGLWGFSESLIRGAAGRSLYFGENRLRSTQAATQVVLNVPET
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 LDLELEIENMGAHLNAYTSREQTVYYAKAFSKDLPRAVEILADIIONSTLGEAEIERERGV
 LREMQUEVETNLQEVVFDYLHATAYQNTALGRTILGPTENIKSISRKDLVDYITTHYKGPRI

VLAAAGGVSHDELLDLAKFHFGDSLCTHKGEIPALPPCKFTGSEIRVRDDKMPLAHLAIA
 VEAVGWAHPDTICLMVANTLIGNWDRSFGGGMNLSSKLAQLTCHGNLCHSFQSFNTSY
 TDTGLWGLYMVCESTVADMLHVQKEWMRLCTSVTESEVARARNLLKTNMMLQLDG
 STPICEDIGRQMLCYNRRRIPIPELEARIDAVNAETIREVCTKYIYNRSPAIAAVGPIKQLPDF
 KQIRSNMCWLRD

SEQID No:257

MGAYLSQPNTVKCSGDGVGAPRLPLPYGFSAMQGWRVSMEDAHNCIPELDSETAMFS
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 GRPTEDEDEKEKVADEDDVDNEEAALLHEEATMTIEELLTRYGQNCHKGPPHSGSGGG
 TGEEPGSQGLNGEAGPEDSTRETPSQENGPTAKAYTGFSNSERGTEAGQVGEPIGIP
 TGEAGPSCSSASDKLPRVAKSKFFEDSEDESDEAEEDSEECSEEDGYSSEEAEEN
 EDEDDTEEAEDDEEEEEEMMVPGMGEGKEEPGSDSGTTAVVALIRGKQLIVANAGDS
 RCVVSEAGKALDMSYDHKPEDEVELARIKNAGGKVTMDGRVNGGLNLSRAIGDHFYKR
 NKNLPPEEQMISALPDIKVLTLTDDHEFMVIACDGIWNVMSSQEVVDFIQSKISQRDENG
 ELRLSSIVEELLQCLAPDTSGDGTGCDNMTCIICFKPRNTAELQPESGKRKLEEVNST
 EGAEENGNSDKKKKAKRD

SEQID No:258

MMETPLPKAPEKRQVTAIIFLLLLWEAGSATIKYSVLEERDSGSFVANLAKDLGLGVGEL
 AARGARILSKGNKQYLQLERKSGNLLLKEKLDREELCGDIDPCILHFQMLLKNPVQFIQG
 ELQLQDVNDHAPEFLENEILLKISEGSHPGTSFPLKIAQDLDVGSNTVQNYSSISTNSYFHL
 FTRNHS DGKKYPELVLDQALDREEQPQLRLTLTALDGGSPPRGTGSQVLIVVDINDNVP
 EFAQRRYEYVQVPENTPIGSLVITVSARDLDAGTHGELSYSFFQYSNQIIQAFEINSITGEIR
 FKKALDFEEIQSYHMEVEASDGGGLSGKCTVAIEVMDINDNAPELTMSLLISDILENSPET
 VVAVFGISDPDSGNNGKMMCSIQDHLPLKPTLENFYTLTTEGALDRESRAEYNITITVT
 DLGTPRLKTEYNITLRVSDVNDNAPAFTQTSYTLFVRENNSPALHIGSVSATDRDSGTN
 AQVTYSLLPPQNPHLPLASLVSINTDNHGLFALRSLDYALQEFEFVFGASDRGSPALS
 SEALVRVLVCWTPTTTRPSCCTRCRTAPRPAPSWCPGRPSRATW

SEQID No:259

MLRMRTAGWARGWCLGCCLLLPLSFSLAAAKQLLRYRLAEEGPADVRIGNVASDLGIV
 TGSGEVTFSLGSEYKIDNLTGELSTSEERRIDREKL PQCMIFDENECFLDFEVSIG
 PSQSWVDLFEGQVIVLDINDNTPTFPSPVLTLTVEENRPVGTLYLLPTATDRDFGRNGIE

RYELLQEPGGGGSGGESRRAGAADSAPYPGGGGNGASGGGSGGSKRRLDASEGGG
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 QAILRVLITDVNDNSPRFEKSVYEADLAENSAPGTPILQLRAADLDVGVNGQIEYVFGAA
 TESVRLLRLDETSGWLSVLHRIDREEVNQLRFTVMARDRGQPPKTDKATVVLNIKDEN
 DNVPSEIRKIGRIPLKDGVANVAEDVLVDTPIALVQVSDRDQGENGVTCTVVGDPFQ
 LKPASDTEGDQNKKKYFLHTSTPLDYEATREFNVVIVAVDSGSPSLSSKNSLIVKVGDTN
 DNPPMFGQSVVEVYFPENNIPGERVATVLATDADSGKNAEIAYSLDSSVMGIFAIDPDS
 GDILVNTVLDREQTDREYEFKVNADKKGIPVLQGSTTVIVQVADKNDNDPKFMQDVFTFY
 VKENLQPNSPVGMVTVMADKGRNAEMSLYIEENNNIFSIENDTGTIYSTMSFDREHQT
 TYTFRVKAVDGGDPPRSATATVSLFVMDENDNAPT VTLPKNISYTLPPSSNVRTVVAT
 VLATSDDDGINADLNYSIVGGNPFLFEIDPTSGVVSLVGKLTQKHVGLHRLVVQVNS
 GQPSQSTTTVVHVFNESVSNATAIDSQIARSLHIPLTQDIAGDPSYEISKQRLSIVIGVVA
 GIMTVILILIVVMARYCRSKNKNNGYEAGKKDHEDFFTQQHDKSKKPKKDKKNKSKQP
 LYSSIVTVEASKPNGQRYDSVNEKLSDSPSMGRYRSVNGGPGSPDLARHYKSSSPLPT
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 PYITVFG

SEQID No:260

MEIGWMHNRQRQVLVFFVLLSLSGAGAE LGSYSVVEETERGSFVANLGKDLGLGLTE
 MSTRKARIISQGNKQHLQLKAQTGDLLINEKLDREELCGPTEPCILHFQVL MENPLEIFQ
 AELRVIDINDHSPMFTEKEMILKIPENSPLGTEFPLNHALDLDVGSNNVQNYKISPSSHFR
 VLIHEFRDGRKYPELVLDKELDREEEPQLRLTLTALDGGSPPRSGTAQVRIEVDINDNA
 PEFEQPIYKVQIPENSPLGSLVATVSARDLDGGANGKISYTLFQPSDISKTLEVNPMTG
 EVRLRKQVDFEMVTSYEVRIKATDGGGLSGKCTLLLQVVDVNDNPPQVTMSALT SPIE
 NSPEIVVAVFSVSDPD SGNNGKTISSIQEDLPFLKPSVKNFYTLVTERALDREARAEYNI
 TLTVTDMGTPRLKTEHNITVQISDVNDNAPTFTQT SYTLFVRENNSPALHIGSVSATDRD
 SGTNAQVTYSLLPPQDPHLPLASLV SINADNGHLFALRSLDYEALQAFEF RVGATDRGS
 PALSREALVRVLVDANDNSPFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDS
 GQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLLSERDAAKQRLVVLVKDNGEPPRS
 ATATLHVLLVDGFSQPFLPLPEAAPGQTQANSLTVYLVVALASVSSLFLFSVLLFVAVRL
 CRRSRAASVGRCSMPEGPFPGRLVDVSGTGTL SQSYQYEVCLTGGSETSEFKFLKPIIP
 NFSP

SEQID No:261

MDEDVLTTLKILIIGESGVGKSSLLLRFTDDTFDELAATIGVDFKVKTISVDGNKAKLAIW
DTAGQERFRTLTPSYRGAQGVILVYDVTRRDTFVKLDNWLNELETYCTRNDIVNMLVG
NKIDKENREVDRNEGLKFARKHSMLFIEASAKTCDGVQCAFEELVEKIIQTPGLWESEN
QNKGVKLSHREEGQGGGACGGYCSVL

SEQID No:262

MESRDHNNPQEGPTSSSGRRRAVEDNHLLIKAVQNEDVDLVQQLLEGGANVNFQEEE
GGWTPHNAVQMSREDIVELLRRHGADPVLRRKNGATPFILAAIAGSVKLLKLFLSKGAD
VNECDFYGFATFMEAAYGKVKALKFLYKRGANVNLRRKTKEDQERLRKGGATALMDA
AEKGHVEVLKILLDEMADVACDNMGRNALIHALLSSDDSDVEAITHLLLDHGADVNV
RGERGKTPLILAVEKKHLGLVQRLLEQEHEINDTSDGKTALLLAVELKLKKIAELLCKR
GASTDCGDLVMTARRNYDHSVLKVLLSHGAKEDFHPPAEDWKPQSSHWGAALKDLHR
IYRPMIGKLKFFIDEKYKIADTSEGGIYLGfYEKQEVAVKTFCEGSPRAQREVSCLOSSR
ENSHLVTFYGSSESHRGHLFVCVTLCEQTLACLVDHVRGEDVENEEDFARNVLSSIFKA
VQELHLSCGYTHQDLQPQNILIDSKAAHLADFDKSIKWAGDPQEVKRDLEDLGRVLVY
VVKKGSISFEDLKAQSNEEVVQLSPDEETKDLIHRFLFHPGEHVRDCLSDLLGHPFFWTW
ESRYRTLNRNVGNESDIKTRKSESEILRLLQPGPSEHSKSFDKWTTKINECVMKKMNKFY
EKRGNFYQNTVGDLLKFIRNLGEHIDEKHKMKMLKIGDPSLYFQKTFPDLVIYVYTKLQ
NTEYRKHFQTHSPNKPQCDGAGGASGLASPGC

SEQID No:263

MACSIVQFCYFQDLQAARDFLFPHLREEILSGALRRDPSKSTDWEDDGWGAWEENEP
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QFAVGWWSGLNVEEGECVTSALCIPLASQKRSSTGRPDWTCIVVGFTSGYVRFYTENG
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QVAKAAASGNENIQPPPLAYKKWGLQDIDTIIDHASVGIMTLSPFDQMKTASNIGGFNAA
IKNSPPAMSQYITVGSNPFTGFFYALEGSTQPLLSHVALAVASKLTSALFNAASGWLGW
KSKHEEEAVQKQKPKVEPATPLAVRFGLPDSRRHGESICLSPCNTLAAVTDDFGRVILL
DVARGIAIRMWKG YRDAQIGWIQTVEDLHERVPEKADFSPFGNSQGSPRVAQFLVIYAP
RRGILEVWSTQQGPRVGAFNVGKHCRLLYPGYKIMGLNNVTSQSWQPQTYQICLVDPV
SGSVKTVNVPFHLALSDKKSERAKDMHLVKKLAALLKTKSPNLDLVETEIKELILDIKYP
TKKQALESILASERLPFSCLR NITQTLMDTLKSQELESVDEGLLQFCANKLKLQLYESVS
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VKTFLEYLEYEKDVLNIKKISEEEYVALGSFFFWKCLHGESSTEDMCHTLESAGLSPQLL
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 CIQSENNGAALLSAHVGHSVAAQISNNMTEKKFSQTVLGADSEALTDSEALSLEDEY
 WKLLLKQLEDCLILQTLLHSGKNTQTSKVSSLQAEPLPRLSVKKLLEGGKGGIADSVAK
 WIFKQDFSPEVLKLANEERDAENPDEPKEGVNRSFLEVSEMEMDLGAIPDLLHLAYEQF
 PCSLELDVLHAHCCWEYVVQWNKDPEEARFFVRSIEHLKQIFNAHVQNGIALMMWNTF
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 QVPVLDTEDAWLSVEGPISIVELALEQKHIHYPLVEHHSILCSILYAVMRFSCLKTVKPLSLF
 DSKGKNAFFKDLTSIQLLPSGEMDPNFISVRQQFLLKVVSAAVQAQHSATKVKDPTEEA
 TPTPFGKDQDWPALAVDLAHLQVSEDVVRHYVGELYNYGVDHLGEEAILQVHDKEV
 LASQLLVLTGQRLAHALLHTQTKEGMELLARLPPTLCTWLKAMDPODLQNTVEPIATTA
 KLVNKVIELLPEKHGQYGLALHLIEAVEAISLPSL

SEQID No:264

MTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAAAYTQALGLDATPQDQ
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 RCVSLEPKNKVFQEALRNIGGQIQEKVRYMSSTDAKVEQMFIILLDPEEKGTETKKQKAS
 QNLVVLAREDAGAIEKIFRSNGVQLLQRLLDMGETDLMLAALRTLVGICSEHQSRVTATL
 SILGTRRVVSILGVESQAVSLAACHLLQVMFDALKEGVKKGFRGKEGAIIVDPARELKVLI
 SNLLDLLTEVGVSGQGRDNALTLLIKAVPRKSLKDPNNSLTLWVIDQGLKKILEVGGSLQ
 DPPGELAVTANSRMSASILLSKLFDDLKCDARENFHRLCENYIKSWFEGQGLAGKLRA
 IQTVSCLLQGPCDAGNRALELSGVMESVIALCASEQEEELVAVEALIHAAGKAKRASFI
 TANGVSLLKDLYKCSEKDSIRIRALVGLCKLGSAGGTDFSMKQFAEGSTLKLAKQCRKW
 LCNDQIDAGTRRWAVEGLAYLTFDADVKEEFVEDAAALKALFQLSRLEERSVLF AVASA
 LVNCTNSYDYEEPDPKMVELAKYAKQHVPEQHPKDKPSFVRARVKKLLAAGVVSAMVC
 MVKTESPVLTSRELLSRVFLALVEEVEDRGTVVAQGGGRALIPLALEGTDVGQTKAA
 QALAKLTITSNPEMTFPGERIYEVVRPLVSLLHLNCSGLQNFEALMALTNLAGISERLRQ
 KILKEKAVPMIEGYMFEEHEMIRRAATECMCNLAMSKEVQDLFEAQGNDRKLLVLYSG
 EDELLQRAAAGGLAMLTSMRPTLCSRIPQVTTHWLEILQALLSSNQELQHRGAVVVL
 NMVEASREIASTLMESEMMEILSVLAKGDHSPVTRAAAACLDKAVEYGLIQPNQDGE

SEQID No:265

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QDFENFYTRNLYMRIRDNWNRPICSVPGARVDIMERQSHDYNWSFKYTGNIIKGVINMG
 SYNLYGFARNTGSCQEAAAKVLEEYGAGVCSTRQEIGNLDKHEELEELVARFLGVEAA
 MAYGMGFATNSMNIPALVGKGCLILSDELNHASLVLGARLSGATIRIFKHNNMQSLEKLL
 KDAIVYGQPRTRRPWKKILILVEGIYSMEGSIVRLPEVIALKKKYKAYLYLDEAHSIGALGP
 TGRGVVEYFGLDPEDVDVMMGTFTKSFGASGGYIGGKELIDYLRTHSHSAVYATSLS
 PPVVEQIITSMKCIMGQDGTSLGKECVQQLAENTRYFRRRLKEMGFIIYGNEDSPVVPL
 MLYMPAKIGAFGREMLKRNIGVVVVGFAPATPIIESRARFCLSAAHTKEILDALKEIDEVG
 DLLQLKYSRHLVPLLDLPFDETTYEETED

SEQID No:266

MSGELPPNINIKEPRWDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRQGIVP
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 WQWINQSFNAVVNYTNRSGDAPLTVNELGTAYVSATTGAVATALGLNALTKHVSPLIGR
 FVPFAAVAAANCINIPLMRQRELKVGIPVTDENGNRLLGESANAQAITQVVVSRILMAA
 PGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCLVFATPLCCALFPQKSSMSVTSL
 EAELQAKIQESHPELRRVYFNKGL

SEQID No:267

MSQWYELQQLDSKFLEQVHQLYDDSFPMERQYLAQWLEKQDWEHAANDVSFATIRF
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 NAQRFNQAQSGNIQSTVMLDKQKELDSKVRNVKDKVMCIEHEIKSLEDLQDEYDFKCK
 TLQNREHETNGVAKSDQKQEQLLLKKMYLMLDNKRKEVVHKIIELLNVTELTQNALINDE
 LVEWKRRQQSACIGGPPNACLDQLQNWFTIVAESLQQVRQQLKKLEELEQKYTYEHDP
 ITKNKQVLWDRTFSLFQQLIQSSFVVERQPCMPHTPQRPLVLKTGVQFTVKLRLLVKLQ
 ELNYNLKVKVLFDKDVNERNTVKGFRKFNLGTHTKVMNMEESTNGSLAAEFRHLQLKE
 QKNAGTRTNEGPLIVTEELHSLSFETQLCQPGGLVIDLETTSLPVVISNVSQLPSGWASIL
 WYNMLVAEPRNLSFFLTPPCARWAQLSEVLWSQFSSVTKRGLNVDQLNMLGEKLLGP
 NASPDGLIPWTRFCKENINDKNFPFWLWIESILELIKHLPLWNDGCIMGFISKERERAL
 LKDQQPGTFLRLFSESSREGAITFTWVERSQNGGEPDFHAVEPYTKKELSAVTFPDIIR
 NYKVMAAENIPENPLKYLYPNIDKDHAFGKYYSRPKEAPEPMELDGPKGTYIKTELISV
 SEVHPSRLQTTDNLLPMSPEEFDEVSRIVGSVEFDSMMNTV

SEQID No:268

MEAVLNELVSVEDLLKFEKKFQSEKAAGSVSKSTQFEYAWCLVRTRYND DIRKGIVLLE

ELLPKGSKEEQRDYVFYLA VGN YRLKEYEKALKYVRGLLQTEPQNNQAKELERLIDKAM
KKDGLVGMAIVGGMALGVAGLAGLIGLAVSKSKS

SEQID No:269

MGAVARAHGGLRVARARESVAGGRHRGAGRPGARAAGAAAGLVRAEAGGRRAGRG
RRPGRGLPTGGGGGLAAA VGREVAQGLCDAIRLDGGLDLLRLLQAPELETRVQAARL
LEQILVAENRDRVARIGLGVILNLAKEREPVELARSVAGILEHMFKHSEETCQRLVAAGG
LDAVLYWCRRTDPALLRHCALALGNCALHGGQAVQRRMVEKRAAEWLFPLAFSKEDE
LLRLHACLAVAVLATNKEVEREVERSGTLALVEPLVASLDPGRFARCLVDASDTSQGRG
PDDLQRLVPLLD SNRLEAQCIGAFYLCAEAAIKSLQGKTKVFSDIGAIQSLKRLVSYSTNG
TKSALAKRALRLLGEEVPRPILPSVPSWKEAEVQTWLQQIGFSKYCESFREQQVDGDL
LRLTEEELQTDLGMKSGITRKRFFRELTELKTFANYSTCDRSNLADWLGS LDPFRFRQYT
YGLVSCGLDRSLLHRVSEQQLLED CGIHLGVHRARILTAAREMLHSPLPCTGGKPSGDT
PDVFISYRRNSGSQLASLLKVHLQLHGFSVFIDVEKLEAGKFEDKLIQSVMGARNFVLVL
SPGALDKCMQDHDCKDWVHKEIVTALSCGKNIVPIIDGFEWPEPQVLPEDMQAVLTFN
GIKWSHEYQEATIEKIIRFLQGRSSRDSSAGSDTSLEGAAPMGPT

SEQID No:270

MVGEEKMSLRNRLSKSRENPEEDEDQRNPAKESLETPSNGRIDIKQLIAKKIKLTAEAE
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KIFIARRSLLDELLEVDHIRT IYHMFIAL LILFILSTLVVDYIDEGRLVLEFSLLSYAFGKFPTV
VWTWWMFLSTFSVPYFLFQHWATGYSKSSHPLIRSLFHGFLFMIFQIGVLGFGPTYVVL
AYTLPPASRFIIIFEQIRFVMKAHSFVRENVPRVLNSAKEKSSTVPIPTVNQYLYFLFAPTLI
YRDSYPRNPTVRWGYVAMKFAQVFGCFFYVYIFERLCAPLFRNIKQEPFSARVLVLCV
FNSILPGVLILFLTFFAFLHCWLN AFAEMLRFGDRMFYKDWWNSTSYSNYYRTWNVVV
HDWLYYYAYKDFLWFFSKRFS AAMLAVFAVSAVVHEYALAVCLSFFYPVLFVLFMFFG
MAFNFIVNDSRKKPIWNVLMWTS LFLGNGVLLCFYSQEWYARRHCPLKNPTFLDYVRP
RSWTCRYVF

SEQID No:271

MKAMDVLPIKKEKVAYLSGGRDKRGGPILTFPARSNHDRIRQEDLRRLISYLACIPSEEV
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GNADLQNLLPKVSTMLDRLHSTRQHHLHQMWHVRKLKLDQCFQLRLFEQDAEKMFDWI
 THNKGLFLNSYTEIGTSHPHAMELQTQHNHFAMNCMVYVNINRIMSVANRLVESGHY
 ASQQIRQIASQLEQEWKAFAAALDERSTLLDMSSIFHQKAEKYMSNVDSWCKACGEVD
 LPSELQDLEDAIH HHQGIYE HITLAYSEVSQDGKSLDDKLQRPLTPGSSDSL TASANYSK
 AVHHVLDVIHEVLHHQRHVRTIWQHRKVRLHQRLQLCVFQQEVQQVLDWIENHGEAFL
 SKHTGVGKSLHRARALQKRHEDFEEVAQNTYTNADKLEAAEQLAQTGECDPEEIYQA
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 DLIKRFQGGQQQTTLQVTNVVIKEGEDLIQQLRDSAISSNKTPHNSSINHIETVLQQLDEAQ
 SQMEELFQERKIKLELFLHVRIFERDAIDIISDLESWNDELSQQMNDFTEDLTIAEQRLQ
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 LQREHEQFQHAIEKTHQSALQVQQKAEAMLQANHYDMDMIRDCAEKVASHWQQMLK
 MEDRLKLVNASVAFYKTSEQVCSVLESLEQYKREEDWCGGADKLGPNSETDHVTPMI
 SKHLEQKEAFLKACTLARRNADVFLKYLHRNSVNMPGMVTHIKAPEQQVKNILNELFQR
 ENRVLHYWTMRKRRLDQCQQYVVFERSAKQALEWIHDNGEFYLTSTHTSTGSSIQHTQ
 ELLKEHEEFQITAKQTKERVKLLIQLADGFCEKGHAAAEIKKCVTAVDKRYRDFSLRME
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 AELIQTEKAYVRDLRECM DTYLWEMTSGVEEIPPGIVNKELIFGNMQEIYEFHNNIFLKE
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 SISSYLIKPVQRITKYQLLLKELLTCCEEGKGEIKDGLEVMLSVPK RANDAMHLSMLEGF
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 LFTSELGVTEHVEGDPCKFALWVGRTPTSDNKIVLKASSIENKQDWIKHIREVIQERTIHL
 KGALKEPIHIPKTAPATRQKGRRDGEDLDSQGDGSSQPD TISIASRTSQNTLDSDKLSG
 GCELT VVIHDFTACNSNELTIRRGQTVEVLERPHDKPDWCLVRTTDRSPAAEGLVPCGS
 LCIAHSRSSMEMEGIFNHKDSL SVSSNDASPPASVASLQPHMIGAQSSPGPKRPGNTL
 RKWLTSPVRRLLSSGKADGHVKKLAHKHKSREVRKSADAGS QKDSDDSAATPQDET V
 EERGRNEGLSSGTL SKSSSSGMQSCGEEEGEEGADAVPLPPPMAIQQHSL LQPD SQD
 DKASSRLLVRPTSSETPSAAELVSAIEELVKSKMALED RPSSLLVDQGDSSSPSFNPSD
 NSLLSSSSPIDEMEERKSSSLKRRHYVLQELVETERDYVRDLGYVVEGYMALMKEDGV
 PDDMKGKDKIVFGNIHQIYDWHRDFFLGELEKCLEDP EKLGS LFKHERRLHMYIAYCQ
 NPKKSEHIVSEYIDTFFEDLKQRLGHR LQLTDLLIKPVQRIMKYQLLLKDFLKYSKKASLD
 TSELERAVEVMCIVPRRCNDMMNVGRLQGFDGKIVAQ GKLLLQDTFLVTDQDAGLLPR
 CRERRIFLFEQIVIFSEPLDKKKGFSMPGFLFKNSIKV SCLCLEENVENDPCKFALT SRTG
 DVVETFILHSSSPSVRQTWIHEINQILENQRNFLNALT SPIEYQRNHSGGGGGGGSGAA

AGVGAAAAAGPPVAAAATVAAPAAAAAPPARAGAGPPGSPSLSDTTPPCWSPLQPR
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 KLENGYRKSREGLSNKVSVKLLNPNIYDVPPEFVIPLSEVTCETGETVVLRCRVCGRP
 KASITWKGPENHTLNNDGHYSISYSDLGEATLKIVGVTTEDDGIYTCIAVNDMGSASSA
 SLRVLGPGMDGIMVTWKDNFDSFYSEVAELGRGRFSVVKKCDQKGTKRAVATKFNK
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 HQLLGNPEFAAPEIILGNPVSLSDTWSVGVLTIVLLSGVSPFLDDSVETCLNICRLDF
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 SFIERRKHQNDVRPIRSIKNFLQSRLLPRV

SEQID No:272

MRKGLRATAARCGLGLGYLLQMLVLPALALLSASGTGSAAQDDDDFFHELPETFPSPDP
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 REVSIEISRQQVEELFGPEDYWCQCVAWSSAGTTKSRKAYVRIAYLRKTFEQEPLGKEV
 SLEQEVLLQCRPPEGIPVAEVEWLKNEIDIIPVEDRNFYITIDHNLIIKQARLSDTANYTCV
 AKNIVAKRKSTTATVIVYVNGGWSTWTEWSVCNSRCGRGYQKRTRTCTNPAPLNNGGA
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 GLVLQSKNCTDGLCMQTAPDSDDVALYVGIVIAVIVCLAISVVVALFVYRKNHRDFESDII
 DSSALNGGFQPVNIKAARQDLLAVPPDLTSAAAMYRGPVYALHDVSDKIPMTNSPILDP
 LPNLKIKVYNTSGAVSPQDDLSEFTSKLSPQMTQSLENEALS LKNQSLARQTDPSCTA
 FGSFNSLGGHLIVPNSGVSLIPAGAIPQGRVYEMYVTVHRKETMRPPMDDSQTLLTPV
 VSCGPPGALLTRPVVLTMHHCADPNTEDWKILLKNQAAQGWEDVVVVGEENFTTPC
 YIKLDAEACHILTENLSTYALVGHSTTKAAAKRLKLAIFGPLCCSSLEYSIRVYCLDDTQD
 ALKEILHLERQTGGQLLEPKALHFKGSTHNLRLSIHDIAHSLWWSKLLAKYQEIPFYHV
 WSGSQRNHCTFTLERFSLNTVELVCKLCVRQVEGEGQIFQLNCTVSEEPTGIDLPLLD
 PANTITTVTGPSAFSIPRQKLCSSLDAPQTRGHDWRMLAHKLNLDRLNYFATKSSP
 TGVILDLWEAQNFDPGNLSMLAAVLEEMGRHETVVSLAAEGQY

SEQID No:273

MAVFVLLALVAGVLGNEFSILKSPGSVFRNGNWPPIGERIPDVAALSMGFSVKEDLS
 WPGLA VGNLFHRPRATVMVMVKGVNKLALPPGSVISYPLENAVPFSLDSVANSIHSLS
 EETPVVLQLAPSEERVYMGKANSVFEDLSVTLRQLRNRLFQENSVLSSLPLNSLSRNN

EVDLLFLSELQVLHDISSLLSRHKHLAKDHSPDLYSLELAGLDEIGKRYGEDSEQFRDAS
 KILVDALQKFADDMYSLYGGNAVVELVTVKSFDTSIRKTRTILEAKRAKNPASPYNLAY
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SEQID No:274

MTFYLFGIRSF PKLWKSPYLGLGPGHSYVSLFLADRCGIRNQQRLFSLKTMSPQNTKAT
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 LNSEEWDK LKEDLKENTGKTSFESWIISQMAGCHSSIDVAKSLLAWVAAKNNGIVSYDL
 LVKYLYLCVFHMQTSEVIDVFEIMKARYKTLEPRGYSLIRGLIHSDRWREALLLLEDIKK
 VITPSKKNYND CIIQGALLHQDVNTAWNLYQELLGHDIVPMLET LKAFFDFGKDIDDDNYS
 NKLLDILSYLRNNQLYPGESFAHSIKTWFE SGGCSGCGKTIESIQLSPEEYECLKGKIMR
 DVIDGGDQYRK TTPQELKRFENFIKS RPPFDVVIDGLNVAKMFPKVRESQ LLLNVVSQL
 AKRNLRLVLGRKHMLRRSSQWSRDEMEEVQKQASCFFADDISEDDPFLLYATLHSGN
 HCRFITRDLMRDHKACLPDAKTQRLFFKWQQGHQLAIVNRFP GSKLTFQRILSYDTV VQ
 TTGDSWHIPYDEDLVERCSCEVPTKWLC LHQKT

SEQID No:275

MALALAALAAVEPACGSRYQQ LQNEEESGEPEQAAGDAPPPYSSISAESAAYFDYKDE
 SGFPKPPSYNVATTLP SYDEAERTKAEATIPLVPGRDEDFVGRDDFD DADQLRIGNDGI
 FMLTFFMAFLFNWIGFFLSFCLT TSAAGRYGAISGFGLSLIKWILIVRFSTYFPGYFDGQY
 WLWWVFLVLGFLFLRGFINYAKVRKMPETFSNLPRTRVLFIY

SEQID No:276

MDPECAQLLPALCAVLVDPGQP VADDTCLEKLLDWFKTVTEGESSVLLQEHPCLVELL
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 TVRSGWIIQGLRSLAQHPSALRFLADHGAVDTIFSLQGDSSLFVASAASQLLVHVLALSM
 RGGAEGQPCLPGGDWPACAQKIMDHVEESLCSAATPKVTQALNVLT TTFGRCQSPWT
 EALWVRLSPRVACLLERDPIPAAHSFVDLLLCVARSPVFSSSDGSLWETVARALSCLGP
 THMGPLALGILKLEHCPQALRTQAFQVLLQPLACVLKATVQAPGPPGLLDGTADDATTV
 DTLLASKSSCAGLLCRTLAHLEELQPLPQRPSWPQASLLGATVTVLRLCDGSAAPASS
 VGGHLCGTLAGCVRVQRAALDFLGTLSQGTGPQELVTQALAVLLECLESPGSSPTVLK
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 SRHWGGQADFRCALLASEVPQALQLLQDPESYVRASAVTAMGQLSSQGLHAPTSPE
 HAEARQSLFLELLHILSV DSEGFP RRAVMQVFTEWLRDGHADAAQDTEQFVATVLQAA

SRDLWEVRAQGLELALVFLGQTLGPPRTHCPYAVALPEVAPAQPLTEALRALCHVGL
 FDFAFCALFDCDRPVAQKSCDLLFLRDKIASYSSLREARGSPNTASAEATLPRWRAGE
 QAQPPGDQEPEAVLAMLRLSDLEGLRSTLAESSDHVEKSPQSLLQDMLATGGFLOGDE
 ADCY

SEQID No:277

MVNYAWAGRSQRKLWWRSVAVLTCKSVVRPGYRGGLQARRSTLLKTCARARATAPG
 AMKMVAPWTRFYNSCCLCHVRTGTILLGVWYLIINAVVLLILLSALADPDQYNFSSE
 LGGDFEFMDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAIT
 VLIYPNSIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGYLISCVWNCYRYING
 RNSSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA

SEQID No:278

MNIFDRKINF DALLKFSHITPSTQQHLKKVYASFALCMFVAAAGAYVH MVTHFIQAGLLS
 ALGSLILMIWLMATPHSHETE QKRLGLLAGFAFLTGVGLGPALEFCIAVNPSILPTAFMGT
 AMIFTCFTLSALYARRRSYLFLGGILMSALSLLLLSSLGNVFFGSIWLFQANLYVGLVVMC
 GFVLFD TQLIEKA EHGDQDYIWHCIDLFDITVFRKLMMILAMNEKDKKKEKK

SEQID No:279

MASILDEYENSLSRSAVLQPGCPSVGIPHSGYVNAQLEKEVPIFTKQRIDFTP SERITSLV
 VSSNQLCMSLGKDTLLRIDLGKANEPNHVELGRKDDAKVHKMFLDHTGSHLLIALSSTE
 VLYVNRNGQKVRPLARWK GQLVESVGWNKALGTESSTGPILVGTAQGHIFEAE LSASE
 GGLFGPAPDLYFRPLYVLNEEGGPAPVCSLEAERGP DGRSFVIATTRQRLFQFIGRAAE
 GAEAQGFSGLFAAYTDHPPPFREFPSNLGYSELAFYTPKLRSAPRAFAWMMGDGVLY
 GALDCGRPDSLLSEERVWEYPEGVGPGASPLAIVLTQFHFLLLADRVEAVCTLTGQV
 VLRDHFLEKFGPLKHMVKDSSTGQLWAYTERAVFRYHVQREARDVWRTYLD MNRFDL
 AKEYCRERPDCLDTVLAREADFCFRQRRYLESARCYALTQSYFEEIALKFLEARQEEAL
 AEFLQRKLASLKPAERTQATLLTTWLTELYLSRLGALQGDPEALTLYREVRNLTQFHPLP
 LAPLLSLSFPTHVLFTSREREREHLSSVCSLCGLWNPSSSLSEEAFSSSCL

SEQID No:280

MTSATSPIILKWDPKSLEIRTLTVERLLEPLVTQVTTLVNTSNKGPSGKKKGRSKKAHVL
 AASVEQATQNFLEKGEQIAKESQDLKEELVAAVEDVRKQGETMRIASSEFADDP CSSVK
 RGTMVRAARALLSAVTRLLILADMADVMRLLSHLKIVEEAEAVKNATNEQDLANRFKEF

GKKMVKLNYVAARRQQELKDPHCRDEMAAARGALKKNATMLYTASQAFLRHPDVAAT
 RANRDYVFKQVQEAIAGISNAAQATSPTDEAKGHTGIGELAAALNEFDNKIILDPMTFSE
 ARFRPSLEERLESIIISGAALMADSSCTRDDRRERIVAECNAVRQALQDLLSEYMNNTGR
 KEKGDPLNIAIDKMTKKTRDLRRQLRKAVMDHISDSFLETNVPLLVLIEAAKSGNEKEVK
 EYAQVFREHANKLVEVANLACISISNNEEGVKLVIRMAATQIDSLCPQVINAALTAAARPQS
 KVAQDNMDVFKDQWEKQVRVLTEAVDDITSVDDFLSVSENHILEDVNKCVIALQEGDVD
 TLDRTAGAIRGRAARVIHIINAEMENYEAGVYTEKVLEATKLLSETVMPRFAEQVEVAIEA
 LSANVPQPFEENEFDASRLVYDGVDRDIRKAVLMIRTPEELEDDSDFEQEDYDVRRTGS
 VQTEDDQLIAGQSARAIMAQLPQEEKAKIAEQVEIFHQEKSKLDAEVAKWDDSGNDIIVL
 AKQMCMIMMEMTDFTRGKGPLKNTSDVINAACKIAEAGSRMDKLARAVADQCPDSACK
 QDLLAYLQRIALYCHQLNICKVKAQVQNLGGELIVSGTGVQSTFTTFYEVDVCDVIDGGR
 ASQLSTHLPTCAEGAPIGSGSSDSSMLDSATSLIQAACKNLMAVVLTVKASYVASTKYQ
 KVYGTAAVNSPVVSWKMKAPKPLVKREKPEEFQTRVRRGSQKKHISPVQALSEFKA
 MDSF

SEQID No:281

MSGDSERAVAPGVVPAPCASKVELRLSCRHLLDRDPLTKSDPSVLLQQAQGWLQV
 DRTEVVKSSLHPVFSKVFTVDYYFEGVQKLRFVYDTHGPSGLTCQDDDFLGGMECTL
 GQIVAQKKMTRPLLLRFRGNAGKSTITVIAEDISGNNGYVELSFQARKLDDKDLFSKSDP
 FLELYRVNDDGSEQLVYRTEVVKNLNPVWEPFKVSLNSLCSCEETRPLKCLVWDYDS
 RGKHDFIGDFTTTFAEMQKAFEEEEQQAQWDCVNAKYKQKKRNYKNSGVVILADKLHR
 VHSFLDYIMGGCQIHCTVAIDFTASNGDPRNSCSLHHINPYQPNEYLRALVAVGEVCQD
 YDSDKRFSALGFGARIPPKYEVSHDFAINFPEDDECEGIQGVVEAYQNCLPKVQLYGP
 TNVAPIISKVARMAAAEESTGEASQYYILLITDGVVTDMSDTREAIVRASHLPMSVIIVGV
 GNADFTDMQILDGDDGVLRSRPGEPALRDIVQFVPFRELKNASPAALAKCVLAEVPKQV
 VEYYSHKELPPRSLGAQTGEAAASSAP

SEQID No:282

MAAQCVTKVALNVSCANLLDKDIGSKSDPLCVLFLNTSGQQWYEVERTERIKNCLNPQF
 SKTFIIDYYFEVVQKLKFGVYDIDNKTIELSDDDFLGECECTLGQIVSSKKLTRPLVMKTG
 RPAGKGSITISAEIKNRVLFFEMEARKLDNKDLFGKSDPYLEFHKQTSNGNWLMMVHR
 TEVVKNLNPVWRPFKISLNSLCYGDMDKTIKVECYDYDNDGSHDLIGTFQTTMTKLKE
 ASRSSPVEFECINEKKRQKKKSYKNSGVISVKQCEITVECTFLDYIMGGCQLNFTVGVD
 TGSNGDPRSPDSLHYISPNGVNEYLTALWSVGLVIQDYDADKMFPAGFGAQIPPQWQ

VSHEFPMNPNPSNPYCNGIQGIVEAYRSCLPQIKLYGPTNFSPIINHVARFAAAATQQQT
 ASQYFVLLIITDGVITDLDETRQAIVNASRLPMSIIIVGVGGADFSAMEFLDGDGGSLRSPL
 GEVAIRDIVQFVPFRQFQNPKEALAQCVLAEIPQQVVGYFNTYKLLPPKNPATKQQKQ

SEQID No:283

MAVSASPVISATSSGAGVPGGLFRAEPLYSTPREPPRLTPNMINSFVVNNHSNSAGGG
 GRGNTNTNECRMVDMHGMKVASFLMDGQELICLPQVFDLFLKHLVGGLHTVYTKLRRL
 DISPVVCTVEQVRILRGLGAIQPGVNRCKLITRKDFETLFTDCTNARRKRQMTRKQAVN
 SSRPGRPPKRSLGVLQENARLLTHAVPGLLSPGLITPTGITAAAMAEAMKLQKMCLMAM
 NTLQGNGSQNGTESEPDDLNSNTGGSESSWDKDKMQSPFAAPGPQHGIHAALAGQ
 PGIGGAPTLNPLQQNHLLTNRLDLPFMMMPHPLLPSLPPASVAMAMNQMNLNTIAN
 MAAAAQIHSPLSRAGTSVIKERIPESPSAPSLEENHRPGSQTSSHTSSSVSSSPSQMD
 HHLERMEEVPVQIPIMKSPLDKIQLTPGQALPAGFPGFIFADSLSSVETLLTNIQGLLKV
 ALDNARIQEKQIQQEKELRLELYREREIRENLERQLAVELQSRTTMQKRLKKEKTKRK
 LQEALEFESKRREQVEQALKQATTSDSGLRMLKDTGIPDIEIENNGTPHDSAAMQGGNY
 YCLEMAQQLYSA

SEQID No:284

MDDSEVESTASILASVKEQEAQFEKLTRALEEERRHVSAQLERVRVSPQDANPLMANG
 TLTRRHQNGRFVGDADLERQKFSDLKLNGPQDHSLLYSTIPRMQEPGQIVETYTEED
 PEGAMSVVSVETSDDGTTRRTETTIVKKVVKTVTTRTVQPVAMGPDGLPVDASSVSNNY
 IQTLGRDFRKNNGGPGPYVGQAGTATLPRNFHYPPDGYSRHYEDGYPGGSDNYGSL
 SRVTRIEERYRPSMEGYRAPSRQDVYGPQPQVRVGGSSVDLHRFHPEPYGLEDDQRS
 MGYDDL DYGMMSDYGTARRTGTPSDPRRRLRSYEDMIGEEVPSDQYYWAPLAQHER
 GSLASLDSLRLKGGPPPPNWRQPELPEVIAMLGFRDLDAVKSNAAAYLQHLCYRNDKVKT
 DVRKLKGIPVLVGLLDHPKKEVHLGACGALKNISFGRDQDNKIAIKNCDGVPALVRLLRK
 ARDMDLTEVITGTLWNLSSHDSIKMEIVDHALHALTDEVIIPHSGWEREPNEDCKPRHIE
 WESVLTNTAGCLRVSSERSEARRKLRECDGLVDALIFIVQAEIGQKDSDSLKLVENCVC
 LLRNLSYQVHREIPQAERYQEAAPNVANNTGPHAASCFGAKKGKGKKPIEDPANDTVD
 FPKRTSPARGYELLFQPEVVRIYISLLKESKTPAILEASAGAIQNLCAGRWTYGRYIRSAL
 RQEKALSAIADLLTNEHERVVKAASGALRNLAVDARNKELIGKHAIPNLVKNLPGGQQN
 SSWNFSEDTVISILNTINEVIAENLEAAKKLRETQGIEKLVLINKSGNRSEKEVRAAALVLQ
 TIWGYKELRKPLEKEGWKKSDFQVNLNNASRSQSSHSYDDSTLPLIDRNQKSDNNYST

PNERGDHNRTLDRSGDLGDMEPLKGTTPLMQDEGQESLEEELDVLVLDDDEGGQVSYP
SMQKI

SEQID No:285

MACPALGLEALQPLQPEPPPEPAFSEAQKWIEQVTGRSFGDKDFRTGLENGILLCELLN
AIKPGLVKKINRLPTPIAGLDNIILFLRGCKELGLKESQLFDPSDLQDTSNRVTVKS LDYSR
KLKNVLVTIYWLGKAANSCTSYSGTTLNLKEFEGLLAQMRKDTDDIESPKRSIRD SGYID
CWDSESRSDSLSPPRHGRDDSFDSLDSFGSRSRQTPSPDVVLRGSSDGRGSDSESDLP
HRKLPDVKKDDMSARRTSHGEPKSAVPFNQYLPNKS NQTAYVPAPLRKKKAEREEYR
KSWSTATSPLGGERPFRYGPRTPVSDDAESTSMFDMRCEEEAAVQPHSRARQEQLQL
INNQLREEDDKWQDDLARWKSRRRSVSQDLIKKEEERKKMEKLLAGEDGTSERRKSIK
TYREIVQEKERRERELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPKILERSHS
TEPNLSSFLNDPNPMKYLRQQSLPPP KFTATVETTIARASVLDTSMSAGSGSPSKTVTP
KAVPMLTPPKPYSQPKNSQDVLKTFKVDGKVSNGETVHREEEKERECPTVAPAHSLTK
SQMFEGVARVHGSPLELKQDN GSIENIKKPNSVPQELAAATTEKTEPNSQEDKNDGGKS
RKGNIELASSE PQHFTTTVTRCSPTVAFVEFPSSPQLKNDVSEEKDQKKPENEMSGKV
ELVLSQKVVKPKSPEPEATLTFPFLDKMPEANQLHLPNLNSQVDS PSSEKSPVMTPFKF
WAWDPEEEERRRQEKWQQEQERLLQERYQKEQDKLKEEWEKAQKEVEEEEERRYYEE
ERKIIEDTVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDLGNCQDEKQDRRWKKS FQG
DDSDLLLKTRES DRLEEKGSLTEGALAHSGNPVSKGVHEDHQLDTEAGAPHC GTNPQL
AQDPSQNNQTSNPTHSSSEDVKPKTLPLDKSINHQIESPSERRKKSPREHFQAGPFSPC
SPTPPGQSPNRSISGKKLCSSCGLPLGKGAAMIIETLNLYFHIQCFRCGICKGQLGDAVS
GTDVRI RNGLLNCNDCYMRSR SAGQPTTL

SEQID No:286

MAARGRRAEPQGREAPGPAGGGGGGSRWAESGSGTSPESGDEEVSGAGSSPVSGG
VNL FANDGSFLELFKRKMEEEEQRQRQEPPPGPQRPDQSAAAAGPGDPKRKGGPGS
TLSFVGKRRGGNKLALKTGIVAKKQKTEDEVLT SKGDAWAKYMAEVKKYKAHQCGDD
DKTRPLVK

SEQID No:287

MAAETQTLNFGPEWLRALSSGGSITSPPLSPALPKYKLADYRYGREEM LALFLKDNKIP
SDLLDKEFLPILQEEPLPPLALVPFTEEEQRNFSMSVNSAAVLRLTGRGGGGGT VVGAPR
GRSSSRGRGRGRGECGFYQRSFDEVEGVFGRGGG REMHRSQSWEERGDRRFEKP

GRKDVGRPNFEEGGPTSVGRKHEFIRSESENWRIFREEQNGEDEDGGWRLAGSRRD
 GERWRPHSPDGPRSAGWREHMERRRRFEFDFRDRDDERGYRRVRSGSGSIDDDR
 SLPEWCLEDAEEEMGTFDSSGAFLSLKKVQKEPIPEEQEMDFRPVDEGEECSDSEGS
 NEEAKEPDKTNKKEGEKTDRVGVEASEETPQTSSSSARPGTPSDHQSQEASQFERKD
 EPKTEQTEKAEETRMEENSLPAKVPSRGDEMADVQQPLSQIPSDTASPLILPPPVPN
 PSPTLRPVETPVVGAPGMGVSSTEPDDEEGLKHLEQQAEKMOVAYLQDSALDDERLASK
 LQEHRAKGVSIPLMHEAMQKWYYKDPQGEIQGPFNNQEMAWEWFQAGYFTMSLLVKRA
 CDES FQPLGDIMKMWGRVPFSPGPAPPPHMGELDQERLTRQQELTALYQMQLQYQ
 QFLIQQQYAQVLAQQQKAALSSQQQQQLALLLQQFQTLKMRISDQNIIPSVTRSVSPD
 TGSIWELQPTASQPTVWEGGSVWDLPLDTTTPGPALEQLQQLEKAKAAKLEQERREAE
 MRAKREEEERKRQEELRRQQEEILRRQQEEERKRREEEELARRKQEEALRRQREQEIA
 LRRQREEEERQQQEEALRRLEERRREEEERRKQEELLRKQEEEAAKWAREEEEAQR
 LEENRLRMEEEAARLRHEEEERKRKELEVQRQKELMRQRQQQQEALRRLQQQQQQQ
 QLAQMKLPSSTWGQQSNTTACQSQATLSLAEIQKLEEEERERQLREEQRRQQRELMK
 ALQQQQQQQQQKLSGWGNVSKPSGTTKSLLEIQQEEARQMOKQQQQQQQHQQPNR
 ARNNTHSNLHTSIGNSVWGSINTGPPNQWASDLVSSIWSNADTKNSNMGFWD DAVKE
 VGPRNSTNKNKKELK

SEQID No:288

MVGKCLKQNLLACLVISSVTVFYLGQHAMECHHRIEERSQPVKLESTRTTVRTGLDLKA
 NKTFAYHKDMPLIFIGGVPRSGTTLMRAMLDAHPDIRCGEETRVIPRILALKQMWSSRSK
 EKIRLDEAGVTDEVLD SAMQAFLEIIVKHGEPAPYLCNKDPFALKSLTYLSRLFPNAKFL
 LMVRDGRASVHSMISRKVTIAGFDLNSYRDCLTKWNRAIETMYNQCMVEVGYKKCMLVH
 YEQLVLHPERWMRTLLKFLQIPWNHSLVHHEEMIGKAGGVSLSKVERSTDQVIKPVNV
 GALSKWVGKIPPDVLQDMAVIAPMLAKLGYDPYANPPNYGKPDPKIIENTRRVYKGEFQ
 LPDFLKEKPQTEQVE

SEQID No:289

MSTFRQEDVEDHYEMGEELGSGQFAIVRKCRQKGTGKEYAAKFIKKRRLSSSRRGVSR
 EEIEREVNILREIRHPNIITLHDIFENKTDVVLILELVSGGELFDLAEKESL TEDEATQFLK
 QILDGVHYLHSHKRIA HFDLKPENIMLLDKNVPNPRIKLIDFGIAHKIEAGNEFKNIFGTPEF
 VAPEIVNYEPLGLEADMWSIGVITYILLSGASPFLGETKQETLTNISAVNYDFDEEYFSNT
 SELAKDFIRRLLVKDPKRRMTIAQSLEHSWIKAIRRRNVRGEDSGRKPERRRLKTTRLKE
 YTIKSHSSLPPNNSYADFERFSKVLEEA AAAEEGLRELQRSRRLCHEDVEALAAIYEEKE

AWYREESDSLQDLRRLRQELLKTEALKRQAQEEAKGALLGTSGLKRRFSRLENRYEA
LAKQVASEMRVQDLVRALEQEKLGVECGLR

SEQID No:290

MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPS
GTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYR
CLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPC
GIDKFRGVFVCCPLAEESDNVDSADAEEDDSVWWGGADTDYADGSEDKVVEVAEE
EEVAEEVEEEEADDDDEDDGDEVEEEAEOPYEEATERTTSIATTTTTTTESVEEVVRVP
TTAASTPDAVDKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKN
LPKADKKAVIQHFQEKVESLEQEAAANERQQLVETHMARVEAMLNDRRLALENYITALQ
AVPPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYE
RMNQSLSLLYNVPAAVEEQDEVDLLQKEQNYSDVLNMISEPRISYGNLALMPSLT
ETKTTVELLPVNGEFLDDLPWHSFGADSVANTENEVEPVDARPAADRGLTTRPGS
GLTNIKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIV
ITLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN

SEQID No:291

MMHALEVLNSQETGPTLPRQNSQLPAQVQNGPSQEELEIQRRLQEQQRQKELERER
LERERMERERLERERLERERLERERLEQEQLERERQERERQERLERQERLERQERLE
RQERLDRERQERQERERLERLERERQERERQEQLEREQLEWERERRISSAAAPASVE
TPLNSVLGDSSASEPGLQAASQPAETPSQQGIVLGPLAPPPPPPLPPGPAQASVALPPP
PGPPPPPPPLPSTGPPPPPPPPPLPNQVPPPPPPPPAPPLPASGFFLASMSDNRPLTGL
AAAIAGAKLRKVS RMEDTSFPGGNAIGVNSASSKTD TGRGNGPLPLGGSGLMEEMSA
LLARRRRRIA EKGSTIETE QKEDKGEDSEPVTSKASSTSTPEPTRKPWERTNTMNGSKSP
VISRPKSTPLSQPSANGVQTEGLDYDRLKQDILDEMRELTKLKEELIDAIRQELSKSNT
A

SEQID No:292

RHTRTHRDTRHTYTHAHTDAHTCTHMHRDTQMHTHTICRKKYALTNIQAAMGLSDPAA
QPLLGNGSANIKLVKNGENQLRKAAEQGQQDPNKNLSPTAVINITSEKLEGKEPHQDS
SSCEILPSQPRRTKSFLNYYADLETSARELEQNRGNHHGTAEKSSQPVQGGQASTIIGNG
DLLLQKPNRPQSSPEDGQVATVSSSPETKKDHPKTGAKTDCALHRIQNLAPSDEESSW
TTLSQDSASPSSPDETDIWSDFSQTDPLPPGWKRVSDIAGTYWHIPTGTTQWERP

VSIPADLQGSRKGSLSVTPSPPTPENЕКQPWSDFAVLNGGKINSIDIWKDLHAATVNPDP
 SLKEFEGATLRYASLKL RNAPHPDDDDSCSINS DPEAKCFAVRSLGWVEMAEEDLAPG
 KSSVAVNNCIRQLSYCKNDIRDTVGIWGEKGDMYLILENDMLSLVDPMDRSVWHSQPIV
 SIRVWGVGRDNGRDFAYVARDKDTRILKCHVFRCDTPAKAIATSLHEICKIMAERKNAK
 ALACSSLQERANVNLDVPLQVDFPTPKTEL VQKFHVQYLGMLPVDPKPVGMDILNSAIEN
 LMTSSNKEDWLSVNMNVADATVTVISEKNEEEVLVECRVRFLSFMGVGKDVHTFAFIM
 DTGNQRFECHVFWCEPNAGNVSEAVQAACMLRYQKCLVARPPSQKVRPPPPPADSV
 TRRVTTNVKRGVLSLIDTLKQKRPVTEMP

SEQID No:293

MAQVAMSTLPVEDEESSESRMVVTF LMSALESMCKELAKSKAEVACIAVYETDVFVVG
 TERGRAFVNTRKDFQKDFVKYCVEEEEKAAEMHKMKSTTQANRMSVDAVEIETLRKTV
 EDYFCFCY GKALGKSTVVPVPEYKMLRDQSAVVVQGLPEGVAFKHPENYDLATLKWIL
 ENKAGISFIIKRPFLPKKHVGGRVMVTDADRSILSPGGSCGPIKVKTEPTEDSGISLEMA
 AVTVKEESED PDYYQYNIQAGPSETDDVDEKQPLSKPLQGSHHSSEGNEGTEMEVPA
 EDSTQHVPSETSEDPEVEVTIEDDDYSPPSKRPKANELPQPPVPEPANAGKRKRVREFN
 FEKWNARITDLRKQVEELFERKYAQAIAKAGPVTIPYPLFQSHVEDLYVEGLPEGIPFRR
 PSTYGIPRLERILLAKERIRFVIKKHELLNSTREDLQLDKPASGVKEEWYARITKL RKMVD
 QLFCKKFAEALGST EAKAVPYQKFEAHPNDLYVEGLPENIPFRSPSWYGIPRLEKIIQVG
 NRIKFVIKRPELLTHSTTEVTQPRNTNPVKEDWNVRITKL RKQVEEIFNLKFAQALGLTEA
 VKVPYPVFESNPEFLYVEGLPEGIPFRSPTWFGIPRLERIVRGSNKIKFVVKPELVISYL
 PPGMASKINTKALQSPKRPRSPGSNSKVPEIEVTVEGPNNNNPQTSAVRTPTQTNGSN
 VPFKPRGREFSFEAWNAKITDLKQKVENL FNEKCGEALGLKQAVKVPFALFESFPEDFY
 VEGLPEGVPFRRPSTFGIPRLEKILRNKAKIKFIIKKPEMFETAIKESTSSKSPPRKINSSP
 NVNTTASGVEDLNIIQVTIPDDDNERLSKVEKARQLREQVNDLFSRKFGAIGMGFPVKV
 PYRKITINPGCVVVDGMPPGVSFKAPSYLEISSMRRILDSAEFIKFTVIRPFPGLVINNQLV
 DQSESEGPVIQESAEPSQLEVPATEEIKETDGSSQIKQEPDPTW

SEQID No:294

MAFVCLAIGCLYTF LISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLD
 HFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQ
 SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEG
 DHALQCVDYIKADGQNI GCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLQNIVKP
 LPPVYLTFTRESSCEIKLKW SIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE

TRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
 LLLRKPNTYPKMIEFFCDT

SEQID No:295

MAERESGGLGGGAASPPAASPFLGLHIASPPNFRRLTHDISLEEFEDLSEITDECGISL
 QCKDTLSLRPPRAGLLSAGGGGAGSRLQAEMQLQMDLIDATGDTPGAEDDEEDDDEER
 AARRPGAGPPKAESGQEPASRGQGQSQGQSGGSGDTYRPKRPTTLNLFQVPRS
 QDTLNNNSLGKKHSWQDRVSRSSSPLKTGEQTPPHEHICLSDELPPQSGPAPTDRGT
 STDSPCRRSTATQMAPPGGPPAAPPGGRGHSHRDRIHYQADVRLATEEIIYLTVPVQRP
 PDAAEPTSAFLPPTESRMSVSSDPDAAYPSTAGRPHPSISEEEEGFDCLSSPERAAPP
 GGGWRGSLGEPPPPPRASLSSDTSALSYDSVKYTLVVDEHAQLELVSLRPCFGDYSDE
 SDSATVYDNCASVSSPYESAIGEEYEEAPRPQPPACLSDESTPDEPDVHFSKKFLNVF
 MSGRSRSSSAESFGLFSCIINGEEQEQTTHRAIFRFVPRHEDELELEVDDPLLVELQAED
 YWYEAYNMRTGARGVFAYYAIEVTKEPEHMAALAKNSDWVDQFRVKFLGSGVQVPYH
 KGNDVLCAAMQKIATTRRLTVHFNPSSCVLEISVRGVKIGVKADDSQEAKGNKCSHFF
 QLKNISSFCGYHPKNNKYFGFITKHPADHRFACHVFVSEDSTKALAESVGRAFQQFYKQF
 VEYTCPTEDIYLE

SEQID No:296

GSELETAMETLINVFHAHSGKEGDKYKLSKKELKELLQTELSGFLDAQKDVEDAVDKVMK
 ELDENGDEVDQFQYVVLVAALTVACNNFFWENS

SEQID No:297

MASTTTCTRFTDEYQLFEELGKGAFSVVRRCMKIPTGQGYAAKIINTKKLSARDHQKLE
 REARICRLLKHPNIVRLHDSISEEGFHVLVFDLVTGGELFEDIVAREYYSEADASHCIQQI
 LESVNHCHLNGIVHRDLKPENLLLASKSKGAAVKLADFGLAIEVQGDQQAWFGFAGTP
 GYLSPEVLRKDPYGKPVDMWACGVILYILLVGYPFFWDEDQHRLYQQIKAGAYDFPSP
 EWDVTVPKADLINKMLTINPAKRITASEALKHPWICQRSTVASMHRQETVDCLKKFN
 ARRLKLGAILTTMLATRNFSAAKSLLKKPDGVKESTESSNTTIEDVDKARKQEIIKVTEQ
 LIEAINNGDFEAYTKICDPGLTAFEPEALGNLVEGMDFHRFYFENALSKSNKPIHTIILNPH
 VHLVGDDAACIAYIRLTQYMDGSGMPKTMQSEETRVWHRRDGKWQNVHFHRSGSPT
 VPIKPPCIPNGKENFSGGTSBWQNI

SEQID No:298

MTATEALLRVLLLLLAFGHSTYGAECFPACNPQNGFCEDDNVCRCQPGWQGGLCDQC
 VTSPGCLHGLCGEPGQCICTDGWDGELCDRDVRACSSAPCANNGTCVSLDGGLYECS
 CAPGYSGKDCQKKDGPCVINGSPCQHGGTCTVDDEGRASHASCLCPPGFSGNFCEIVA
 NSCTPNPCENDGVCTDIGGDFRCRCPAGFIDKTCSRPTNCASSPCQNGGTCLQHTQ
 VSYECLCKPEFTGLTCVKKRALSPQQVTRLPSGYGLAYRLTPGVHELPPVQQPEHRILKV
 SMKELNKKTPLLTEGQAICFTILGVLTSLVVLTGVIVFLNKCETWVSNLRYNHMLRKKK
 NLLLQYNSGEDLAVNIIFPEKIDMTTFSKEAGDEEI

SEQID No:299

MATIPDWKLQLLARRRQEEASVRGREKAERERLSQMPAWKRGLLERRRAKLGLSPGE
 PSPVLGTVEAGPPDPDESAVLLEAIGPVHQNRFRIRQERQQQQQQQQQRSEELLAERKPG
 PLEARERRPSPGEMRDQSPKGRESREERLSPRETRERRLGIGGAQELSLRPLEARDW
 RQSPGEVGDRSSRLSEAWKWRLSPGETPERSLRLAESREQSPRRKEVESRLSPGESA
 YQKLGLTEAHKWRPDSRESQEQSLVQLEATEWRLRSGEERQDYSEECGRKEEWPVP
 GVAPKETAELSETLTREAQGNSSAGVEAAEQRPVEDGERGMKPTGKWTNLNSGKA
 REWTPRDIEAQTQKLEPPESAELLESPPGVEAGEGEAEKEEAGAQQRPLRALQNCCSV
 PSPLPPEDAGTGGLRQQEEEAVELQPPPPAPLSPPPPAPTAPQPPGDPLMSRLFYGVK
 AGPGVGAPRRSGHTFTVNPRRSVPPATPATPTSPATVDAAVPGAGKKRYPTAEELVL
 GGYLRLSRSLAKGSPERHHKQLKISFSETALETYQYPSESSVLEELGPEPEVPSAPN
 PPAAQPDDEEDEEELLLLQPELQGGGLRTKALIVDESCRR

SEQID No:300

MSEHVEPAAPGPGPNGGGGGPAPARGPRTPNLNPINVRDRLFHALFFKMAVTYS
 RLFPPAFRRLEFFVLLKALFVLFVLAYIHIVFSRSPINCLEHVRDKWPREGILRVEVRHN
 SSRAPVFLQFCDSGGGRGSFPGLAVEPGSNLDMEDEEEELTMEMFGNSSIKFELDIEP
 KVFKPPSSTEALNDSQEFPFPETPTKWVPQDEYIVEYSLEYGFLRLSQATRQRLSIPVM
 VVTLDPTRDQCFGDRFSRLLLDEFLGYDDILMSSVKGLAENEENKGFLRNVSSEHYRF
 VSMWMARTSYLAFAIMVIFTLSVSMMLRYSHHQIFVFIVDLLQMLEMNMAIAFPAAPLLT
 VILALVGMEAIMSEFFNDTTTAFYIILIVWLADQYDAICCHTSTSKRHWLRFYLYHFAFYA
 YHYRFNGQYSSLALVTSWLFIQHSMIYFFHHYELPAILQQVRIQEMLLQAPPLGPGTPTA
 LPDDMNNSGAPATAPDSAGQPPALGPVFELVSKERGWGSAEGSGGVLVGLQ

SEQID No:301

KEQSELDQDLDDVEEVEEEEETGEETKLKARQLTVQMMQNPQILAAALQERLDGLVETPT
 GYIESLPRVVKRRVNALKNLQVKCAQIEAKFYEEVHDLERKYAVLYQPLFDKRFEIINAIY
 EPTEEECWKPDEEDEISEELKEKAKIEDEKKDEEKEDPKGIPEFWLTVFKNVDLLSDM
 VQEHDEPILKHLKDIKVKFSDAGQPMSFVLEFHFEPNEYFTNEVLTKTYRMRSEPDDSD
 PFSFDGPEIMGCTGCQIDWKKGKNVTLKTIKKKQKHKGRTVTVTKTVSNDSEFFNFFA
 PPEVIPKFSADFDDAEAILAADFEIGHFLRERIIPRSVLYFTGEAIEDDDDDYDEEGEEAD
 EGYQLFEEVKSCSKLFQRWLQ

SEQID No:302

GKQNSKLRPEVMQDLLESTDFTEHEIQEWYKGFLRDCPSGHLSMEEFKKIYGNFFPYG
 DASKFAEHVFRFTDANGDGTIDFREFIIALSVTSRGKLEQKLKWAFSMYDLGNGYISKA
 EMLEIVQAIYKMVSSVMKMPPEDESTPEKRTEKIFRQMDTNRDGKLSLEEFIRGAKS DPSI
 VRLLQCDPSSAGQF

SEQID No:303

MVEKGPEVSGKRRGRNNAASASAAAAASAAASAACASPAATAASGAAASSASAAAAAS
 AAAAPNNGQNKSLAAAAPNGNSSSNSWEEGSSGSSSDEEHGGGGMRVGPQYQAVV
 PDFDPAKLARRSQERDNLGMLVWSPNQNLSEAKLDEYIAIAKEKHGYNMEQALGMLFW
 HKHNIEKSLADLPNFTFPDEWTVEDKVLFEQAFSFGKTFHRIQQMLPDKSIASLVKFY
 YSWKKTRTKTSVMDRHARKQKREREESEDELEEANGNNPIDIEVDQNKESKKEVPTE
 TVPQVKKEKHSTQAKNRAKRPKGMFLSQEDVEAVSANATAATTVLRQLDMELVSVK
 RQIQNIKQTNSALKEKLDGGIEPYRLPEVIQKCNARWTTTEEQLLAVQAIRKYGRDFQAIS
 DVIGNKSVVQVKNFFVNYRRRFNIDEVLQEWEAEHGKEETNGPSNQKPKVSPDNSIKM
 PEEEDEAPVLDRVRYASAS

SEQID No:304

MSELEKAMVALIDVFHQYSGREGDKHKLKKSELKELINNELSHFLEEIKEQEVDKVMET
 LDNDGDGECDFQEFMAFVAMVTTACHEFFEHE

SEQID No:305

MDDDIAALVVDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGVMMGMGQKDSYVGD
 EAQSKRGILTLYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANR
 EKMTQIMFETFNTPAMYVAIQAVLSLYASGRTTGIVMDSGDGVTHTVPIYEGYALPHAIL

RLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRDIKEKLCYVALDFEQEMATAASSSSL
EKSYELPDGQVITIGNERFRCPEALFQPSFLGMESCGIHETTFNSIMKCDVDIRKDLNAN
TVLSGGTTMYPGIADRMQKEITALAPSTMKIKIIPPERKYSVWIGGSILASLSTFQQMWI
SKQEYDESGPSIVHRKCF

SEQID No:306

MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGA
GKHVPRAVFDLEPTVIDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVL
DRIRKLADQCTGLQGFLVFHSFGGGTGSGFTSLLMERLSVDYGKKSLEFSIYPAPQVS
TAVVEPYNSILTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNLISQIVSSITA
SLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEEKAYHEQLSVAEITNACFEPAN
QMVKCDPRHGYMACCLLYRGDVVPKDVNAAIATIKTKRSIQFVDWCPTGFKVGINYQ
PPTVVPGGDLAKVQRAVCMLSNTTAAIEAWARLDHKFDLMYAKRAVHWYVGEEMEE
GEFSEAREDMAALEKDYEYEEVGVDSVEGEGEEEGEEY

SEQID No:307

MREIVHIQAGQCGNQIGAKFWEVISDEHGIDPTGTYHGDSDLQLDRISVYYNEATGGKY
VPRAILVDLEPGTMDSVRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDSVL
DVVRKEAESCDCLQGFLTHSLGGGTGSGMGTLLISKIREEYPDRIMNTFSVVPSPKVS
DTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFRTLKLTPTYGDLNHLVSATMSGV
TTCLRFPGLNADLRKLAVNMVPPRLHFFMPGFAPLTSRGSQQYRALTVPCLTQQVF
DAKNMMAACDPRHGRYLTVAAVFRGRMSMKEVDEQMLNVQKNSSYFVEWIPNNVK
TAVCDIPPRGLKMAVTFIGNSTAIQELFKRISEQFTAMFRRKAFLHWYTGEGMDEMEFT
EAESNMNDLVSEYQQYQDATAEEEEEDFGEEAEEEE

SEQID No:308

MEGSLEREAPAGALAAVLKHSSTLPPESTQVRGYDFNRGVNYRALLEAFGTTGFQATN
FGRAVQQVNAMIEKKLEPLSQDEDOHADLTQSRRLTSCTIFLGYTSNLISSGIRETIRYL
VQHNMDVVLVTTAGGVEEDLIKCLAPTYLGEFSLRGKELRENGINRIGNLLVPNENYCKF
EDWLMPILOQMVMEQNTGKWTSPKMIARLGKEINNPEVSVYYWAQKNHIPVFSPALT
DGSGLGDMIFFHSYKNPGLVLDIVEDLRLINTQAIFAKCTGMILGGGVVKHHIANANLMRN
GADYAVYINTAQEFDGSDSGARPDEAVSWGKIRVDAQPVKVYADASLVFPLLVAETFA
QKMDAFMHEKNED

SEQID No:309

MADPKYADLPGIARNEPDVYETSDLPEDDQAEFDAEELTSTSVEHIIVNPNAAYDKFKDK
RVGTKGLDFSDRIGKTKRTGYESGEYEMLGEGLVKETPQQKYQRLLHEVQELTTEVE
KIKTTVKESATEEKLTPVLLAKQLAALKQQLVASHLEKLLGPDAAINLTDPDGALAKRLLL
QLEATKNSKGGSGGKTTGTPPDSSLVTYELHSRPEQDKFSQAAKVAELEKRLTELETA
VRCDQDAQNPLSAGLQGACLMETVELLQAKVSALDLAVLDQVEARLQSVLGKVNIAK
HKASVEDADTQSKVHQLYETIQRWSPIASTLPELVQRLVTIKQLHEQAMQFGQLLTHLD
TTQQMIANSLKDNTTLLTQVQTTMRENLATVEGNFASIDERMKKLGK

SEQID No:310

MRKETPPPLVPPAAREWNLPPNAPACMERQLEAARYRSDGALLLGASSLSGRCWAGS
LWLFDPCAAPNEGFCASAGVQTEAGVADLTWVGGERGILVASDSGAVELWELDENETLI
VSKFCKYEHDDIVSTVSVLSSGTQAVSGSKDICKVWDLAQQVVLSSYRAHAAQVTCVA
ASPHKDSVFLSCSEDNRILLWDTRCPKPASQIGCSAPGYLPTSLAWHPQQSEVVFVFGD
ENGTVSLVDTKSTSCVLSSAVHSQCVTGLVFSPHSVPFLASLSEDCSLAVLDSSLSLSELF
RSQAHRDFVRDATWSPLNHSLLTTVGWDHQVVHHVVPTEPLPAPGPASVTE

SEQID No:311

MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYVEA
EVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAAAAASQQ
GSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNAKAVVLRGHESEVFICAWNP
VSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEG
TLLATGSYDGFARIWTKDGNLASTLGQHKGPFIKWNKKGNFILSAGVDKTTIWDHAHT
GEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAI
KWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANL
MLASASFDSTVRLWDVDRGICHTLTKHQEPVYSVAFSPDGRYLASGSFSDKCVHIWNTQ
TGALVHSYRGTTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK

SEQID No:312

MDEKVFTKELDQWIEQLNECKQLSESQVKSLEKAKEILTKESNVQEVRCPTVCGDV
HGQFHDLMELEFRIGGKSPDTNYLFMGDYVDRGYYSVETVTLVALKVRYRERITILRGN
HESRQITQVYGFYDECLRKYGANVWKYFTDLFDYLPLTALVDGQIFCLHGGLSPSIDTL
DHIRALDRLQEVPHEGPMCDLLWSDPDGRGGWGISPRGAGYTFGQDISETFNHANGL

TLVSRAHQLVMEGYNWCHDRNVVTIFSAPNYCYRCGNQAAIMELDDTLKYSFLQFDPA
 PRRGEPHVTRRTPDYFL

SEQID No:313

MDDKAFTKELDQWVEQLNECKQLNENQVRTLCEKAKEILTKESNVQEVRCPVTVC GDV
 HGQFHDLME LFRIGGKSPDTNYLFMGDYVDRGYYSVETVTLLVALKVRYPERITILRGN
 HESRQITQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALVDGQIFCLHGGLSPSIDTL
 DHIRALDRLQEVPHGPMCDLLWSDPDDRGGWGISPRGAGYTFGQDISETFNHANGL
 TLVSRAHQLVMEGYNWCHDRNVVTIFSAPNYCYRCGNQAAIMELDDTLKYSFLQFDPA
 PRRGEPHVTRRTPDYFL

SEQID No:314

AAADGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSTIALALGVERTRSSELLPFLTDTIYDED
 EVLLALAEQLGTFTTLVGGPEYVHCLLPPLSLATVEETVVRDKAVESLRAISHEHSPSD
 LEAHFVPLVKRLAGGDWFTSRTSACGLFSVCYPRVSSAVKAELRQYFRNLCSDDTPMV
 RRAAASKLGEFAKVL ELDNVKSEIIPMFSNLASDEQDSVRL LAVEACVNIAQLLPQEDLE
 ALVMPTLRQAAEDKSWAVRYMVADKFTELQKAVGPEITKTDLVPAFQNL MKDCEAEVR
 AAASHKVKEFCENLSADCRENVMSQILPCIKELVSDANQHVKSALASVIMGLSPILGKD
 NTIEHLLPLFLAQLKDECPEVRLNIISNLDCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRL
 AIIEYMP LLAGQLGVEFFDEKLSNLCMAWLVDHVYAIREAATSNLKKLVEKFGKEWAHA
 TIIPKVLAMSGDPNYLHRMTTLFCINVLSEVCGQDITTKHMLPTVLRMAGDPVANVRFNV
 AKSLQKIGPILDNSTLQSEVKPILEKLTQDQDQDVVKYFAQEALTVLSLA

SEQID No:315

MAEPRQEFV MEDHAGTYGLGDRKDQGGYTMHQDQEGD TDAGLKESPLQTPTEDGS
 EEPGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAQPHTEIPEGTTAEEAGIGDTPSLE
 DEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPP GQKGQANATRIP
 AKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREP KKVAVVR
 TPPKSPSSAKSRLQTAPVPMPLKKNVSKSIGSTENLKHQPGGGKVQIINKKLDLSNVQS
 KCGSKDNIKHVPGGGSVQIVYKPV DLSKVT SKCGSLGNIHHKPGGGQVEVKSEKLD FK
 DRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVS GDTSPR
 HLSNVSS TGSIDMVDSPLATLADEV SASLAKQGL

